



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 197724

TO: Jane Zara  
Art Unit: 1635  
Location: rem/2A59/2C18  
Case Serial Number: 10/636065

Friday, August 11, 2006

From: Beverly Shears  
Location: Biotech-Chem Library  
REM-1A54  
Phone: (571)272-2528

beverly.shears@uspto.gov

### Search Notes

Your queries have completed processing. You may access an electronic version via eDAN (SCORE) and /or <http://es/ScoreAccessWeb>. If the result files have been separated into two (2) or more versions, you may view additional files via the "[View version list for this application](#)" link.

#### Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

#### Published Applications Database - November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid database searches now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published Applications\_New databases; older published applications make up the Published Applications\_Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions .rnpbm (Published Applications\_NA\_Main) and .rnpbn (Published Applications\_NA\_New).

Searches run against Amino Acid Published Applications produce two sets of results, with the extensions .rapbm (Published Applications\_AA\_Main) and .rapbn (Published Applications\_AA\_New).



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ACCESS DB # 1977  
PLEASE PRINT CLEAR

Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 8-7-  
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 10/636,065  
Location (Bldg/Room#): 2A54 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER D  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: ANTISENSE LAP OLIGOS

Inventors (please provide full names): KORNECIUK et al.

Earliest Priority Date: 8/7/03

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

21 NA 19 Please Search Seq ID No:

22 NA 19 21

29 NA 19 — size limit to 70 NT's.

— EXACT IDENTITY needed.

may — NO INTERFERENCE SEARCH PLEASE.

THANKS.

\*\*\*\*\*  
STAFF USE ONLY

Searcher: Beverly 2528

Searcher Phone #: \_\_\_\_\_

Searcher Location: \_\_\_\_\_

Date Searcher Picked Up: \_\_\_\_\_

Date Completed: \_\_\_\_\_

Searcher Prep & Review Time: \_\_\_\_\_

Online Time: \_\_\_\_\_

Type of Search

\_\_\_\_ NA Sequence (#)

\_\_\_\_ AA Sequence (#)

\_\_\_\_ Structure (#)

\_\_\_\_ Bibliographic

\_\_\_\_ Litigation

\_\_\_\_ Fulltext

\_\_\_\_ Other

Vendors and cost where applicable

\_\_\_\_ STN \_\_\_\_\_ Dialog

\_\_\_\_ Questel/Orbit \_\_\_\_\_ Lexis/Nexis

\_\_\_\_ Westlaw \_\_\_\_\_ WWW/Internet

\_\_\_\_ In-house sequence systems CGW

\_\_\_\_ Commercial \_\_\_\_\_ Oligomer \_\_\_\_\_ Score/Length  
\_\_\_\_ Interference \_\_\_\_\_ SPDI \_\_\_\_\_ Encode/Transl  
\_\_\_\_ Other (specify) \_\_\_\_\_

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 07:05:47 / Search time 221.333 Seconds  
(without alignments)  
598.521 Million cell updates/sec

Title: US-10-636-065-29  
Perfect score: 19  
Sequence: 1 cgcacgcatcccttcac 19

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5484110

Minimum DB seq length: 0  
Maximum DB seq length: 70

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
1: N\_Geneseq\_8:\*  
2: geneseqn1980s:\*  
3: geneseqn1990s:\*  
4: geneseqn2000s:\*  
5: geneseqn2001as:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	6	ABK93682
2	19	100.0	19	14	AEA10008
3	19	100.0	19	14	AEA10086
4	18	94.7	23	3	AAA64903
5	16	84.2	29	14	AEA17843
6	15	78.9	19	14	ADX86146
7	15	78.9	19	14	ADX86613
8	14	73.7	19	10	ADFE68184
9	14	73.7	19	10	ADFE68262
10	14	73.7	19	14	AEA10122
11	14	73.7	19	14	AEA10076
12	14	73.7	19	14	AEA10108
13	14	73.7	19	14	AEA09518
14	14	73.7	19	14	AEA10267
15	14	73.7	19	14	AEA09596
16	13.8	72.6	33	6	ABA97854
17	13.8	72.6	33	8	ACC70715
18	13.8	72.6	59	2	AAV76807

19	13.8	72.6	60	14	AE827488	AEb27488 P. radiat
20	13.4	70.5	24	2	AA053958	Ag53958 Human OTC
21	13.4	70.5	37	2	AA16221	Ad16221 Bryodin 1
22	13.4	70.5	60	6	ABN37919	ABn37919 Human spl
23	13.2	69.5	20	2	AAx93159	Aax93159 PCR prime
24	13.2	69.5	21	12	ADM72682	Adm72682 Human TAS
25	13.2	69.5	29	10	ADL01767	Adl01767 Tobacco t
26	13.2	69.5	42	10	ADG76422	Adg76422 Primer #4
27	13.2	69.5	42	12	ADJ21021	Adj21021 Citrate s
28	13.2	69.5	55	12	ADQ26310	Adq26310 Internal
29	13.2	69.5	60	12	ADQ26317	Adq26317 Internal
30	13.2	69.5	65	6	ABN28183	ABn28183 Rat splic
31	13	68.4	19	14	AEC23674	Aec23674 Forward P
32	12.8	67.4	22	2	AAx36205	Aax36205 Primer us
33	12.8	67.4	23	2	AAx36207	Aax36207 Primer us
34	12.8	67.4	25	9	ACI49799	Act49799 Human mic
35	12.8	67.4	25	9	ACK16942	Ack16942 Human mic
36	12.8	67.4	25	9	ACK02223	Ack02223 Human mic
37	12.8	67.4	25	9	ACI07104	Act07104 Human mic
38	12.8	67.4	25	10	ACF79228	Actf79228 Human Nek
39	12.8	67.4	31	14	ABN31091	ABn31091 Hog chole
40	12.8	67.4	38	11	AD051609	Ado51609 Human TAG
41	12.8	67.4	38	11	AD051606	Ado51606 Human TAG
42	12.8	67.4	38	15	AEF03242	Aef03242 Primer KC
43	12.8	67.4	52	4	AAI65699	Aai65699 Nucleotid
44	12.8	67.4	52	4	AAI65700	Aai65700 Nucleotid
45	12.8	67.4	52	6	AAI18208	Aai18208 Partial D
46	12.8	67.4	52	6	ABV73812	ABv73812 Partial s
47	12.8	67.4	52	8	ABX14804	ABx14804 Chimeric
48	12.8	67.4	52	8	ABX11364	ABx11364 DNA seque
49	12.8	67.4	52	8	ABX11381	ABx11381 DNA seque
50	12.8	67.4	52	10	ADD44679	Add44679 DNA encod
51	12.8	67.4	52	10	ADD64184	Add64184 PLC871 pl
52	12.8	67.4	52	10	ADD63596	Add63596 Plasmid p
53	12.8	67.4	52	10	ADG27453	Adg27453 PLC871 pa
54	12.8	67.4	52	10	ACA61168	Ac61168 DNA encod
55	12.8	67.4	52	11	ADM15666	Adm15666 PLC871 pl
56	12.8	67.4	52	11	ADM15668	Adm15668 PLC871 pl
57	12.8	67.4	52	11	ADM83172	Adm83172 PLC671 ve
58	12.8	67.4	52	12	ADP89634	Adp89634 Vector pl
59	12.8	67.4	52	13	ADG60297	Adg60297 Human Igg
60	12.8	67.4	52	13	ADP47341	Adp47341 Plasmid p
61	12.8	67.4	52	14	ADX97620	Adx97620 PLC871 re
62	12.8	67.4	52	14	ADZ19096	Adz19096 PLC871 pl
63	12.8	67.4	52	14	AE81631	Ae81631 PLC871 pl
64	12.8	67.4	52	14	AE804268	Ae804268 Anti-TNF
65	12.8	67.4	52	15	AEF54755	Aef54755 PLC871 pa
66	12.8	67.4	52	15	AEF07126	Aef07126 Partial n
67	12.8	67.4	52	15	AEF38563	Aef38563 PLC871 pa
68	12.8	67.4	52	15	AEF40635	Aef40635 PLC871 DN
69	12.8	67.4	70	2	AAQ56709	Aaq56709 Sequence
70	12.8	67.4	70	2	AAQ56707	Aaq56707 Sequence
71	12.6	66.3	19	14	AEA10089	Aea10089 Antisense
72	12.6	66.3	21	12	ADK97924	Adk97924 Primer of
73	12.6	66.3	30	3	AA638824	Aa638824 Bovine hi
74	12.6	66.3	35	12	AD026814	Ad026814 CD40 tran
75	12.6	66.3	35	12	AD026923	Ad026923 CD40 vari
76	12.6	66.3	39	2	AAV72614	Aav72614 Rat Facto
77	12.6	66.3	39	2	AAZ09550	Aaz09550 Rat Facto
78	12.6	66.3	50	6	ABZ02105	Abz02105 Human Ieu
79	12.6	66.3	50	12	ADP33437	Adp33437 Human DNA
80	12.6	66.3	50	12	ADP10127	Adp10127 50-mer ol
81	12.6	66.3	50	13	ADU24922	Adu24922 Retroelem
82	12.6	66.3	50	13	ADU22389	Adu22389 Human tra
83	12.6	66.3	59	3	AAA49666	Aaa49666 Pig costi
84	12.6	66.3	60	6	ABN33040	ABn33040 Human spl
85	12.6	66.3	65	6	ABN54850	ABn54850 Mouse spl
86	12.4	65.3	19	12	AD061052	Ad061052 Anti-HCK
87	12.4	65.3	20	14	ADZ97966	Adz97966 Human ant
88	12.4	65.3	21	3	AAx90860	Aax90860 Oligonuc
89	12.4	65.3	21	3	AAZ74577	Aaz74577 Human bla
90	12.4	65.3	21	13	ADU27486	Adu27486 Knock-dow
91	12.4	65.3	21	14	ACI48718	Act48718 FOLH1 tar

```
c 92 12.4 65.3 21 14 ACL48720 FOLH1 SIR
93 12.4 65.3 21 14 ACL48719 FOLH1 SIR
94 12.4 65.3 21 14 ACL48716 FOLH1 SIR
95 12.4 65.3 21 14 ACL48715 FOLH1 tar
96 12.4 65.3 21 14 ACL48717 FOLH1 SIR
97 12.4 65.3 24 13 AdQ98314 Human PSM
98 12.4 65.3 24 14 AdW80073 Human HGF
99 12.4 65.3 25 9 AC161573 Human m1c
c 100 12.4 65.3 25 9 ACK13870 Human m1c
```

## ALIGNMENTS

```
RESULT 1
ID ABRK93682 standard; DNA; 19 BP.
AC ABRK93682;
XX
XX
XX 26-AUG-2002 (first entry)
XX
XX Human inhibitor of apoptosis, XIAP, antisense oligonucleotide #29.
DE
XX Human; ss; antisense; inhibitor of apoptosis; H1AP1; H1AP2; XIAP;
XX cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
XX pancreatic cancer; embryonic development; viral pathogenesis;
XX autoimmune disorder; neurodegenerative disease; multiple sclerosis;
XX lupus erythematosus; herpes virus infection; pox virus infection;
XX adenovirus infection; proliferative disease.
XX
XX Homo sapiens.
OS
XX
XX WO200226968-A2.
XX
XX 04-APR-2002.
XX
XX 27-SEP-2001; 2001WO-CA001379.
XX
XX 28-SEP-2000; 2000US-00672717.
XX
XX (UYOT-) UNIV OTTAWA.
XX (ABGE-) ABERGIA THERAPEUTICS INC.
XX
XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX
XX WPI; 2002-479562/51.
XX
XX Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
XX apoptosis in a cell, for treating cancer and other proliferative
XX diseases.
XX
XX Claim 8; Page 33; 135pp; English.
XX
XX The invention relates to an inhibitor of apoptosis (IAP) antisense
XX nucleic acid (1) that inhibits IAP biological activity, regardless of
XX length of the antisense nucleic acid, the IAP proteins may be mouse or
XX human XIAP, H1AP1 or H1AP2. Also included are a pharmaceutical
XX composition comprising a mammalian IAP antisense molecule and a method of
XX enhancing apoptosis in a cell, comprising administering a negative
XX regulator of the IAP anti-apoptotic pathway to the cell. The IAP
XX antisense inhibitor is useful for enhancing apoptosis in a cell in a
XX mammal diagnosed with a proliferative disease. The method is useful for
XX treating a patient diagnosed with a proliferative disease like cancer.
XX The IAP antisense molecule is useful to treat, ameliorate, improve,
XX sustain or prevent proliferative diseases (e.g. ovarian cancer,
XX adenocarcinoma, lymphoma, pancreatic cancer) and also in diseases or
XX conditions where apoptosis is involved or implicated (e.g. embryonic
XX development, viral pathogenesis, autoimmune disorders, neurodegenerative
XX diseases, multiple sclerosis, lupus erythematosus and infection by herpes
XX virus, pox virus and adenovirus). The present sequence is an IAP
XX antisense molecule of the invention
```

Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 6; Length 19;

Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CGCAGCGTATCTCCTTCAC 19
DB 1 CGCAGCGTATCTCCTTCAC 19
```

## RESULT 2

AEAL0008

ID AEAL0008 standard; DNA; 19 BP.

AC AEAL0008;

XX 14-JUL-2005 (first entry)

DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 29.

XX Cytostatic; neoplasia; cancer; Antisense; apoptosis inhibitor; ss.

OS Homo sapiens.

XX Synthetic.

XX WO2005042030-A1.

XX 12-MAY-2005.

XX 29-OCT-2004; 2004WO-CA001900.

XX 30-OCT-2003; 2003US-0516263P.

XX (ABGE-) ABERGIA THERAPEUTICS INC.

XX Lacasse E, Mcmanus D, Durkin JP;

XX WPI; 2005-366517/37.

XX Treating proliferative disease such as hepatoma, bile duct carcinoma,  
XX choriocarcinoma, seminoma and embryonal carcinoma comprises administering  
XX antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic  
XX agent.

XX Claim 6; SEQ ID NO 29; 285pp; English.

XX The invention relates to a method of treating a patient having a  
XX proliferative disease, comprising administering to the patient, an  
XX antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a  
XX chemotherapeutic agent, in amounts that together are sufficient to treat

XX the patient. The method is useful for treating a patient having a  
XX proliferative disease. The proliferative disease is cancer. A composition  
XX comprising an antisense IAP nucleobase oligomer and a chemotherapeutic

XX agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or  
XX human cancer cell in vivo or ex vivo, which involves contacting the cell

XX with the composition. The present sequence represents an antisense  
XX inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the

XX sequence represents either T or U. There are multiple versions of this  
XX sequence in the patent, the present sequence represents the sequence

XX shown in the main body of the specification.

XX Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 19; DB 14; Length 19;

Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CGCAGCGTATCTCCTTCAC 19
DB 1 CGCAGCGTATCTCCTTCAC 19
```

```

RESULT 3
ID AEA10086 standard, DNA; 19 BP.
XX
XX AEA10086;
XX
XX 14-JUL-2005 (first entry)
XX
XX Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 107.
XX
XX Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key
XX modified_base 1..3
XX modified_base /mod_base= OTHER
XX modified_base /note= "OTHER = 2'-O-methyl X RNA"
XX modified_base 17..19
XX modified_base /*tag= b
XX modified_base /mod_base= OTHER
XX modified_base /note= "OTHER = 2'-O-methyl X RNA"
XX
XX WO2005042030-A1.
XX
XX 12-MAY-2005.
XX
XX 29-OCT-2004; 2004WO-CA001900.
XX
XX 30-OCT-2003; 2003US-0516263P.
XX
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Lacasease E, Mcmanus D, Durkin JP;
XX
XX WPI; 2005-366517/37.
XX
XX
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
XX choriocarcinoma, seminoma and embryonal carcinoma comprises administering
XX antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
XX agent.
XX
XX Example 1; SEQ ID NO 107; 285bp; English.
XX
XX The invention relates to a method of treating a patient having a
XX proliferative disease, comprising administering to the patient, an
XX antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a
XX chemotherapeutic agent, in amounts that together are sufficient to treat
XX the patient. The method is useful for treating a patient having a
XX proliferative disease. The proliferative disease is cancer. A composition
XX comprising an antisense IAP nucleobase oligomer and a chemotherapeutic
XX agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
XX human cancer cell in vivo or ex vivo, which involves contacting the cell
XX with the composition. The present sequence represents an antisense
XX inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
XX sequence represents either T or U. There are multiple versions of this
XX sequence in the patent, the present sequence represents the sequence
XX shown in the main body of the specification.
XX
XX Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 14; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 5.7;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 1 CGCAGCGTATCTCTTTCAC 19
XX |||||
XX 1 CGCAGCGTATCTCTTTCAC 19

```

XX	AAA64903	
XX	ID	AAA64903 standard; DNA; 23 BP.
XX	AC	AAA64903;
XX	DT	07-NOV-2000 (first entry)
XX	DE	Reverse PCR primer targeted to human X-linked inhibitor of apoptosis.
XX	KM	X-linked inhibitor of apoptosis; XIAP; hILP; MTA; antisense;
XX	KW	antiinflammatory; cytostatic; tumour; PCR primer; ss.
XX	OS	Homo sapiens.
XX	PN	US6087173-A.
XX	PD	11-JUL-2000.
XX	PP	09-SEP-1999; 99US-00392580.
XX	PR	09-SEP-1999; 99US-00392580.
XX	PA	(ISIS-) ISIS PHARM INC.
XX	PI	Bennett CF, Cowseert LM, Ackermann EJ;
XX	DR	WP1; 2000-498201/44.
XX	PT	Antisense compound useful for research reagents, diagnosis, prophylaxis
XX	PT	and for treating disorders associated with X-linked inhibitor of
XX	PT	apoptosis, modulates expression of X-linked inhibitor of apoptosis.
XX	PS	Example 13; Col 38; 33pp; English.
XX	CC	The present invention relates to antisense oligonucleotides designed to
XX	CC	inhibit expression of the human X-linked inhibitor of apoptosis. Modified
XX	CC	phosphorothioate 2'-MOE oligonucleotides are more effective inhibitors
XX	CC	than unmodified oligonucleotides. The oligonucleotides may be used to
XX	CC	inhibit X-linked inhibitor of apoptosis expression in cells and tissues
XX	CC	in vitro. The oligonucleotides are also useful for treating animals or
XX	CC	humans, prone to a disease associated with X-linked inhibitor of
XX	CC	apoptosis. The oligonucleotides may also be used prophylactically to
XX	CC	prevent infection, inflammation or tumour formation. Inhibition was
XX	CC	measured by comparing the level of X-linked inhibitor of apoptosis mRNA
XX	CC	to that of GAPDH. The present sequence is the reverse PCR primer used in
XX	CC	RT-PCR to measure X-linked inhibitor of apoptosis mRNA
XX	SO	Sequence 23 BP; 5 A; 8 C; 4 G; 6 T; 0 U; 0 Other;
XX	Query Match	94.7%; Score 18; DB 3; Length 23;
XX	Best Local Similarity	100.0%; Pred. No. 19;
XX	Matches 18; Conservative 0; Mismatches	0; Indels 0; Gaps 0
QY	2 GCACGGTATCTCCTTCAC 19	
Db	1 GCACGGTATCTCCTTCAC 18	
RESULT 5		
AEAI7843/C		
ID	AEAI7843 standard; DNA; 29 BP.	
XX	AEAI7843;	
XX	AC	
XX	DT	14-JUL-2005 (first entry)
XX	DE	Human IAP-specific inhibitory oligonucleotide - SEQ ID 37.
XX	KM	inhibitor of apoptosis protein; gene silencing; apoptosis stimulation;
XX	KW	cancer; cytostatic; ss; IAP.
XX	OS	Homo sapiens.
XX	XX	

```

FH Key Location/Qualifiers
FT misc_difference 2
FT /*tag= a
FT /note= "N = T or U"
FT misc_difference 5
FT /*tag= b
FT /note= "N = T or U"
FT misc_difference 8
FT /*tag= c
FT /note= "N = T or U"
FT misc_difference 17
FT /*tag= d
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FT misc_difference 22
FT /*tag= e
FT /note= "N = T or U"
FT misc_difference 27
FT /*tag= f
FT /note= "N = T or U"
XX WO2005042558-A1.
XX
XX 12-MAY-2005.
XX
XX 29-OCT-2004; 2004WO-CA001902.
XX
XX 30-OCT-2003; 2003US-0516192P.
XX
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Lacasease E, Mcmannus D;
XX
XX WPI; 2005-346849/35.
XX
XX New pure nucleobase oligomer comprising a duplex comprising at least
XX eight but no more than 30 consecutive nucleobases corresponding to XIAP,
XX hIAP-1 or hIAP-2, useful in preparing a composition for treating cancer.
XX
XX Claim 9; SEQ ID NO 37; 112pp; English.
XX
XX The invention comprises oligonucleotides which are capable of educing the
XX expression of X-linked inhibitor of apoptosis protein (XIAP), hIAP-1 or
XX hIAP-2. The oligonucleotides of the invention are useful for the
XX treatment of proliferative disease (e.g. cancer). The present DNA
XX sequence represents an IAP-specific inhibitory oligonucleotide of the
XX invention.
XX
XX Sequence 29 BP, 7 A; 5 C; 11 G; 0 T; 0 U; 6 Other;
XX
XX Query Match 84.2%; Score 16; DB 14; Length 29;
XX Best Local Similarity 84.2%; Pred. No. 2.2e+02;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 CGCAGCGTATCTCTCTTCCAC 19
XX |||||
XX 25 CGCNCGGTNTCTCTCTTCCAC 7
XX
XX RESULT 6
XX ADX86146/c
XX ID ADX86146 standard; RNA; 19 BP.
XX
XX ADX86146;
XX
XX 05-MAY-2005 (first entry)
XX
XX XIAP targeting siRNA SEQ ID NO 17.
XX
XX de; primer; short interfering RNA; siRNA;
XX X-linked inhibitor of apoptosis protein; XIAP; RNA interference; RNAi;
XX cyostatic; cancer; gene silencing.
XX
XX OS Synthetic.
```

```

XX XX
XX WO2005014811-A2.
XX
XX 17-FEB-2005.
XX
XX 06-AUG-2004; 2004WO-US025589.
XX
XX 08-AUG-2003; 2003US-0493561P.
XX 23-OCT-2003; 2003US-00693059.
XX 24-NOV-2003; 2003US-00720448.
XX 03-DEC-2003; 2003US-00727780.
XX 14-JAN-2004; 2004US-00757803.
XX 10-FEB-2004; 2004US-0543480P.
XX 13-FEB-2004; 2004US-00780447.
XX 16-APR-2004; 2004US-00826966.
XX 30-APR-2004; 2004WO-US013456.
XX 24-MAY-2004; 2004WO-US016390.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Chowrira BM;
XX
XX WPI; 2005-163247/17.
XX
XX New chemically synthesized double stranded short interfering nucleic acid
XX that directs cleavage of an X-linked inhibitor of apoptosis protein
XX (XIAP) RNA via RNA interference, useful in preparing a composition for
XX treating cancer.
XX
XX Claim 33; SEQ ID NO 17; 202pp; English.
XX
XX This invention describes novel chemically synthesized double stranded
XX short interfering nucleic acid (siRNA) molecules which direct cleavage of
XX a X-linked inhibitor of apoptosis protein (XIAP) RNA via RNA interference
XX (RNAi), where each strand of the siRNA molecule is about 18-23
XX nucleotides in length and one strand of the siRNA molecule comprises
XX nucleotide sequence having sufficient complementarity to the XIAP RNA.
XX The siRNA molecules can be used to make a cyostatic composition
XX comprising the siRNA molecule in a carrier or diluent. The sense and
XX antisense strands are connected via a linker molecule. The pyrimidine
XX nucleotides in the sense region are 2'-O-methyl pyrimidine nucleotides.
XX The purine nucleotides in the sense region are 2'-deoxy purine
XX nucleotides and the pyrimidine nucleotides are 2'-deoxy-2'-fluoro
XX pyrimidine nucleotides. The fragment comprising the sense region includes
XX a terminal cap moiety at a 5'-end, a 3'-end, or both of the 5' and 3'
XX ends of the fragment comprising the sense region. The terminal cap moiety
XX is an inverted deoxy abasic moiety. The pyrimidine nucleotides of the
XX antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the
XX purine nucleotides are 2'-O-methyl purine nucleotides. The purine
XX nucleotides present in the antisense region comprise 2'-deoxy- purine
XX nucleotides. The antisense region comprises a phosphorothioate
XX internucleotide linkage at the 3' end of the antisense region. The
XX antisense region comprises a glyceryl modification at a 3' end of the
XX molecule are base-paired to the complementary nucleotides of the other
XX fragment of the siRNA. The 5'-end of the fragment comprising the
XX antisense region optionally includes a phosphate group. The XIAP RNA
XX comprises Genbank Accession No. NM_001157. The chemically synthesized
XX double stranded short interfering nucleic acid (siRNA) molecule is useful
XX in preparing a composition for treating cancer. ADX86130-ADX87180
XX represent siRNA molecules which are used in RNA interference mediated
XX inhibition of XIAP gene expression.
XX
XX Sequence 19 BP; 6 A; 3 C; 7 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 78.9%; Score 15; DB 14; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 7.1e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 CGGTATCTCTCTTCCAC 19
XX |||||
XX DB 19 CGGTATCTCTTCCAC 5
```

RESULT 7  
AD86613  
ID AD86613 standard; RNA; 19 BP.  
XX  
AC AD86613;  
XX  
DT 05-MAY-2005 (first entry)  
XX  
DE XIAP targeting siRNA SEQ ID NO 484.  
XX  
KM ds; primer; short interfering RNA; siRNA;  
KM X-linked inhibitor of apoptosis protein; XIAP; RNA interference; RNAi;  
KM cytosolic; cancer; gene silencing.  
XX  
OS Synthetic.  
XX  
PN WO2005014811-A2.  
XX  
PD 17-FEB-2005.  
XX  
PF 06-AUG-2004; 2004WO-US025589.  
XX  
PR 08-AUG-2003; 2003US-0493561P.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00727780.  
PR 14-JAN-2004; 2004US-00757803.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826966.  
PR 30-APR-2004; 2004WO-US013456.  
PR 24-MAY-2004; 2004WO-US016390.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Chowitra BM;  
XX  
XX WPI; 2005-163247/17.  
XX  
PT New chemically synthesized double stranded short interfering nucleic acid  
PT that directs cleavage of an X-linked inhibitor of apoptosis protein  
PT (XIAP) RNA via RNA interference, useful in preparing a composition for  
PT treating cancer.  
XX  
XX  
PS Claim 33; SEQ ID NO 484; 202bp; English.  
XX  
XX This invention describes novel chemically synthesized double stranded  
CC short interfering nucleic acid (siRNA) molecules which direct cleavage of  
CC a X-linked inhibitor of apoptosis protein (XIAP) RNA via RNA interference  
CC (RNAi), where each strand of the siRNA molecule is about 18-23  
CC nucleotides in length and one strand of the siRNA molecule comprises  
CC nucleotide sequence having sufficient complementarity to the XIAP RNA.  
CC The siRNA molecule can be used to make a cytostatic composition  
CC comprising the siRNA molecule in a carrier or diluent. The sense and  
CC antisense strands are connected via a linker molecule. The sense and  
CC nucleotides in the sense region are 2'-O-methyl pyrimidine nucleotides.  
CC The purine nucleotides in the sense region are 2'-deoxy-2'-fluoro  
CC pyrimidine nucleotides. The fragment comprising the sense region includes  
CC a terminal cap moiety at a 5'-end, a 3'-end, or both of the 5' and 3'  
CC ends of the fragment comprising the sense region. The terminal cap moiety  
CC is an inverted deoxy abasic moiety. The pyrimidine nucleotides of the  
CC antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the  
CC purine nucleotides are 2'-O-methyl purine nucleotides. The purine  
CC nucleotides present in the antisense region comprise 2'-deoxy- purine  
CC nucleotides. The antisense region comprises a phosphorothioate  
CC internucleotide linkage at the 3' end of the antisense region. The  
CC antisense region comprises a glyceryl modification at a 3' end of the  
CC antisense region. About 19 nucleotides of each fragment of the siRNA  
CC molecule are base-paired to the complementary nucleotides of the other  
CC fragment of the siRNA. The 5'-end of the fragment comprising the  
CC antisense region optionally includes a phosphate group. The XIAP RNA

CC comprises Genbank Accession No. NM\_001167. The chemically synthesized  
CC double stranded short interfering nucleic acid (siRNA) molecule is useful  
CC in preparing a composition for treating cancer. ADX86130-ADX87180  
CC represent siRNA molecules which are used in RNA interference mediated  
CC inhibition of XIAP gene expression.  
XX  
SQ Sequence 19 BP; 3 A; 7 C; 3 G; 0 T; 6 U; 0 Other;  
Query Match 78.9%; Score 15; DB 14; Length 19;  
Best Local Similarity 66.7%; Pred. No. 7.1e+02;  
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
OY 5 CGGATCTCCTGCAC 19  
Db 1 CGGUAUCCUUCAC 15  
RESULT 8  
AD86184  
ID AD86184 standard; DNA; 19 BP.  
XX  
AC AD86184;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human antisense XIAP nucleobase oligomer SEQ ID NO:29.  
XX  
KM nucleobase oligomer; inhibitor-of apoptosis inhibitor; IAP inhibitor;  
KM cytosolic; antisense therapy; apoptosis enhancer; cancer;  
KM lymphoproliferative disorder; leukemia; myelodysplastic syndrome;  
KM polycythemia vera; lymphoma; Hodgkin's disease;  
KM Waldenstrom's macroglobulinemia; breast cancer; basal cell carcinoma;  
KM lung carcinoma; melanoma; retinoblastoma; human; ss.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1..19  
FT /\*tag= a  
FT /note= "N = T or U where each nucleobase may be part of a  
FT ribonucleotide, deoxyribonucleotide, or nucleotide  
FT analogue"  
XX  
XX  
PN WO2003080638-A2.  
XX  
PD 02-OCT-2003.  
XX  
PF 27-MAR-2003; 2003WO-1B001670.  
XX  
PR 27-MAR-2002; 2002US-0367853P.  
XX  
PA (AEGE-) AEGERA THERAPEUTICS INC.  
XX  
PI Lacasease E, Mcmannus D, Durkin JP;  
XX  
XX WPI; 2003-779241/73.  
XX  
PT New nucleobase oligomers that inhibit expression of inhibitor of  
PT apoptosis gene, useful for treating cancer and other lymphoproliferative  
PT disorders by inducing apoptosis.  
XX  
XX  
PS Claim 54; SEQ ID NO 29; 259pp; English.  
XX  
XX The present invention describes a substantially pure nucleobase oligomer  
CC (I) of up to 30 nucleobases in length or comprising eleven DNA residues  
CC flanked on each side by four 2'-O-methyl RNA residues that inhibits the  
CC expression of an inhibitor-of apoptosis (IAP) in the cell. Also  
CC described: (1) a pharmaceutical composition (II) comprising (I) and a  
CC carrier; (2) a catalytic RNA molecule (III) capable of cleaving XIAP,  
CC H1AP1, or H1AP2 mRNA; (3) an expression vector (IV) comprising a nucleic  
CC acid encoding one or more (III) positioned for expression in a mammalian  
CC cell; (4) a double-stranded RNA molecule (IV) consisting of 21-29

CC nucleobases comprising at least eight consecutive nucleobases  
CC corresponding to a sequence comprising 19 nucleotides, as given in  
CC specification; (5) a double-stranded hairpin RNA molecule (V) consisting  
CC of 50-70 nucleobases, comprising a first domain of 21-29 nucleobases that  
CC comprise at least eight consecutive nucleobases corresponding to a  
CC sequence fully defined in the specification, comprising, e.g. 19  
CC nucleotides, and a second domain complementary to the first domain, and a  
CC loop domain situated between the first and the second domains such that  
CC the first domain and the second domain are capable of duplexing to form  
CC the double-stranded hairpin RNA molecule; and (6) an expression vector  
CC (VI) comprising a nucleic acid molecule encoding the double stranded RNA  
CC molecule positioned for expression in a mammalian cell. (I) has  
CC cytosolic activity, and can be used in antisense therapy. (I) is useful  
CC for enhancing the apoptosis of a cell in an animal, preferably human  
CC where (I) inhibits the expression of an IAP in the cell. (I) is also  
CC useful for treating an animal having a cancer or lymphoproliferative  
CC disorder. The cancer includes acute leukemia, acute lymphocytic  
CC leukemia, acute myelocytic leukemia, acute myeloblastic leukemia,  
CC acute promyelocytic leukemia, acute myelomonocytic leukemia, acute  
CC monocytic leukemia, acute erythroleukemia, chronic leukemia, chronic  
CC myelocytic leukemia, myelodysplastic syndrome, chronic lymphocytic  
CC leukemia, polycythemia vera, lymphoma, Hodgkin's disease, Waldenstrom's  
CC macroglobulinemia, breast cancer, basal cell carcinoma, lung carcinoma,  
CC melanoma and retinoblastoma. The present sequence is used in the  
CC exemplification of the present invention.

Query Match	73.7%	Score 14	DB 10	Length 19
Best Local Similarity	73.7%	Pred. No 2.4e+03		
Matches 14, Conservative	0	Mismatches 5	Indels 0	Gaps 0
QY	1	GGCAAGGTATCTCTTCAC	19	
Db	1	GGCAAGGNANCNCCNNAC	19	

RESULT 9	
ADFe68262	
ID	ADFe68262 standard; DNA, 19 BP.
XX	
AC	
XX	ADFe68262;
XX	
D7	12-FEB-2004 (first entry)
XX	
DE	Human antisense IAP nucleobase oligomer SEQ ID NO:107.
XX	
KW	nucleobase oligomer; inhibitor-of apoptosis inhibitor; IAP inhibitor;
KW	cyclostatic; antisense therapy; apoptosis enhancer; cancer;
KW	lymphoproliferative disorder; leukæmia; myelodysplastic syndrome;
KW	polycythemia vera; lymphoma; Hodgkin's disease;
KW	Maidenstrom's macroglablinemia; breast cancer; basal cell carcinoma;
KW	lung carcinoma; melanoma; retinoblastoma; human; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
FH	
FT	Key
FT	misc_feature
FT	
FT	Location/Qualifiers
FT	1..19
FT	/tag= a
FT	/note= "N = T or U where each nucleobase may be part of a
FT	ribonucleotide, deoxyribonucleotide, or nucleotide
FT	analogue"

PN	WO2003080638-A2.
XX	
PD	02-OCT-2003.
XX	
PF	27-MAR-2003; 2003WO-IB001670.
XX	
PR	27-MAR-2002; 2002US-0367853P.
PA	(AEGE-) AEGERA THERAPEUTICS INC.

XX Lacasease E, Mcmannus D, Durkin JP;  
PI WPI; 2003-779241/73.  
XX  
DR  
XX  
XX New nucleobase oligomers that inhibit expression of inhibitor of  
PT apoptosis gene, useful for treating cancer and other lymphoproliferative  
PT disorders by inducing apoptosis.  
XX  
XX Claim 54; SEQ ID NO 107; 259pp; English.  
PS

The present invention describes a substantially pure nucleobase oligomer (I) of up to 30 nucleobases in length or comprising eleven DNA residues flanked on each side by four 2'-O-methyl RNA residues that inhibits the expression of an inhibitor-of apoptosis (IAP) in the cell. Also described: (1) a pharmaceutical composition (II) comprising (I) and a carrier; (2) a catalytic RNA molecule (III) capable of cleaving XIAP, HAIAP, or HIMP2 mRNA; (3) an expression vector (IV) comprising a nucleic acid encoding one or more (III) positioned for expression in a mammalian cell; (4) a double-stranded RNA molecule (IV) consisting of 21-29 nucleobases, comprising at least eight consecutive nucleobases corresponding to a sequence comprising 19 nucleotides, as given in specification; (5) a double-stranded hairpin RNA molecule (V) consisting of 50-70 nucleobases, comprising a first domain of 21-29 nucleobases that comprise at least eight consecutive nucleobases corresponding to a sequence fully defined in the specification, comprising, e.g. 19 nucleotides, and a second domain complementary to the first domain, and loop domain situated between the first and the second domains such that the first domain and the second domain are capable of duplexing to form the double-stranded hairpin RNA molecule; and (6) an expression vector (VI) comprising a nucleic acid molecule encoding the double stranded RNA molecule positioned for expression in a mammalian cell. (I) has cytostatic activity, and can be used in antinease therapy. (I) is useful for enhancing the apoptosis of a cell in an animal, preferably human where (I) inhibits the expression of an IAP in the cell. (I) is also useful for treating an animal having a cancer or lymphoproliferative disorder. The cancer includes acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, acute myeloblastic leukemia, acute promyelocytic leukemia, acute myelomonocytic leukemia, acute monocytic leukemia, acute erythroleukemia, chronic lymphocytic leukemia, myelodysplastic syndrome, chronic lymphocytic leukemia, polycythemia vera, lymphoma, Hodgkin's disease, Waldenstrom's macroglobulinemia, breast cancer, basal cell carcinoma, lung carcinoma, melanoma and retinoblastoma. The present sequence is used in the exemplification of the present invention.

```

SQ Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;
Query Match 73.7%; Score 14; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. NO. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps
QY 1 CGCAGGTTATCTCCTTCAC 19
    |||||
DB 1 CGCAGGNNANCCNNNCAC 19
    |||||

```

Key	Location/Qualifiers
RESULT 10	
AEAl0122	
ID	AEAl0122 standard; DNA, 19 BP.
XX	
XX	
AC	AEAl0122;
XX	
DT	14-JUL-2005 (first entry)
XX	
DE	Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 143
XX	
KW	Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	

FT	modified_base	1..4	/tag = a
PT		/mod_base= OTHER	
FT		/note="OTHER = 2'-O-methyl X RNA"	
FT		16..19	
FT	modified_base		/tag= b
FT		/mod_base= OTHER	
FT		/note="OTHER = 2'-O-methyl X RNA"	
XX			
PN	WO2005042030-A1.		
XX			
PD	12-MAY-2005.		
XX			
PE	29-OCT-2004; 2004WO-CA001900.		
XX			
PR	30-OCT-2003; 2003US-0516263P.		
XX			
PA	(AEGE-) AEGERA THERAPEUTICS INC.		
XX			
PI	Lacasse E, Mcmanus D, Durkin JP;		
XX			
DR	WPI; 2005-366517/37.		
PT	Treating proliferative disease such as hepatoma, bile duct carcinoma,		
PT	choriocarcinoma, seminoma and embryonal carcinoma comprises administering		
PT	antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic		
PT	agent.		
XX			
PS	Claim 6; SEQ ID NO 143; 285bp; English.		
XX			
CC	The invention relates to a method of treating a patient having a		
CC	proliferative disease, comprising administering to the patient, an		
CC	antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a		
CC	chemotherapeutic agent, in amounts that together are sufficient to treat		
CC	the patient. The method is useful for treating a patient having a		
CC	proliferative disease. The proliferative disease is cancer. A composition		
CC	comprising an antisense IAP nucleobase oligomer and a chemotherapeutic		
CC	agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or		
CC	human cancer cell in vivo or ex vivo, which involves contacting the cell		
CC	with the composition. The present sequence represents an antisense		
CC	inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the		
CC	sequence represents either T or U. There are multiple versions of this		
CC	sequence in the patent, the present sequence represents the sequence		
CC	shown in the main body of the specification.		
SQ			
Sequence	19 BP; 4 A; 6 C; 3 G; 4 T; 2 U; 0 Other;		
Query Match	73.7%; Score 14; DB 14; Length 19;		
Best Local Similarity	92.9%; Pred. No. 2.4e+03;		
Matches	13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
QY	6 GGATTCCTCCTCAC 19		
	:		
Db	1 GGUATCTCCTTACC 14		
RESULT 11			
ID	AEA10076		
AEAI0076	standard; DNA; 19 BP.		
AC	AEA10076;		
XX			
DT	14-JUL-2005 (first entry)		
DE	Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 97.		
XX			
KX	Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.		
XX			
OS	Homo sapiens.		
XX	Synthetic.		
Key	Location/Qualifiers		
FT	modified_base 1..2		

FT		/tag= a
FT		/mod_base= OTHER
FT		/note= "OTHER = 2'-O-methyl x RNA"
FT	modified_base	18. .19
FT		/tag= b
FT		/mod_base= OTHER
FT		/note= "OTHER = 2'-O-methyl x RNA"
XX		
PN	WO2005042030-A1.	
XX		
PD	12-MAY-2005.	
XX		
PF	29-OCT-2004; 2004WO-CA001900.	
XX		
PR	30-OCT-2003; 2003US-0516263P.	
XX		
PA	(AEGE-) AEGERA THERAPEUTICS INC.	
XX		
PI	Lacasse E, Mcmanus D, Durkin JP,	
XX	WPI; 2005-366517/37.	
DR		
PT	Treating proliferative disease such as hepatoma, bile duct carcinoma,	
PT	choriocarcinoma, seminoma and embryonal carcinoma comprises administering	
PT	antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic	
PT	agent.	
XX		
PS	Claim 6; SEQ ID NO 97; 285bp; English.	
XX		
CC	The invention relates to a method of treating a patient having a	
CC	proliferative disease, comprising administering to the patient, an	
CC	antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a	
CC	chemotherapeutic agent, in amounts that together are sufficient to treat	
CC	the patient. The method is useful for treating a patient having a	
CC	proliferative disease. The proliferative disease is cancer. A composition	
CC	comprising an antisense IAP nucleobase oligomer and a chemotherapeutic	
CC	agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or	
CC	human cancer cell in vivo or ex vivo, which involves contacting the cell	
CC	with the composition. The present sequence represents an antisense	
CC	inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the	
CC	sequence represents either T or U. There are multiple versions of this	
CC	sequence in the patent, the present sequence represents the sequence	
CC	shown in the main body of the specification.	
XX		
SQ	Sequence 19 BP; 4 A; 6 C; 3 G; 5 T; 1 U; 0 Other;	
	Query Match 73.7%; Score 14; DB 14; Length 19;	
	Best Local Similarity 100.0%; Pred. No. 2,4e+03;	
	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	6 GGATCCTCCTTCAC 19	
Db	1 GGATCCTCCTTCAC 14	
	RESULT 12	
	AEA10108	
ID	AEA10108 standard; DNA, 19 BP.	
XX		
AC	AEA10108;	
XX		
DT	14-JUL-2005 (first entry)	
XX		
DE	Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 129.	
XX		
KW	Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.	
OS	Homo sapiens.	
XX	Synthetic.	
XX		
FN	WO2005042030-A1.	
XX		
DD	12-MAY-2005.	

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XX 29-OCT-2004; 2004WO-CA001900.
XX
XX 30-OCT-2003; 2003US-0516263P.
XX
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Lacasease E, Mcmanus D, Durkin JP;
XX
XX WPI; 2005-366517/37.
XX
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
XX choriocarcinoma, seminoma and embryonal carcinoma comprises administering
XX antisenase inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
XX agent.
XX
XX Example 1; SEQ ID NO 129; 285pp; English.
XX
XX The invention relates to a method of treating a patient having a
XX proliferative disease, comprising administering to the patient, an
XX antisenase inhibitor of apoptosis (IAP) nucleobase oligomer and a
XX chemotherapeutic agent, in amounts that together are sufficient to treat
XX the patient. The method is useful for treating a patient having a
XX proliferative disease. The proliferative disease is cancer. A composition
XX comprising an antisenase IAP nucleobase oligomer and a chemotherapeutic
XX agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
XX human cancer cell in vivo or ex vivo, which involves contacting the cell
XX with the composition. The present sequence represents an antisenase
XX inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
XX sequence represents either T or U. There are multiple versions of this
XX sequence in the patent, the present sequence represents the sequence
XX shown in the main body of the specification.
XX
SQ Sequence 19 BP; 4 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
XX
Query Match 73.7%; Score 14; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 6 GGTATCTCCTTCAC 19
DB 1 GGTATCTCCTTCAC 14
XX
RESULT 13
AEA09518
ID AEA09518 standard; DNA; 19 BP.
XX
XX AEA09518;
XX
XX 14-JUL-2005 (first entry)
XX
DE Antisenase inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 29.
XX
XX Cytostatic; neoplasm; cancer; Antisenase; apoptosis inhibitor; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT misc_difference 1..19
XX FT /tag= a
XX FT /note= "The residues represented by N are either T or U"
XX
XX PN WO2005042030-A1.
XX
XX 12-MAY-2005.
XX
XX 29-OCT-2004; 2004WO-CA001900.
XX
XX 30-OCT-2003; 2003US-0516263P.
XX
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX PA
```

```
XX Lacasease E, Mcmanus D, Durkin JP;
XX
XX WPI; 2005-366517/37.
XX
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
XX choriocarcinoma, seminoma and embryonal carcinoma comprises administering
XX antisenase inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
XX agent.
XX
XX Claim 6; SEQ ID NO 29; 285pp; English.
XX
XX The invention relates to a method of treating a patient having a
XX proliferative disease, comprising administering to the patient, an
XX antisenase inhibitor of apoptosis (IAP) nucleobase oligomer and a
XX chemotherapeutic agent, in amounts that together are sufficient to treat
XX the patient. The method is useful for treating a patient having a
XX proliferative disease. The proliferative disease is cancer. A composition
XX comprising an antisenase IAP nucleobase oligomer and a chemotherapeutic
XX agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or
XX human cancer cell in vivo or ex vivo, which involves contacting the cell
XX with the composition. The present sequence represents an antisenase
XX inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the
XX sequence represents either T or U. There are multiple versions of this
XX sequence in the patent, the present sequence represents the sequence
XX shown in the sequence listing.
XX
SQ Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;
XX
Query Match 73.7%; Score 14; DB 14; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 1 CGCAGGTATCTCCTTCAC 19
DB 1 CGCAGGTATCTCCTTCAC 19
XX
RESULT 14
AEA10267
ID AEA10267 standard; DNA; 19 BP.
XX
XX AEA10267;
XX
XX 14-JUL-2005 (first entry)
XX
DE Antisenase inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 289.
XX
XX Cytostatic; neoplasm; cancer; Antisenase; apoptosis inhibitor; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX WO2005042030-A1.
XX
XX 12-MAY-2005.
XX
XX 29-OCT-2004; 2004WO-CA001900.
XX
XX 30-OCT-2003; 2003US-0516263P.
XX
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX PI Lacasease E, Mcmanus D, Durkin JP;
XX
XX WPI; 2005-366517/37.
XX
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,
XX choriocarcinoma, seminoma and embryonal carcinoma comprises administering
XX antisenase inhibitor of apoptosis nucleobase oligomer and chemotherapeutic
XX agent.
XX
XX Claim 6; SEQ ID NO 289; 285pp; English.
XX
XX PS
```



XX The invention relates to a method of treating a patient having a  
CC proliferative disease, comprising administering to the patient, an  
CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a  
CC chemotherapeutic agent, in amounts that together are sufficient to treat  
CC the patient. The method is useful for treating a patient having a  
CC proliferative disease. The proliferative disease is cancer. A composition  
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic  
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or  
CC human cancer cell in vivo or ex vivo, which involves contacting the cell  
CC with the composition. The present sequence represents an antisense  
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the  
CC sequence represents either T or U. There are multiple versions of this  
CC sequence in the patent, the present sequence represents the sequence  
CC shown in the main body of the specification.

SQ Sequence 19 BP; 4 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 73.7%; Score 14; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGATCTCTCTTAC 19  
Db 1 GGATCTCTCTTAC 14

RESULT 15  
AEA09596  
ID AEA09596 standard; DNA; 19 BP.  
XX AEA09596;  
AC  
XX 14-JUL-2005 (first entry)  
DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 107.  
XX  
XX Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.  
XX Homo sapiens.  
OS Synthetic.  
XX Key Location/Qualifiers  
FT misc\_difference 1..19  
FT /\*tag= a  
FT /note= "The residues represented by N are either T or U"  
XX  
XX MO2005042030-A1.  
PN  
XX 12-MAY-2005.  
PD  
XX 29-OCT-2004; 2004MO-CA001900.  
PF  
XX 30-OCT-2003; 2003US-0516263P.  
PR  
XX  
XX (AEGE-) AEGERA THERAPEUTICS INC.  
PA  
XX Lacasease E, Mcmanus D, Durkin JP;  
PI  
XX WPI; 2005-366517/37.  
DR  
XX  
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,  
PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering  
PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic  
PT agent.  
XX  
XX Example 1; SEQ ID NO 107; 2855pp; English.  
XX  
XX The invention relates to a method of treating a patient having a  
CC proliferative disease, comprising administering to the patient, an  
CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a  
CC chemotherapeutic agent, in amounts that together are sufficient to treat  
CC the patient. The method is useful for treating a patient having a

CC proliferative disease. The proliferative disease is cancer. A composition  
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic  
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or  
CC human cancer cell in vivo or ex vivo, which involves contacting the cell  
CC with the composition. The present sequence represents an antisense  
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the  
CC sequence represents either T or U. There are multiple versions of this  
CC sequence in the patent, the present sequence represents the sequence  
CC shown in the sequence listing.

SQ Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;

Query Match 73.7%; Score 14; DB 14; Length 19;  
Best Local Similarity 73.7%; Pred. No. 2.4e+03;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTAC 19  
Db 1 CGCAGCGTATCTCTTAC 19

RESULT 16  
ABA97854/c  
ID ABA97854 standard; DNA; 33 BP.  
XX ABA97854;  
AC  
XX 10-APR-2002 (first entry)  
DE Oligonucleotide ME1-anti.  
XX  
XX Drug; cell wall; GPI anchor protein; ss.  
XX  
XX Synthetic.  
OS  
XX MO200183733-A1.  
PN  
XX 08-NOV-2001.  
PD  
XX 26-APR-2001; 2001MO-JP003630.  
PF  
XX 01-MAY-2000; 2000JP-00132041.  
PR  
XX (DAUC ) DAICHI PHARM CO LTD.  
PA  
XX Kitanura A, Someya K, Nakajima R;  
PI  
XX WPI; 2002-097496/13.  
DR  
XX  
XX Screening for drugs that act on cell walls, involves culturing  
PT microorganisms with a reporter protein acting as a GPI anchor protein in  
PT their cell walls.  
XX  
XX Disclosure; Page 13; 44pp; Japanese.  
PS  
XX  
XX The invention relates to screening for drugs that act on cell walls,  
CC comprising culturing microorganisms with a reporter protein acting as a  
CC GPI anchor protein in their cell walls in the presence of the test  
CC substance and assaying the amount of reporter protein produced in the  
CC culture. The present sequence is that of an oligonucleotide useful to the  
CC invention  
XX  
XX Sequence 33 BP; 10 A; 7 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 72.6%; Score 13.8; DB 6; Length 33;  
Best Local Similarity 88.2%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTAC 17  
Db 26 CTCACGGTATCGCCTTC 10

RESULT 17  
ACCT0715/c  
ID ACC70715 standard; DNA; 33 BP.  
XX  
AC ACC70715;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Yeast PCR primer ME11-anti1.  
XX  
KW Yeast; antifungal; cell wall; fungal infection; PCR; primer; ss.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN W02003035898-A1.  
XX  
PD 01-MAY-2003.  
XX  
PF 22-OCT-2002; 2002WO-JP010932.  
XX  
PR 22-OCT-2001; 2001JP-00323293.  
XX  
PA (DAUC ) DAIICHI PHARM CO LTD.  
XX  
PI Kitamura A, Nakajima R;  
XX  
WP; 2003-430423/40.  
XX  
PT Screening drugs acting on cell wall based on reporter protein as GPI  
PT anchor protein with analysis of its derived sugar chain, useful in  
PT judging action points of drugs particularly in developing antifungal  
PT agents.  
XX  
XX  
PS Example 1; Page 15; 51pp; Japanese.  
XX  
CC The present invention relates to a method for screening drugs which act  
CC on cell walls. The method comprises culturing a microorganism immobilised  
CC on its cell wall with a reporter protein as a GPI anchor protein, in the  
CC presence of a test drug, analysing a receptor-originated sugar chain in  
CC the liquid culture medium, and presuming the action point of the cell  
CC wall-acting drug based on the data of the sugar chain thus obtained. The  
CC method is useful for judging action points of drugs particularly in  
CC developing cell-wall inhibitors for treatment of deep-site fungal  
CC infection. The present sequence is a PCR primer used in an example from  
CC the invention  
XX  
SQ Sequence 33 BP; 10 A; 7 C; 11 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 72.6%; Score 13.8; DB 8; Length 33;  
Best Local Similarity 88.2%; Pred.No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
OY 1 CGACGGATCTCCTTC 17  
DB | ||||| |||||  
26 CTCACGGATCGCCTTC 10  
XX  
RESULT 18  
AAV76807  
ID AAV76807 standard; DNA; 59 BP.  
XX  
AC AAV76807;  
XX  
DT 16-MAR-1999 (first entry)  
XX  
DE Staphylococcus aureus contig SEQ ID #2496.  
XX  
KW Computer readable medium; vaccine; S.aureus infection; immunodetection;  
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
KW skin infection; surgical wound infection; scalded skin syndrome;  
KW toxic shock syndrome; ds.  
XX  
OS Staphylococcus aureus.  
XX

XX EP186519-A2.  
XX  
XX  
XX 30-JUL-1997.  
XX  
XX  
XX 07-JAN-1997; 97EP-00100117.  
XX  
XX PF  
XX 05-JAN-1996; 96US-0009861P.  
XX  
XX PR  
XX (HUMA-) HUMAN GENOME SCT INC.  
XX  
XX PA  
XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA,  
XX PI  
XX WPI; 1997-374922/35.  
XX  
XX DR  
XX Polynucleotide(s) and proteins derived from *Staphylococcus aureus* -  
XX PT stored on computer readable medium and used in the production of anti-  
XX S.aureus vaccines.  
XX  
XX PT  
XX  
XX PS  
XX Claim 1; Page 2254-2255; 3271pp; English.  
XX  
XX This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences  
XX of the invention. The DNA sequences are recorded on a computer readable  
XX medium, preferably selected from a floppy or hard disk, random access  
XX memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
XX the *S.aureus* DNA sequences allows putative functions to be assigned so  
XX that protein-encoding or regulatory regions of commercial, therapeutic or  
XX industrial importance can be obtained. Specifically, sequences which are  
XX likely to encode antigens have been identified and these polypeptides can  
XX be used in a vaccine composition against *S.aureus* infection. The  
XX polypeptides can also be used in a kit for the immunodetection of  
XX *S.aureus* in a sample. *S.aureus* is implicated in numerous human diseases,  
XX including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
XX skin and surgical wound infections, scalded skin syndrome, toxic shock  
XX syndrome, etc. Organisms transformed with the DNA sequences can be used  
XX for recombinant production of the polypeptides. The new DNA sequences  
XX (and their fragments) are useful as primers or probes for isolating  
XX homologues of any of the *S.aureus* DNA sequences contained on the computer  
XX readable medium  
XX  
XX SQ  
XX Sequence 59 BP; 19 A; 12 C; 8 G; 20 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 72.6%; Score 13.8; DB 2; Length 59;  
XX Best Local Similarity 88.2%; Pred. NO. 3.4e+03;  
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0.  
XX  
XX QY  
XX 1 CGCAGCGATCTCCTTC 17  
XX ||||| |||||  
XX 14 CGCAGCGATTTCTTCTC 30  
XX  
XX  
XX RESULT 19  
XX AEB27488  
XX ID AEB27488 standard; DNA; 60 BP.  
XX AC  
XX AEB27488;  
XX  
XX DT 22-SEP-2005 (first entry)  
XX  
XX XX P. radiata cell cycle gene microarray oligo SEQ ID NO 649.  
XX DE plant protectant; fungicide; plant growth regulant; gene therapy;  
XX KW cell cycle; gene expression; plant; transgenic plant; microarray; wood;  
XX 88.  
XX  
XX XX Pinus radiata.  
XX OS  
XX WO2005065339-A2.  
XX PN  
XX 21-JUL-2005.  
XX  
XX 30-DEC-2004; 2004WO-US043804.  
XX  
XX PF  
XX

PR 30-DEC-2003; 2003US-0533036P.  
XX (ARBO-) ARBOGEN LLC.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
PI Forster RL, Connert MB, Emerson SJ, Grigor MR, Higgins CM,  
PI Lund ST, Magusin A, Kodrzycki RJ;  
XX WPI; 2005-506765/51.  
XX  
XX New polynucleotide encoding a plant cell cycle protein, useful for  
PT modifying plant development and altering plant phenotype.  
XX  
XX  
PS Claim 43; SEQ ID NO 649; 499pp; English.  
XX  
XX The invention describes an isolated polynucleotide comprising: (1) a  
CC sequence of SEQ ID NOS: 1-237 or their conservative variants; (11) a  
CC sequence encoding the catalytic or substrate-binding domain of a  
CC polypeptide of SEQ ID NOS: 261-497, where the polynucleotide encodes a  
CC polypeptide having the activity of the polypeptide of SEQ ID NOS: 261-497  
CC ; or (11) a nucleic acid sequence of SEQ ID NOS: 471-657. Also described  
CC are: (1) a DNA construct comprising at least one polynucleotide having  
CC the sequence of SEQ ID NOS: 1-237 or their conservative variants; (2) a  
CC plant cell transformed with the DNA construct of (1); (3) a transgenic  
CC plant comprising the plant cell of (2); (4) a method of making a  
CC transformed plant; (5) a wood or a wood pulp obtained from a transgenic  
CC tree which has been transformed with the DNA construct of (1); (6) a  
CC method of making wood or wood pulp; (7) an isolated polypeptide  
CC comprising an amino acid sequence encoded by the new isolated  
CC polynucleotide or comprising any of the amino acid sequences of SEQ ID  
CC NOS: 261-497; (8) a method of altering a plant phenotype of a plant; (9)  
CC a method of correlating gene expression in two different samples; (10) a  
CC method of correlating the possession of a plant phenotype to the level of  
CC gene expression in the plant of one or more genes; (11) a method of  
CC correlating gene expression to a stage of the cell cycle; (12) a  
CC combination, for detecting expression of one or more genes, comprising  
CC two or more oligonucleotides, where each oligonucleotide is capable of  
CC hybridizing to a nucleic acid sequence of SEQ ID NOS: 1-237 or to gene  
CC product encoded by a nucleic acid sequence of SEQ ID NOS: 1-237; (13) a  
CC microarray comprising the combination of (12) provided on a solid  
CC support, where each of the two or more oligonucleotides occupies a unique  
CC location on the solid support; (14) a method for detecting one or more  
CC genes in a sample; (15) a method for detecting one or more nucleic acid  
CC sequences encoded by one or more genes in a sample; and (16) a kit, for  
CC detecting gene expression, comprising the microarray of (13) together  
CC with one or more buffers or reagents for a nucleotide hybridization  
CC reaction. The polynucleotides, polypeptides, DNA construct, composition,  
CC and methods are useful for modifying plant development and altering plant  
CC phenotype. This sequence represents an oligonucleotide used in the  
CC creation of a microarray for detection of cell cycle genes.  
XX  
SQ Sequence 60 BP; 18 A; 13 C; 9 G; 20 T; 0 U; 0 Other;  
Query Match 72.6%; Score 13.8; DB 14; Length 60;  
Best Local Similarity 88.2%; Pred. No. 3.4e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 CACGGTATCTCCTTCAC 19  
Db 24 CACGGTATCTCCTTCAC 40  
RESULT 20  
AAQ53958 standard; DNA; 24 BP.  
XX  
XX AAQ53958;  
XX  
XX 03-AUG-1995 (first entry)  
XX  
XX Human OTC gene antisense primer, binds to bases 260-283.  
DE  
XX  
XX Human; OTC; identification; mutation; amplify; PCR; diagnosis;

KW fluorescence-label; primer; electrophores; genetic disease;  
KW single stranded conformation polymorphism; SSCP; detection; ss.  
XX  
XX Synthetic.  
XX  
XX JP05317048-A.  
XX  
XX  
XX 03-DEC-1993.  
XX  
XX 30-SEP-1992; 92JP-00286605.  
XX  
XX 30-SEP-1991; 91JP-00280835.  
XX  
XX (SHIO ) SHIONOGI & CO LTD.  
PA (MATS/) MATSUDA I.  
XX  
XX WPI; 1994-011017/02.  
XX  
XX  
XX Gene mutation identification for genetic disease diagnosis - includes  
PT specific gene or fragment amplification by polymerase chain reaction  
PT using fluorescence-labelled primer and electrophoresis.  
XX  
XX Disclosure; Page 11; 14pp; Japanese.  
XX  
XX The sequences given in AAQ53956-78 are primers which were used in the  
CC method of the invention to detect mutations in the human OTC gene. The  
CC gene is amplified by PCR using a fluorescence-labelled primer and the  
CC amplified gene or fragment is electrophoresed by single stranded  
CC conformation polymorphism (SSCP) and detecting the mutated gene via the  
CC primer. This method can be used to detect the presence of mutation in a  
CC gene with a precision equal to or higher than that of RFL labelling  
CC methods. This method may be used in the diagnosis of genetic disease  
XX  
SQ Sequence 24 BP; 7 A; 7 C; 3 G; 7 T; 0 U; 0 Other;  
Query Match 70.5%; Score 13.4; DB 2; Length 24;  
Best Local Similarity 93.3%; Pred. No. 5e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 CACGGTATCTCCTTC 17  
Db 10 CACGGTATCTCCTTC 24  
RESULT 21  
AAT16221 standard; cDNA; 37 BP.  
XX  
XX AAT16221;  
XX  
XX 11-JUL-1996 (first entry)  
XX  
XX Bryodin 1 PCR primer 4.  
DE  
XX  
XX Bryodin 1; ribosome-inactivating protein; ligand; toxin; immunotoxin;  
KW cytotoxin; cancer; Bryonia dioica; primer; PCR;  
KW polymerase chain reaction; ss.  
XX  
XX Synthetic.  
XX  
XX CA2148724-A.  
XX  
XX 18-NOV-1995.  
XX  
XX 05-MAY-1995; 95CA-02148724.  
XX  
XX 17-MAY-1994; 94US-00245754.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA  
XX  
XX Siegal1 CB;  
PI  
XX  
XX WPI; 1996-077793/09.

XX Oligo:nucleotide encoding ribosome-inactivating bryodin 1 from Bryonia  
PT dioica - inhibits protein synthesis in vitro and is useful as ligand or  
PT toxin conjugates or fusion proteins to selectively kill, e.g. cancer  
PT cells.  
XX  
PS Example 4; Page 24; 46pp; English.  
XX  
CC Following PCR amplification of cDNA coding for bryodin 1 (see also  
CC AAT16208) and insertion of the product into vector pET22b, the pElb  
CC leader sequence contained in the resulting intermediate vector was  
CC removed by digesting with XbaI and NcoI, and ligating the resulting  
CC bp fragment with an oligoduplex formed by the annealing of primers 3  
CC (AAT16220) and 4 (AAT16221). The resulting plasmid, pSEI3.0, was used for  
CC transformation of E. coli BL21. Recombinant bryodin 1 (see also AAR92481)  
CC was produced that had potent protein synthesis inhibitory activity (ED50  
CC = 3-4 µM)  
XX  
SQ Sequence 37 BP; 13 A; 6 C; 3 G; 15 T; 0 U; 0 Other;  
XX  
Query Match 70.5%; Score 13.4; DB 2; Length 37;  
Best Local Similarity 93.3%; Pred. No. 5.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 CACGATCTCTCTTC 17  
DB 1 CATGGTATCTCTTTC 15  
RESULT 22  
ABN37919/C  
ID ABN37919 standard; DNA; 60 BP.  
XX  
AC ABN37919;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:10667.  
XX  
KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
KM splice variant; transcriptome; oligonucleotide library; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-IB001903.  
XX  
PR 28-JUL-2000; 2000US-0221607P.  
XX  
PR 02-MAY-2001; 2001US-0287724P.  
XX  
PA (COMP-) COMPUGEN INC.  
XX  
PI Shoshan A, Maeserman A, Mintz E, Mintz I, Faigler S;  
XX  
PI WPI; 2002-257383/30.  
XX  
DR WPI; 2002-257383/30.  
XX  
PT New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
XX  
PS Example 1; SEQ ID NO 10667; 47pp; English.  
XX  
CC The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridising selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The

CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcripts. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the primed specification, but was obtained in electronic format  
CC directly from WIGO at ftp.wigo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 60 BP; 21 A; 10 C; 20 G; 9 T; 0 U; 0 Other;  
XX  
Query Match 70.5%; Score 13.4; DB 6; Length 60;  
Best Local Similarity 93.3%; Pred. No. 5.6e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 CGGTATCTCTCTTAC 19  
DB 27 CTGTATCTCTTTCAC 13  
RESULT 23  
AAK93159/C  
ID AAK93159 standard; DNA; 20 BP.  
XX  
AC AAK93159;  
XX  
DT 13-SEP-1999 (first entry)  
XX  
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.  
XX  
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;  
KW neutralising epitope; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
OS Chlamydia pneumoniae.  
XX  
PN WO9927105-A2.  
XX  
PD 03-JUN-1999.  
XX  
PF 20-NOV-1998; 98WO-IB001890.  
XX  
PR 21-NOV-1997; 97FR-00014673.  
XX  
PR 04-NOV-1998; 98US-0107078P.  
XX  
PA (GENST ) GENSET.  
XX  
PI Griffats R;  
XX  
PI WPI; 1999-357842/30.  
XX  
DR WPI; 1999-357842/30.  
XX  
PT Genome sequence of Chlamydia pneumoniae.  
XX  
PS Page 1568; Disclosure; 1912pp; English.  
XX  
CC AAX1991-X97517 represent PCR primers used to amplify open reading frames  
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae  
CC (see AAX91990). C. pneumoniae causes respiratory disease such as  
CC pneumonia and bronchitis and is thought to be a contributing factor in  
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema  
CC nodosum or pharyngitis. The polypeptides encoded by the open reading  
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used  
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae  
CC nucleotide sequences can also be used as immunogenic compositions,

CC especially where the vector directs the expression of a neutralising  
 CC epitope of C. pneumoniae  
 XX  
 SQ Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 2; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 6.3e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCACGATCTCTCTTCA 19  
 |||||  
 DB 18 GCACGATCTCTCTTCA 1

RESULT 24  
 ADM72682/C  
 ID ADM72682 standard; RNA; 21 BP.  
 XX  
 AC ADM72682;  
 XX

DT 17-JUN-2004 (first entry)  
 XX  
 DE Human TASK120(1) siRNA antisense oligo.

XX TASK; tumour-associated kinase; cytostatic; tumour;  
 KM cell proliferative disorder; cancer; transgenic;  
 KM chromosome identification; tissue typing; TASK120; siRNA;  
 KM small interfering RNA; ds.  
 XX

OS Synthetic.

XX WO2004024063-A2.

XX 25-MAR-2004.

XX 05-SEP-2003; 2003WO-US027886.

XX 11-SEP-2002; 2002US-0410166P.

XX (GETH ) GENENTECH INC.

XX Davis DP, Desauvage FJ, Wood WJ, Zhang Z;  
 XX

XX WPI; 2004-282984/26.

PT New tumor-associated kinase nucleic acids and polypeptides, useful as  
 PT hybridization probes for isolating full length TASK DNA, for generating  
 PT transgenic animals, in chromosome identification, or for tissue typing.  
 XX

PS Example 4; Page 92; 140pp; English.

CC The invention relates to tumour-associated kinase (TASK) polypeptides  
 CC (I) and encoding polynucleotides. An antibody, oligopeptide (siRNA) or  
 CC organic molecule that binds to (II) is useful for treating a mammal  
 CC having a tumour comprising cells expressing (II). Antagonists of TASK are  
 CC useful for treating or preventing a cell proliferative disorder (e.g.  
 CC cancer) associated with increased expression or activity of (II). The  
 CC TASK polynucleotides and polypeptides may be used as hybridization probes  
 CC for isolating full length TASK DNA, for generating transgenic animals, in  
 CC chromosome identification, or for tissue typing. Sequences ADM72681-  
 CC ADM72686 represent small interfering RNA (siRNA) oligonucleotides  
 CC specific for TASK120.  
 XX

XX Sequence 21 BP; 4 A; 3 C; 10 G; 2 T; 2 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 12; Length 21;  
 Best Local Similarity 83.3%; Pred. No. 6.3e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGGATCTCTCTTCA 18  
 |||||  
 DB 19 CGCAGGATCTCTCTTCA 2

RESULT 25  
 ADL01767  
 ID ADL01767 standard; DNA; 29 BP.  
 XX  
 AC ADL01767;  
 XX

DT 06-MAY-2004 (first entry)  
 XX

DE Tobacco translationally controlled tumour protein, TCTP, PCR primer #3.  
 XX  
 XX ss; PCR; transgenic; plant; translationally controlled tumour protein;  
 KM agronomic phenotype; tobacco; TCTP; primer.  
 XX

OS Nicotiana tabacum.

XX US2003131384-A1.

XX 10-JUL-2003.

XX 16-JAN-2003; 2003US-00345599.

XX 22-SEP-2000; 2000KR-00055727.

XX 15-DEC-2000; 2000US-00737300.

XX (KANG/) KANG J.

XX (YUN/) YUN J.

XX (SONG/) SONG P.

XX (PARK/) PARK C.

XX Kang J, Yun J, Song P, Park C;  
 XX

XX WPI; 2003-635877/60.

XX New transgenic plant cell or its progeny transformed with a  
 XX PT translationally controlled tumor protein gene, useful for producing  
 XX PT higher plants exhibiting several desirable agronomic phenotypes.  
 XX

PS Disclosure; Page 6; 19pp; English.  
 XX  
 XX The invention relates to a transgenic plant cell or its progeny  
 CC transformed with and expressing a gene encoding the translationally  
 CC controlled tumor protein. The methods and compositions of the present  
 CC invention are useful for providing a new tool to accelerate the growth  
 CC rate of higher plants exhibiting several desirable agronomic phenotypes  
 CC by transforming cells of higher plants with the TCTP gene. The present  
 CC sequence represents a tobacco translationally controlled tumour protein,  
 CC TCTP, PCR primer.  
 XX

PS Sequence 29 BP; 6 A; 10 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 10; Length 29;  
 Best Local Similarity 83.3%; Pred. No. 6.5e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGGATCTCTCTTCA 18  
 |||||  
 DB 9 CGCAGGATCTCTCTTCA 26

RESULT 26  
 ADG76422  
 ID ADG76422 standard; DNA; 42 BP.  
 XX  
 AC ADG76422;  
 XX

DT 11-MAR-2004 (first entry)  
 XX

XX Primer #4 of the invention.

XX Gram-negative bacterium; Enter-Doudoroff pathway;  
 KM 6-phosphogluconate dehydratase; EDP;  
 KM 2-keto-3-deoxy-6-phosphogluconate aldolase; EDA; primer; ss.

```
XX OS Synthetic.
XX PN EP1352966-A2.
XX PD 15-OCT-2003.
XX PF 26-MAR-2003; 2003EP-00006936.
XX PR 27-MAR-2002; 2002JP-00088668.
XX PA (AJIN ) AJINOMOTO CO INC.
XX PI Hara Y, Izui H, Asano T, Watanabe Y, Nakamatsu T;
XX DR WPI; 2003-815163/77.
XX PT Production of L-amino acids in Gram-negative bacteria, useful
XX particularly for making glutamic acid, by increasing activity of Entner-
XX Doudoroff pathway enzymes.
XX PS Disclosure; SEQ ID NO 4; 18pp; English.
XX CC The present invention relates to the production of L-amino acids by
XX culturing a Gram-negative bacterium that contains the Entner-Doudoroff
XX pathway and has been modified so that activity of 6-phosphogluconate
XX dehydratase (EDD) and/or 2-keto-3-deoxy-6-phosphogluconate aldolase (EDA)
XX are increased. The method is specifically used to produce L-glutamic
XX acid. The present sequence represents a primer of the invention.
XX SQ Sequence 42 BP; 11 A; 13 C; 6 G; 12 T; 0 U; 0 Other;

Query Match          69.5%; Score 13.2; DB 10; Length 42;
Best Local Similarity 83.3%; Pred. No. 6.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTCA 18
   |||||
Db 2 CGCAGCATATCCCTTCA 19

RESULT 27
AD121021
ID AD121021 standard; DNA; 42 BP.
XX
XX AC AD121021;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE Citrate synthase (CS) promoter primer seq id 4.
XX
XX KM L-amino acid production; Entner-Doudoroff pathway;
XX 6-phosphogluconate dehydratase activity;
XX 2-keto-3-deoxy-6-phosphogluconate aldolase activity;
XX Entner-Doudoroff pathway; PCR; primer; ss; citrate synthase; CS;
XX promoter.
XX OS Corynebacterium glutamicum.
XX
XX PN US2003219882-A1.
XX
XX PD 27-NOV-2003.
XX
XX PF 26-MAR-2003; 2003US-00396488.
XX
XX PR 26-MAR-2003; 2003US-00396488.
XX
XX PA (AJIN ) AJINOMOTO CO INC.
XX
XX PI Hara Y, Izui H, Asano T, Watanabe Y, Nakamatsu T;
XX DR WPI; 2004-212658/20.
XX
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PT Production of L-amino acid comprises culturing microorganism, which is
PT Gram-negative bacterium having Entner-Doudoroff pathway and which has
PT been modified so that specific activities are enhanced.
XX
XX PS Example; SEQ ID NO 4; 12pp; English.
XX
XX CC The invention describes a method of L-amino acid production comprising
XX culturing a microorganism having an ability to produce an L-amino acid in
XX a medium. The microorganism is a Gram-negative bacterium having the
XX Entner-Doudoroff pathway and which has been modified so that 6-
XX phosphogluconate dehydratase activity or 2-keto-3-deoxy-6-
XX phosphogluconate aldolase activity, or activities of both are enhanced.
XX The method is useful for producing an L-amino acid, e.g. L-glutamic acid,
XX L-arginine, L-glutamine, L-proline, L-leucine, L-isoleucine, L-valine, or
XX L-alanine. The method improves productivity of L-amino acids in bacteria
XX from a viewpoint different from known techniques. This sequence
XX represents a primer used in the isolation of Brevibacterium
XX lactofermentum citrate synthase (CS) promoter used in the creation of an
XX Entner-Doudoroff pathway enhanced strain of Enterobacter agglomerans.
XX SQ Sequence 42 BP; 11 A; 13 C; 6 G; 12 T; 0 U; 0 Other;

Query Match          69.5%; Score 13.2; DB 12; Length 42;
Best Local Similarity 83.3%; Pred. No. 6.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTCA 18
   |||||
Db 2 CGCAGCATATCCCTTCA 19

RESULT 28
ADQ26310
ID ADQ26310 standard; DNA; 55 BP.
XX
XX AC ADQ26310;
XX
XX DT 23-SEP-2004 (first entry)
XX
XX DE Internal primer for siRNA expression construct M.
XX
XX KM Tetracycline; operator; RNA interference; gene silencing; promoter;
XX gene therapy; short interfering RNA; siRNA; PCR; primer; ss.
XX
XX OS Escherichia coli.
XX
XX PN WO2004056964-A2.
XX
XX PD 08-JUL-2004.
XX
XX PF 18-DEC-2003; 2003WO-US040548.
XX
XX PR 18-DEC-2002; 2002US-0434856P.
XX 28-AUG-2003; 2003US-0499313P.
XX
XX PA (GENP-) GENPATH PHARM INC.
XX
XX PI Winston W, O'hagan RC, Heyer J, Rideout W, Etemad-Moghadam B;
XX DR WPI; 2004-500295/47.
XX
XX PT New nucleic acid construct comprising a coding sequence for a small
XX interfering RNA molecule linked operably to a mammalian or viral
XX promoter, useful for treating gene-mediated diseases, such as cancer.
XX
XX PS Example; SEQ ID NO 42; 58pp; English.
XX
XX CC The present sequence is that of an internal primer used to insert a
XX tetracycline operator sequence ADQ26299 into a double-stranded siRNA
XX expression construct ADQ26303 designed for inducible RNA interference of
XX luciferase gene expression. The invention relates to recombinant vectors
XX containing inducible systems for expressing dsRNA molecules that
XX interfere with expression of target genes, including disease-related
XX
```

CC genes (e.g. cancer-related genes such as oncogenes and tumour suppressor  
CC genes). A claimed nucleic acid construct comprises a coding sequence for  
CC a siRNA molecule operably linked to a mammalian or viral promoter (e.g.  
CC the U6 promoter), in which the part of the nucleotide region between the  
CC proximal sequence element and the transcription initiation site of the  
CC promoter is replaced with an operator sequence (e.g. a tetracycline  
CC operator) controlled by a small molecule.  
XX  
SQ Sequence 55 BP; 21 A; 10 C; 11 G; 13 T; 0 U; 0 Other;  
Query Match 69.5%; Score 13.2; DB 12; Length 55;  
Best Local Similarity 83.3%; Pred. No. 7e+03; 3; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 GCACGGTATCTCTTATC 19  
2 GCACGGTATCTCTTATC 19  
Db 2 GCACGGTATCTCTTATC 19  
RESULT 29  
ADQ26317/c  
ID ADQ26317 standard; DNA; 60 BP.  
XX  
AC ADQ26317;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Internal primer for siRNA expression construct M.  
XX  
KM Tetracycline; operator; RNA interference; gene silencing; promoter;  
KM gene therapy; short interfering RNA; siRNA; PCR; primer; ss.  
XX  
OS Escherichia coli.  
XX  
PN WO2004056964-A2.  
XX  
PD 08-JUL-2004.  
XX  
PF 18-DEC-2003; 2003WO-US040548.  
XX  
PR 18-DEC-2002; 2002US-0434856P.  
XX  
PR 28-AUG-2003; 2003US-0499313P.  
XX  
PA (GENP-) GENPATH PHARM INC.  
XX  
PI Winston W, O'hagan RC, Heyer J, Rideout W, Etemad-Moghadam B;  
XX  
DR WPI; 2004-500295/47.  
XX  
XX  
PT New nucleic acid construct comprising a coding sequence for a small  
PT interfering RNA molecule linked operably to a mammalian or viral  
PT promoter, useful for treating gene-mediated diseases, such as cancer.  
XX  
PS Example; SEQ ID NO 49; 58bp; English.  
XX  
XX The present sequence is that of an internal primer used to insert a  
CC tetracycline operator sequence ADQ26299 into a double-stranded siRNA  
CC expression construct ADQ26303 designed for inducible RNA interference of  
CC luciferase gene expression. The invention relates to recombinant vectors  
CC containing inducible systems for expressing dsRNA molecules that  
CC interfere with expression of target genes, including disease-related  
CC genes (e.g. cancer-related genes such as oncogenes and tumour suppressor  
CC genes). A claimed nucleic acid construct comprises a coding sequence for  
CC a siRNA molecule operably linked to a mammalian or viral promoter (e.g.  
CC the U6 promoter), in which the part of the nucleotide region between the  
CC proximal sequence element and the transcription initiation site of the  
CC promoter is replaced with an operator sequence (e.g. a tetracycline  
CC operator) controlled by a small molecule.  
XX  
SQ Sequence 60 BP; 15 A; 16 C; 12 G; 17 T; 0 U; 0 Other;  
Query Match 69.5%; Score 13.2; DB 12; Length 60;  
Best Local Similarity 83.3%; Pred. No. 7.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 GCACGGTATCTCTTATC 19  
2 GCACGGTATCTCTTATC 19  
Db 39 GCACGGTATCTCTTATC 22  
RESULT 30  
ABN28183  
ID ABN28183 standard; DNA; 65 BP.  
XX  
AC ABN28183;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Rat spliced transcript detection oligonucleotide SEQ ID NO:931.  
XX  
KM Human; mouse; rat; splice transcript; detection; RNA transcript;  
KM splice variant; transcriptome; oligonucleotide library; ss.  
XX  
OS Rattus norvegicus.  
XX  
PN WO200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-IB001903.  
XX  
PR 28-JUL-2000; 2000US-0221607P.  
XX  
PR 02-MAY-2001; 2001US-0287724P.  
XX  
PA (COMP-) COMPUGEN INC.  
XX  
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX  
DR WPI; 2002-257383/30.  
XX  
XX  
PT New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
XX  
PS Example 1; SEQ ID NO 931; 47bp; English.  
XX  
XX The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridising selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcripts. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at fcp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 65 BP; 14 A; 24 C; 13 G; 14 T; 0 U; 0 Other;  
Query Match 69.5%; Score 13.2; DB 6; Length 65;  
Best Local Similarity 83.3%; Pred. No. 7.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
OY      1 CGCAGGTATCTCTTCA 18
DB      39 CGCAAGGATCTCTTCA 56

RESULT 31
ID      AEC23674/c
AC      AEC23674;
DT      20-OCT-2005 (first entry)
DE      Forward primer for amplification of genomic CAPN1, seq id 10.
XX      Meat; animal breeding; SNP detection;
KW      micromolar calcium activated neutral protease; mu-calpain; CAPN1; PCR;
XX      primer; ss.
OS      Bos taurus.
XX      US2005181373-A1.
XX      18-AUG-2005.
XX      18-DEC-2003; 2003US-00739904.
XX      18-DEC-2003; 2003US-00739904.
XX      (SMIT/) SMITH T P.
PA      (CASA/) CASAS E.
XX      Smith TP, Casas E;
XX      WPI; 2005-554241/56.
XX      Determining one or more alleles of the gene encoding micromolar calcium
PT      activated neutral protease effecting meat tenderness by assaying a sample
PT      of nucleic acids from a bovine for the presence of single nucleotide
PT      polymorphisms.
XX      Example 2; SEQ ID NO 10; 39pp; English.
XX      The invention relates to a method for determining one or more alleles of
CC      the gene encoding micromolar calcium activated neutral protease effecting
CC      meat tenderness in a bovine animal. The method comprises assaying a
CC      sample of nucleic acids (genomic DNA, cDNA, or RNA) from a bovine for the
CC      presence of one or more single nucleotide polymorphisms in the bovine
CC      CAPN1 gene encoding micromolar calcium activated neutral protease (mu-
CC      calpain). In determining one or more alleles of the gene encoding
CC      micromolar calcium activated neutral protease effecting meat tenderness
CC      in a bovine animal, the single nucleotide polymorphisms correspond to
CC      position 18 of exon 9 of AEC23667, position 17 of exon 14 of AEC23668,
CC      and position 185 on intron 19 of AEC23668. The method further comprises
CC      selecting those bovine for breeding where the polymorphism at position 18
CC      on exon 9 encodes alanine at amino acid 316 of the bovine micromolar
CC      calcium activated neutral protease. The method further comprises
CC      selecting those bovine for breeding where the polymorphism at position 17
CC      on exon 14 encodes valine at amino acid 530 of the bovine micromolar
CC      calcium activated neutral protease. The method further comprises
CC      selecting those bovine for breeding where the polymorphism at position
CC      185 on intron 19 comprises the presence of cytosine. In identifying one
CC      or more mutations in micromolar calcium activated neutral protease of
CC      bovine, the presence of alanine at amino acid 316, or valine at amino
CC      acid 539 of the bovine micromolar calcium activated neutral protease is
CC      indicative of increased meat tenderness. The method is useful for
CC      determining one or more alleles of the gene encoding micromolar calcium
CC      activated neutral protease effecting meat tenderness in a bovine animal.
CC      Sequences given in records for AEC23672-AEC23741 represent primers used
CC      in an example from the invention in the amplification of genomic CAPN1.
XX      Sequence 19 BP; 6 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
SQ
```

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Query Match      68.4%; Score 13; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3 CACGGTATCTCTCT 15
DB      17 CACGGTATCTCTCT 5

RESULT 32
ID      AAX36205/c
AC      AAX36205 standard; DNA; 22 BP.
XX      AAX36205;
XX      16-JUL-1999 (first entry)
XX      Primer used for sequencing of the wheat Rht gene.
DE      Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
XX      antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW      paclobutrazol; sequencing primer; ss.
XX      Synthetic.
XX      WO9909174-A1.
XX      25-FEB-1999.
XX      07-AUG-1998; 98WO-CB002383.
XX      13-AUG-1997; 97GB-00017192.
XX      (PLAN-) PLANT BIOSCIENCE LTD.
XX      Harberd NP, Richards DE, Peng J;
XX      WPI; 1999-181040/15.
XX      New Triticum aestivum polynucleotides - encode a polypeptide which
PT      provides inhibition of the growth of plants, which inhibition is
PT      antagonised by gibberellin, used to confer a dwarf phenotype.
XX      Claim 50; Page 51; 88pp; English.
XX      The specification describes polypeptides encoded by the Rht gene (and its
CC      homologues) that, when expressed in Triticum aestivum, inhibit growth of
CC      the plant. This growth inhibition is antagonised by gibberellin. The
CC      products can be used to provide Rht expression in plants, conferring a
CC      dwarf phenotype on a plant which is correctable by treatment with
CC      gibberellin. In addition, the products can be used to produce Rht mutant
CC      plants which are dwarfed compared with wild-type, the dwarfing being
CC      gibberellin-insensitive. Taller plants may be made by knocking out Rht or
CC      the relevant homologous gene in the plant of interest. Plants may be made
CC      which are resistant to compounds which inhibit gibberellin biosynthesis,
CC      such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis
CC      inhibitor to keep weeds dwarf but let crop plants grow tall. Primers
CC      AAX36199-K36233 were used in the sequencing of the Rht gene, in the
CC      course of the invention
XX      Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
SQ

Query Match      67.4%; Score 12.8; DB 2; Length 22;
Best Local Similarity 87.5%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      4 ACGGTATCTCTCTCAC 19
DB      19 ACGGTATCTCTCTCAC 4

RESULT 33
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AAK36207  
ID AAK36207 standard; DNA; 23 BP.  
XX  
AC AAK36207;  
XX  
DT 16-JUL-1999 (first entry)  
XX  
DE Primer used for sequencing of the wheat Rht gene.  
XX  
KM Rht gene; homologue: Triticum aestivum; wheat; growth inhibition;  
KM antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;  
KM paclobutrazol; sequencing primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9909174-A1.  
XX  
PD 25-FEB-1999.  
XX  
PF 07-AUG-1998; 98WO-GB002383.  
XX  
PR 13-AUG-1997; 97GB-00017192.  
XX  
PA (PLAN-) PLANT BIOSCIENCE LTD.  
XX  
PI Harberd NP, Richards DE, Peng J;  
XX  
DR WPI; 1999-181040/15.  
XX  
PT New Triticum aestivum polynucleotides - encode a polypeptide which  
PT provides inhibition of the growth of plants, which inhibition is  
PT antagonised by gibberellin, used to confer a dwarf phenotype.  
XX  
PS Claim 50; Page 51; 88pp; English.  
XX  
CC The specification describes polypeptides encoded by the Rht gene (and its  
CC homologues) that, when expressed in Triticum aestivum, inhibit growth of  
CC the plant. This growth inhibition is antagonised by gibberellin. The  
CC products can be used to provide Rht expression in plants, conferring a  
CC dwarf phenotype on a plant which is correctable by treatment with  
CC gibberellin. In addition, the products can be used to produce Rht mutant  
CC plants which are dwarfed compared with wild-type, the dwarfing being  
CC gibberellin-insensitive. Taller plants may be made by knocking out Rht or  
CC the relevant homologue gene in the plant of interest. Plants may be made  
CC which are resistant to compounds which inhibit gibberellin biosynthesis,  
CC such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis  
CC inhibitor to keep weeds dwarf but let crop plants grow tall. Primers  
CC AAK36199-X36233 were used in the sequencing of the Rht gene, in the  
CC course of the invention  
XX  
SQ Sequence 23 BP; 5 A; 7 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 67.4%; Score 12.8; DB 2; Length 23;  
Best Local Similarity 87.5%; Pred. No. 1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 ACGGTATCTCTTCAC 19  
DB 4 AGGGTATCTCTTCAC 19  
RESULT 34  
ACI49799/c  
ID ACI49799 standard; DNA; 25 BP.  
XX  
AC ACI49799;  
XX  
DT 13-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 49790.  
XX  
KM EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KM genetic variation; diallelic marker; polymorphism; human;

KM cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
DT 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFY-) AFEWETRIX INC.  
XX  
PI Miltmann MP;  
XX  
DR WPI; 2003-567953/53.  
XX  
PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
PS Claim 1; SEQ ID NO 49790; 9pp; English.  
XX  
CC The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying diallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation. In Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
XX  
SQ Sequence 25 BP; 7 A; 6 C; 6 G; 6 T; 0 U; 0 Other;  
Query Match 67.4%; Score 12.8; DB 9; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 ACGGTATCTCTTCAC 19  
DB 22 ACGGTATCTCTTCAC 7  
RESULT 35  
ACKI6942/c  
ID ACKI6942 standard; DNA; 25 BP.  
XX  
AC ACKI6942;  
XX  
DT 14-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 116923.  
XX  
KM EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KM genetic variation; diallelic marker; polymorphism; human;  
KM cross-species comparison.

OS Homo sapiens.  
XX US2003104410-A1.  
XX  
XX 05-JUN-2003.  
PD  
XX 15-MAR-2002; 2002US-00098263.  
PF  
XX 16-MAR-2001; 2001US-0276759P.  
PR  
XX (AFY-) AFFYMETRIX INC.  
PA  
XX Mitmann MP;  
PI  
XX WPI; 2003-567953/53.  
DR  
XX  
XX  
PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
PS  
XX Claim 1; SEQ ID NO 116923; 9pp; English.  
XX  
XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 25 BP; 11 A; 4 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 67.4%; Score 12.8; DB 9; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 ACGGATCTCCTTCAC 19  
DB 20 ACGGATCTCCTTC 5  
RESULT 36  
ACIO7104/C  
ID ACIO7104 standard; DNA; 25 BP.  
XX  
XX ACKO2223;  
AC  
XX  
XX 14-OCT-2003 (first entry)  
DT  
XX  
XX Human microarray DNA oligonucleotide SEQ ID NO 102204.  
DE  
XX  
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
XX Homo sapiens.  
XX

PN US2003104410-A1.  
XX  
XX 05-JUN-2003.  
PD  
XX 15-MAR-2002; 2002US-00098263.  
PF  
XX 16-MAR-2001; 2001US-0276759P.  
PR  
XX (AFY-) AFFYMETRIX INC.  
PA  
XX Mitmann MP;  
PI  
XX WPI; 2003-567953/53.  
DR  
XX  
XX  
PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
PS  
XX Claim 1; SEQ ID NO 102204; 9pp; English.  
XX  
XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 25 BP; 9 A; 5 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 67.4%; Score 12.8; DB 9; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 ACGGATCTCCTTCAC 19  
DB 17 ACGTATCTCTTGAC 2  
RESULT 37  
ACIO7104/C  
ID ACIO7104 standard; DNA; 25 BP.  
XX  
XX ACIO7104;  
AC  
XX  
XX 13-OCT-2003 (first entry)  
DT  
XX  
XX Human microarray DNA oligonucleotide SEQ ID NO 7095.  
DE  
XX  
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
XX Homo sapiens.  
XX  
XX US2003104410-A1.  
XX

PD 05-JUN-2003.  
 XX  
 PF 15-MAR-2002; 2002US-00098263.  
 XX  
 PR 16-MAR-2001; 2001US-0276759P.  
 XX  
 PA (AFFY-) AFFYMETRIX INC.  
 XX  
 PI Miltmann MP;  
 DR WPI; 2003-567953/53.  
 XX  
 PT New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 XX  
 PS Claim 1; SEQ ID NO 7095; 9pp; English.  
 XX  
 CC The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridization to a DNA library,  
 CC in analysis of genetic variation or in hybridization of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridizing at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridization. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying allelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in in situ hybridization, in Southern, Northern or dot-  
 CC blot hybridization to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at seqdata.uspto.gov/sequence.html  
 XX  
 SQ Sequence 25 BP; 11 A; 4 C; 4 G; 6 T; 0 U; 0 Other;  
 XX  
 QY Query Match 67.4%; Score 12.8; DB 9; Length 25;  
 Db Best Local Similarity 87.5%; Pred. No. 1e+04;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 4 ACGGTATCTCCTTCAC 19  
 17 ACGGTATCTACTTAC 2

PR 24-JAN-2002; 2002US-0352080P.  
 XX  
 PA (CHIR) CHIRON CORP.  
 XX  
 PI Walter AO, Reinhard C;  
 XX  
 DR WPI; 2003-636724/60.  
 XX  
 FT New Nek2 inhibitor, useful for preparing a composition for treating  
 FT neoplastic disease.  
 XX  
 PS Example 1; Page 55; 69pp; English.  
 XX  
 CC The present sequence is that of an oligonucleotide having the reverse  
 CC sequence of CHIR-103-6 (see ACF79218), an antisense oligonucleotide  
 CC targeted to human Nek2, a serine/threonine kinase involved in the  
 CC regulation of mitosis. The oligonucleotide was used to transfect control  
 CC cells in experiments designed to demonstrate the effect of antisense  
 CC oligonucleotides on Nek2 mRNA levels in SW610 tumour cells. The antisense  
 CC oligonucleotides inhibited Nek2 expression, inhibited cell proliferation  
 CC and induced release of lactate dehydrogenase, indicating cell death. The  
 CC invention provides Nek2 inhibitors, such as antisense oligonucleotides  
 CC (see ACF79213-22) and ribozymes, that can be used to treat neoplastic  
 CC disease (claimed). Methods are provided for modulating Nek2 expression  
 CC and for regulating cell growth, particularly tumour cell growth  
 XX  
 SQ Sequence 25 BP; 4 A; 9 C; 4 G; 8 T; 0 U; 0 Other;  
 XX  
 QY Query Match 67.4%; Score 12.8; DB 10; Length 25;  
 Db Best Local Similarity 87.5%; Pred. No. 1e+04;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 4 ACGGTATCTCCTTCAC 19  
 5 ACGGTGCTCCTTCAC 20

RESULT 39  
 ID AEA31091 standard; DNA; 31 BP.  
 AC AEA31091;  
 XX  
 DT 28-JUL-2005 (first entry)  
 XX  
 DE Hog cholera virus E2 antigen-related PCR primer 2.  
 XX  
 KW vaccine; livestock; vibrio cholerae infection; antibacterial;  
 KW gastrointestinal disease; infection; antigen; PCR; primer; ss.  
 XX  
 OS Classical swine fever virus.  
 OS Synthetic.  
 XX  
 PN CN1539989-A.  
 XX  
 PD 27-OCT-2004.  
 XX  
 PF 31-OCT-2003; 2003CN-01103408.  
 XX  
 PR 31-OCT-2003; 2003CN-01103408.  
 XX  
 PA (LANZ-) LANZHOU INST VETERINARY SURGEON CHINESE.  
 PA Liu X, Han X, Xie Q;  
 XX  
 PI Liu X, Han X, Xie Q;  
 XX  
 DR WPI; 2005-143329/16.  
 XX  
 PT Method for producing antigen protein in use for hog cholera vaccine.  
 XX  
 PS Claim 10; Page 3; 18pp; Chinese.  
 XX  
 CC The invention relates to a novel method for preparing an antigen protein  
 CC to be used in a Hog cholera vaccine. The method comprises extracting Hog



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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 07:17:58 ; Search time 610 Seconds  
(without alignments)  
382.730 Million cell updates/sec

Title: US-10-636-065-29  
Perfect score: 19  
Sequence: 1 cgcacgcatctcttcac 19

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24308366

Minimum DB seq length: 0  
Maximum DB seq length: 70

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications NA Main:\*

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- 2: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US09C\_PUBCOMB.seq:\*
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- 13: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/pcodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	19	100.0	19	US-10-636-065-29	Sequence 29, Appl
2	16.4	86.3	25	US-11-036-317-52322	Sequence 52322, A
3	16.4	86.3	25	US-11-036-317-753875	Sequence 753875, A
4	16	84.2	29	US-10-975-974-37	Sequence 37, Appl
5	15.4	81.1	25	US-10-719-900-135048	Sequence 135048, A
6	15.4	81.1	25	US-10-934-048A-13794	Sequence 13794, A
7	15.4	81.1	25	US-10-934-048A-62245	Sequence 62245, A
8	14.8	77.9	25	US-10-956-157-190898	Sequence 190898, A
9	14.8	77.9	25	US-10-956-157-206582	Sequence 206582, A
10	14.8	77.9	25	US-10-956-157-219118	Sequence 219118, A
11	14.8	77.9	25	US-10-956-157-256107	Sequence 256107, A
12	14.8	77.9	25	US-10-956-157-274442	Sequence 274442, A
13	14.8	77.9	25	US-11-036-317-402065	Sequence 402065, A
14	14.8	77.9	25	US-11-036-317-753874	Sequence 753874, A
15	14.4	75.8	19	US-11-083-784-787223	Sequence 787223, A
16	14.4	75.8	19	US-11-101-244-787223	Sequence 787223, A
17	14.4	75.8	25	US-10-719-900-429169	Sequence 429169, A

C 18	14.4	75.8	25	US-10-956-157-235288	Sequence 235288, A
C 19	14.4	75.8	25	US-11-060-756-282641	Sequence 282641, A
C 20	14.4	75.7	25	US-11-060-756-282642	Sequence 282642, A
C 21	14.2	74.7	22	US-10-310-914A-632065	Sequence 632065, A
C 22	14.2	74.7	23	US-10-310-914A-632083	Sequence 632083, A
C 23	14.2	74.7	25	US-11-036-317-811973	Sequence 811973, A
C 24	14.2	74.7	19	US-10-400-382-29	Sequence 29, Appl
C 25	14	73.7	19	US-10-400-382-107	Sequence 107, Appl
C 26	14	73.7	19	US-10-975-790-29	Sequence 29, Appl
C 27	14	73.7	19	US-10-975-790-107	Sequence 107, Appl
C 28	14	73.7	25	US-10-681-773-6411	Sequence 6411, Appl
C 29	14	73.7	25	US-10-681-773-19055	Sequence 19055, A
C 30	14	73.7	25	US-10-681-773-29718	Sequence 29718, A
C 31	14	73.7	25	US-10-681-773-93340	Sequence 93340, A
C 32	14	73.7	25	US-10-681-773-93502	Sequence 93502, A
C 33	13.8	72.6	25	US-10-719-956-157200	Sequence 157200, A
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C 36	13.8	72.6	25	US-10-719-900-135047	Sequence 135047, A
C 37	13.8	72.6	25	US-11-036-317-66927	Sequence 66927, A
C 38	13.8	72.6	25	US-11-036-317-488544	Sequence 488544, A
C 39	13.8	72.6	25	US-11-036-317-531529	Sequence 531529, A
C 40	13.8	72.6	25	US-11-036-317-691674	Sequence 691674, A
C 41	13.8	72.6	25	US-11-036-317-691675	Sequence 691675, A
C 42	13.8	72.6	25	US-11-036-317-826282	Sequence 826282, A
C 43	13.8	72.6	25	US-11-121-849-406343	Sequence 406343, A
C 44	13.8	72.6	25	US-11-121-849-419824	Sequence 419824, A
C 45	13.8	72.6	25	US-11-136-527-236094	Sequence 236094, A
C 46	13.8	72.6	59	US-08-781-986A-2496	Sequence 2496, Appl
C 47	13.8	72.6	59	US-10-329-624-2496	Sequence 2496, Appl
C 48	13.8	72.6	60	US-11-024-959-649	Sequence 649, Appl
C 49	13.4	70.5	19	US-11-083-784-798689	Sequence 798689, A
C 50	13.4	70.5	19	US-11-101-244-798689	Sequence 798689, A
C 51	13.4	70.5	25	US-11-060-756-212609	Sequence 212609, A
C 52	13.4	70.5	25	US-11-060-756-212610	Sequence 212610, A
C 53	13.4	70.5	25	US-11-121-849-530772	Sequence 530772, A
C 54	13.4	70.5	25	US-11-136-527-280358	Sequence 280358, A
C 55	13.4	70.5	50	US-11-175-859-20839	Sequence 20839, A
C 56	13.4	70.5	50	US-11-175-859-80293	Sequence 80293, A
C 57	13.4	70.5	60	US-09-908-975-10667	Sequence 10667, A
C 58	13.4	70.5	20	US-10-289-762-2460	Sequence 2460, Appl
C 59	13.2	69.5	24	US-10-310-914A-73969	Sequence 73969, A
C 60	13.2	69.5	25	US-10-719-956-1398597	Sequence 1398597, A
C 61	13.2	69.5	25	US-10-956-157-198597	Sequence 198597, A
C 62	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
C 63	13.2	69.5	25	US-10-956-157-293738	Sequence 293738, A
C 64	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
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C 70	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
C 71	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
C 72	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
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C 75	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
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C 77	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
C 78	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
C 79	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
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C 81	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
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C 85	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
C 86	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
C 87	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
C 88	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
C 89	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A
C 90	13.2	69.5	25	US-10-956-157-293739	Sequence 293739, A

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91 12.8 67.4 21 9 US-10-751-736-15045 Sequence 15045, A
92 12.8 67.4 21 9 US-10-751-736-30365 Sequence 30365, A
93 12.8 67.4 21 10 US-10-770-726-27103 Sequence 27103, A
94 12.8 67.4 21 10 US-10-770-726-27622 Sequence 27622, A
95 12.8 67.4 21 10 US-10-770-726-28015 Sequence 28015, A
96 12.8 67.4 21 10 US-10-770-726-28102 Sequence 28102, A
97 12.8 67.4 22 10 US-10-809-945-27 Sequence 27, Appl
98 12.8 67.4 22 11 US-10-310-914A-817705 Sequence 817705,
99 12.8 67.4 23 10 US-10-809-945-29 Sequence 29, Appl
c 100 12.8 67.4 23 11 US-10-310-914A-1379474 Sequence 1379474,
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## ALIGNMENTS

```
RESULT 1
US-10-636-065-29
/ Sequence 29, Application US/10636065
/ Publication No. US20040127694A1
/ GENERAL INFORMATION:
/ APPLICANT: Korneluk, Robert G.
/ APPLICANT: Lacasse, Eric
/ APPLICANT: Baird, Stephen
/ APPLICANT: Holcik, Martin
/ APPLICANT: Young, Sean
/ TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
/ TITLE OF INVENTION: Thereof
/ FILE REFERENCE: 07891/025005
/ CURRENT APPLICATION NUMBER: US/10/636,065
/ CURRENT FILING DATE: 2003-08-07
/ PRIOR APPLICATION NUMBER: 09/672,717
/ PRIOR FILING DATE: 2000-09-28
/ NUMBER OF SEQ ID NOS: 231
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 29
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: based on Homo sapiens
US-10-636-065-29
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Query Match 100.0%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGCAGGTATCTCTTCAC 19
DB 1 CGCAGGTATCTCTTCAC 19
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## RESULT 2

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US-11-036-317-52322/C
/ Sequence 52322, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 52322
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-52322
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Query Match 86.3%; Score 16.4; DB 13; Length 25;
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Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2 GCACGGTATCTCTTCAC 19
DB 25 GCACGGTATCTCTTCAC 8
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## RESULT 3

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US-11-036-317-753875/C
/ Sequence 753875, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 753875
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-753875
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Query Match 86.3%; Score 16.4; DB 13; Length 25;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2 GCACGGTATCTCTTCAC 19
DB 25 GCACGGTATCTCTTCAC 8
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## RESULT 4

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US-10-975-974-37/C
/ Sequence 37, Application US/10975974
/ Publication No. US20050148535A1
/ GENERAL INFORMATION:
/ APPLICANT: Lacasse, Eric
/ APPLICANT: McManus, Daniel
/ TITLE OF INVENTION: IAP NUCLEOBASE OLIGOMERS AND OLIGOMERIC
/ TITLE OF INVENTION: COMPLEXES AND USES THEREOF
/ FILE REFERENCE: 07891/038002
/ CURRENT APPLICATION NUMBER: US/10/975,974
/ CURRENT FILING DATE: 2004-10-28
/ PRIOR APPLICATION NUMBER: 60/516,192
/ PRIOR FILING DATE: 2003-10-30
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 37
/ LENGTH: 29
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 2, 5, 8, 17, 22, 27
/ OTHER INFORMATION: n = T or U
/ FEATURE:
/ OTHER INFORMATION: based on Homo sapiens
/ OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,
/ OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog
US-10-975-974-37
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Query Match 84.2%; Score 16; DB 10; Length 29;
Best Local Similarity 84.2%; Pred. NO. 3.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 GCACGGTATCTCTTCAC 19
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```
US-10-956-157-219118/c
; Sequence 219118, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 219118
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-219118

Query Match
Best Local Similarity 77.9%; Score 14.8; DB 10; Length 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTTCAC 19
DB 21 GAACGGTGTCTCCTTCAC 4

RESULT 11
US-10-956-157-256107/c
; Sequence 256107, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 256107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-256107

Query Match
Best Local Similarity 77.9%; Score 14.8; DB 10; Length 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTTCAC 19
DB 25 GAACGGTGTCTCCTTCAC 8

RESULT 12
US-10-956-157-274442/c
; Sequence 274442, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 274442
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-274442

Query Match
Best Local Similarity 77.9%; Score 14.8; DB 10; Length 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTTCAC 19
DB 24 GAACGGTGTCTCCTTCAC 7

RESULT 13
US-11-036-317-402065
; Sequence 402065, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 402065
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-402065

Query Match
Best Local Similarity 77.9%; Score 14.8; DB 13; Length 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTTCAC 19
DB 4 GCACGGTATCTCCTTCAC 21

RESULT 14
US-11-036-317-753874/c
; Sequence 753874, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 753874
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-753874

Query Match
Best Local Similarity 77.9%; Score 14.8; DB 13; Length 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTTCAC 19
DB 25 GCACGGTGTCTCCTTCAC 8
```



RESULT 15  
 US-11-083-784-787223/c  
 ; Sequence 787223, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 787223  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-787223

Query Match 75.8%; Score 14.4; DB 14; Length 19;  
 Best Local Similarity 93.8%; Pred. No. 2.4e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGATCTCCTTCA 18  
 |||||  
 DB 16 CACGGATCTCCTTCA 1

RESULT 16  
 US-11-101-244-787223/c  
 ; Sequence 787223, Application US/1101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 787223  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-101-244-787223

Query Match 75.8%; Score 14.4; DB 15; Length 19;  
 Best Local Similarity 93.8%; Pred. No. 2.4e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGATCTCCTTCA 18  
 |||||  
 DB 16 CACGGATCTCCTTCA 1

RESULT 17  
 US-10-719-900-429169/c  
 ; Sequence 429169, Application US/10719900  
 ; Publication No. US20050026164A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
 ; FILE REFERENCE: 3528.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,900  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,808  
 ; PRIOR FILING DATE: 2002-11-20  
 ; NUMBER OF SEQ ID NOS: 982914  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 429169  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-10-719-900-429169

Query Match 75.8%; Score 14.4; DB 9; Length 25;  
 Best Local Similarity 93.8%; Pred. No. 2.5e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACGGATCTCCTTC 17  
 |||||  
 DB 16 GCACGGATCTCCTTC 1

RESULT 18  
 US-10-956-157-235288/c  
 ; Sequence 235288, Application US/10956157  
 ; Publication No. US20050118625A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William  
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
 ; FILE REFERENCE: 031896-043000 (AM 101081)  
 ; CURRENT APPLICATION NUMBER: US/10/956,157  
 ; CURRENT FILING DATE: 2004-10-04  
 ; NUMBER OF SEQ ID NOS: 319805  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 235288  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Probe Sequence  
 US-10-956-157-235288

Query Match 75.8%; Score 14.4; DB 10; Length 25;  
 Best Local Similarity 93.8%; Pred. No. 2.5e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ACGGTATCTCCTTAC 19  
 |||||  
 DB 25 ACGGTATCTCCTTAC 10

RESULT 19  
 US-11-060-756-282641/c  
 ; Sequence 282641, Application US/11060756  
 ; Publication No. US20050221354A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William Martin  
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
 ; FILE REFERENCE: AM101083 (031896-042000)  
 ; CURRENT APPLICATION NUMBER: US/11/060,756  
 ; CURRENT FILING DATE: 2005-02-18  
 ; NUMBER OF SEQ ID NOS: 303284  
 ; SOFTWARE: PatentIn version 3.2

SEQ ID NO 282641  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-282641

Query Match 75.8%; Score 14.4; DB 13; Length 25;  
Best Local Similarity 93.8%; Pred. No. 2.5e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACGGATCTCTCTTCCAC 19  
Db 25 ACGGATCTCTCTTCCAC 10

RESULT 20  
US-11-060-756-282642/C  
Sequence 282642, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT APPLICATION NUMBER: US/11/060,756  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 282642  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-282642

Query Match 75.8%; Score 14.4; DB 13; Length 25;  
Best Local Similarity 93.8%; Pred. No. 2.5e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACGGATCTCTCTTCCAC 19  
Db 25 ACGGATCTCTCTTCCAC 10

RESULT 21  
US-10-310-914A-632065  
Sequence 632065, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kyuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 632065  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-632065

Query Match 74.7%; Score 14.2; DB 11; Length 22;  
Best Local Similarity 73.7%; Pred. No. 3.1e+03;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGATCTCTCTTCCAC 19  
Db 2 CGCAGGATCTCTCTTCCAC 20

RESULT 22  
US-10-310-914A-632083  
Sequence 632083, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kyuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 632083  
LENGTH: 23  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-632083

Query Match 74.7%; Score 14.2; DB 11; Length 23;  
Best Local Similarity 73.7%; Pred. No. 3.1e+03;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGATCTCTCTTCCAC 19  
Db 4 CGCAGGATCTCTCTTCCAC 22

RESULT 23  
US-11-036-317-811973  
Sequence 811973, Application US/11036317  
Publication No. US20050214823A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Alan  
APPLICANT: Blume, John  
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
FILE REFERENCE: 3654.1  
CURRENT APPLICATION NUMBER: US/11/036,317  
CURRENT FILING DATE: 2005-01-13  
PRIOR APPLICATION NUMBER: US 60/536,639  
PRIOR FILING DATE: 2004-01-13  
NUMBER OF SEQ ID NOS: 991174  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 811973  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-11-036-317-811973

Query Match 74.7%; Score 14.2; DB 13; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGATCTCTCTTCCAC 19  
Db 6 CACACGGTCTCTTCCAC 24

RESULT 24  
US-10-400-382-29  
Sequence 29, Application US/10400382  
Publication No. US20030190659A1  
GENERAL INFORMATION:  
APPLICANT: Lacasse, Eric  
APPLICANT: McManus, Daniel  
APPLICANT: Durkin, Jonathan P.  
TITLE OF INVENTION: Antisense iAP Nucleobase Oligomers and  
FILE REFERENCE: 07891/025004  
CURRENT APPLICATION NUMBER: US/10/400,382  
CURRENT FILING DATE: 2003-03-27  
PRIOR APPLICATION NUMBER: US 60/367,853

Query Match 74.7%; Score 14.2; DB 13; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGATCTCTCTTCCAC 19  
Db 6 CACACGGTCTCTTCCAC 24

RESULT 24  
US-10-400-382-29  
Sequence 29, Application US/10400382  
Publication No. US20030190659A1  
GENERAL INFORMATION:  
APPLICANT: Lacasse, Eric  
APPLICANT: McManus, Daniel  
APPLICANT: Durkin, Jonathan P.  
TITLE OF INVENTION: Antisense iAP Nucleobase Oligomers and  
FILE REFERENCE: 07891/025004  
CURRENT APPLICATION NUMBER: US/10/400,382  
CURRENT FILING DATE: 2003-03-27  
PRIOR APPLICATION NUMBER: US 60/367,853

PRIOR FILING DATE: 2002-03-27  
NUMBER OF SEQ ID NOS: 460  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 29  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: based on Homo sapiens.  
OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,  
OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 8, 10, 12, 15, 16  
OTHER INFORMATION: n = T or U  
US-10-400-382-29

Query Match 73.7%; Score 14; DB 7; Length 19;  
Best Local Similarity 73.7%; Pred. No. 3.9e+03;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCCTTCAC 19  
Db 1 CGCAGCGNANCCNNCACC 19

RESULT 25  
US-10-400-382-107  
Sequence 107, Application US/10400382  
Publication No. US20030190659A1  
GENERAL INFORMATION:  
APPLICANT: Lacasse, Eric  
APPLICANT: McManus, Daniel  
TITLE OF INVENTION: Antisense IAP Nucleobase Oligomers and  
FILE REFERENCE: 07891/025004  
CURRENT APPLICATION NUMBER: US/10/400,382  
CURRENT FILING DATE: 2003-03-27  
PRIOR APPLICATION NUMBER: US 60/367,853  
PRIOR FILING DATE: 2002-03-27  
NUMBER OF SEQ ID NOS: 460  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 107  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: based on Homo sapiens.  
OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,  
OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 8, 10, 12, 15, 16  
OTHER INFORMATION: n = T or U  
US-10-400-382-107

Query Match 73.7%; Score 14; DB 7; Length 19;  
Best Local Similarity 73.7%; Pred. No. 3.9e+03;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCCTTCAC 19  
Db 1 CGCAGCGNANCCNNCACC 19

RESULT 26  
US-10-975-790-29  
Sequence 29, Application US/10975790  
Publication No. US20050119217A1  
GENERAL INFORMATION:  
APPLICANT: Lacasse, Eric  
APPLICANT: McManus, Daniel

APPLICANT: Durkin, Jonathan, P.  
TITLE OF INVENTION: METHODS AND REAGENTS FOR THE TREATMENT  
OF PROLIFERATIVE DISEASES  
FILE REFERENCE: 07891/039002  
CURRENT APPLICATION NUMBER: US/10/975,790  
CURRENT FILING DATE: 2004-10-28  
PRIOR APPLICATION NUMBER: 60/516,263  
PRIOR FILING DATE: 2003-10-30  
NUMBER OF SEQ ID NOS: 490  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 29  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: based on Homo sapiens.  
OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,  
OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 8, 10, 12, 15, 16  
OTHER INFORMATION: n = T or U  
US-10-975-790-29

Query Match 73.7%; Score 14; DB 10; Length 19;  
Best Local Similarity 73.7%; Pred. No. 3.9e+03;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCCTTCAC 19  
Db 1 CGCAGCGNANCCNNCACC 19

RESULT 27  
US-10-975-790-107  
Sequence 107, Application US/10975790  
Publication No. US20050119217A1  
GENERAL INFORMATION:  
APPLICANT: Lacasse, Eric  
APPLICANT: McManus, Daniel  
TITLE OF INVENTION: METHODS AND REAGENTS FOR THE TREATMENT  
OF PROLIFERATIVE DISEASES  
FILE REFERENCE: 07891/039002  
CURRENT APPLICATION NUMBER: US/10/975,790  
CURRENT FILING DATE: 2004-10-28  
PRIOR APPLICATION NUMBER: 60/516,263  
PRIOR FILING DATE: 2003-10-30  
NUMBER OF SEQ ID NOS: 490  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 107  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: based on Homo sapiens.  
OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,  
OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 8, 10, 12, 15, 16  
OTHER INFORMATION: n = T or U  
US-10-975-790-107

Query Match 73.7%; Score 14; DB 10; Length 19;  
Best Local Similarity 73.7%; Pred. No. 3.9e+03;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCCTTCAC 19  
Db 1 CGCAGCGNANCCNNCACC 19

```
RESULT 28
US-10-681-773-6411/c
; Sequence 6411, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 6411
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-6411
```

```
Query Match          73.7%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 ACGGTATCTCCTTC 17
Db      16 ACGGTATCTCCTTC 3
```

```
RESULT 29
US-10-681-773-19055/c
; Sequence 19055, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 19055
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-19055
```

```
Query Match          73.7%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 ACGGTATCTCCTTC 17
Db      15 ACGGTATCTCCTTC 2
```

```
RESULT 30
US-10-681-773-29718/c
; Sequence 29718, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 29718
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-29718
```

```
Query Match          73.7%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 ACGGTATCTCCTTC 17
Db      19 ACGGTATCTCCTTC 6
```

```
RESULT 31
US-10-681-773-93340/c
; Sequence 93340, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 93340
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-93340
```

```
Query Match          73.7%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 ACGGTATCTCCTTC 17
Db      20 ACGGTATCTCCTTC 7
```

```
RESULT 32
US-10-681-773-95502/c
; Sequence 95502, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
```

```
FILE REFERENCE: 3522.2
CURRENT APPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: 60/470,475
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 60/417,190
PRIOR FILING DATE: 2002-10-08
NUMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 95502
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-681-773-95502

Query Match
Best Local Similarity 73.7%; Score 14; DB 8; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ACAGTATCTCTTC 17
Db 18 ACAGTATCTCTTC 5

RESULT 33
US-10-719-956-157200
Sequence 157200, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 157200
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-157200

Query Match
Best Local Similarity 72.6%; Score 13.8; DB 8; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CACGATCTCTCTC 19
Db 4 CACGATCTCTCTC 20

RESULT 34
US-10-719-956-235231/c
Sequence 235231, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 235231
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-235231
```

```
Query Match
Best Local Similarity 72.6%; Score 13.8; DB 8; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CACGATCTCTCTC 19
Db 19 CTCGATCTCTCTC 3

RESULT 35
US-10-719-956-317851/c
Sequence 317851, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 317851
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-317851

Query Match
Best Local Similarity 72.6%; Score 13.8; DB 8; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCAGGATCTCTCTCA 18
Db 24 GCAGGATCTCTCTCA 8

RESULT 36
US-10-719-900-135047
Sequence 135047, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 135047
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-135047

Query Match
Best Local Similarity 72.6%; Score 13.8; DB 9; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCAGGATCTCTCTCA 18
Db 8 GCAGGATCTCTCTCA 24

RESULT 37
US-11-036-317-66927/c
Sequence 66927, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
```

```

; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 66927
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-66927
```

```

Query Match      72.6%; Score 13.8; DB 13; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

Qy      2 GCACGGTATCTCTTCA 18
Db      21 GCACGGCATCTTCTTCA 5
```

```

RESULT 38
US-11-036-317-488544/c
; Sequence 488544, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 488544
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-488544
```

```

Query Match      72.6%; Score 13.8; DB 13; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

Qy      2 GCACGGTATCTCTTCA 18
Db      21 GCACGGCATCTTCTTCA 5
```

```

RESULT 39
US-11-036-317-531529/c
; Sequence 531529, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 531529
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
```

```

US-11-036-317-531529
```

```

Query Match      72.6%; Score 13.8; DB 13; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

Qy      2 GCACGGTATCTCTTCA 18
Db      20 GTACGGATCTCTTCA 4
```

```

RESULT 40
US-11-036-317-691674/c
; Sequence 691674, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 691674
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-691674
```

```

Query Match      72.6%; Score 13.8; DB 13; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

Qy      2 GCACGGTATCTCTTCA 18
Db      19 GTACGGATCTCTTCA 3
```

```

Search completed: August 10, 2006, 08:37:29
Job time : 613 secs
```

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model1

Run on: August 10, 2006, 08:07:12 ; Search time 87.6667 Seconds  
(without alignments)  
344.184 Million cell updates/sec

Title: US-10-636-065-29  
Perfect score: 19  
Sequence: 1 cgcacgctactctcttcac 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 3071694

Minimum DB seq length: 0  
Maximum DB seq length: 70

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

1: Published Applications NA.New:\*  
2: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
3: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
4: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
5: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
6: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
7: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
8: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US11\_NEW\_PUB.seq2:\*  
9: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US11\_NEW\_PUB.seq3:\*  
10: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US60\_NEW\_PUB.seq:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query #	Match Length	ID	Description
1	13.4	70.5	25	US-11-348-413-698648	Sequence 698648,
2	13.4	70.5	25	US-11-348-413-698649	Sequence 698649,
3	13.4	70.5	25	US-11-348-413-698650	Sequence 698650,
4	13.2	69.5	25	US-11-217-529-106544	Sequence 106544,
5	13.2	69.5	25	US-11-348-413-45911	Sequence 45911, A
6	13.2	69.5	25	US-11-348-413-45912	Sequence 45912, A
7	13.2	69.5	25	US-11-348-413-634497	Sequence 634497,
8	13.2	69.5	25	US-11-281-495-4	Sequence 4, Appl1
9	13	68.4	25	US-11-348-413-684532	Sequence 684532,
10	12.8	67.4	25	US-11-217-529-164386	Sequence 164386,
11	12.8	67.4	25	US-11-348-413-251718	Sequence 251718,
12	12.8	67.4	25	US-11-348-413-251719	Sequence 251719,
13	12.8	67.4	25	US-11-348-413-865498	Sequence 865498,
14	12.8	67.4	25	US-11-297-810-26	Sequence 26, Appl
15	12.8	67.4	25	US-11-314-941-26	Sequence 141152,
16	12.6	66.3	25	US-11-217-529-141152	Sequence 141152,
17	12.6	66.3	25	US-11-348-413-198939	Sequence 198939,
18	12.6	66.3	25	US-11-348-413-810033	Sequence 810033,
19	12.6	66.3	50	US-10-511-937-136	Sequence 136, App
20	12.6	66.3	50	US-10-554-711-392	Sequence 392, App
21	12.4	65.3	25	US-11-348-413-257483	Sequence 257483,
22	12.4	65.3	25	US-11-348-413-257484	Sequence 257484,
23	12.4	65.3	25	US-11-348-413-257485	Sequence 257485,

24	12.4	65.3	25	US-11-348-413-257486	Sequence 257486,
25	12.4	65.3	25	US-11-348-413-857440	Sequence 857440,
26	12.4	65.3	25	US-11-348-413-871598	Sequence 871598,
27	12.4	65.3	25	US-11-348-413-871599	Sequence 871599,
28	12.4	65.3	31	US-11-240-651-32	Sequence 32, Appl
29	12.4	65.3	60	US-11-240-651-14	Sequence 14, Appl
30	12.2	64.2	25	US-11-348-413-429142	Sequence 429142,
31	12.2	64.2	25	US-11-348-413-636110	Sequence 636110,
32	12.2	64.2	25	US-11-348-413-661408	Sequence 661408,
33	12.2	64.2	25	US-11-348-413-661409	Sequence 661409,
34	12.2	64.2	25	US-11-348-413-701530	Sequence 701530,
35	12.2	64.2	25	US-11-348-413-812478	Sequence 812478,
36	12.2	64.2	25	US-11-348-413-900939	Sequence 900939, A
37	12	63.2	25	US-11-348-413-90100	Sequence 90100, A
38	12	63.2	25	US-11-348-413-90100	Sequence 90100, A
39	12	63.2	25	US-11-348-413-208705	Sequence 208705,
40	12	63.2	25	US-11-348-413-208706	Sequence 208706,
41	12	63.2	25	US-11-348-413-208707	Sequence 208707,
42	12	63.2	25	US-11-348-413-208708	Sequence 208708,
43	12	63.2	25	US-11-348-413-208709	Sequence 208709,
44	12	63.2	25	US-11-348-413-443433	Sequence 443433,
45	12	63.2	25	US-11-348-413-443434	Sequence 443434,
46	12	63.2	25	US-11-348-413-443435	Sequence 443435,
47	12	63.2	25	US-11-348-413-597819	Sequence 597819,
48	12	63.2	25	US-11-348-413-597820	Sequence 597820,
49	12	63.2	25	US-11-348-413-597821	Sequence 597821,
50	12	63.2	25	US-11-348-413-597822	Sequence 597822,
51	12	63.2	25	US-11-348-413-597818	Sequence 597818,
52	12	63.2	25	US-11-348-413-1267795	Sequence 1267795,
53	12	63.2	25	US-11-348-413-1267796	Sequence 1267796,
54	12	63.2	25	US-11-348-413-1268372	Sequence 1268372,
55	12	63.2	25	US-11-348-413-1268373	Sequence 1268373,
56	12	63.2	25	US-11-348-413-1268374	Sequence 1268374,
57	12	63.2	25	US-11-348-413-820167	Sequence 820167,
58	12	63.2	25	US-11-348-413-1085116	Sequence 1085116,
59	12	63.2	25	US-11-348-413-1267795	Sequence 1267795,
60	12	63.2	25	US-11-348-413-1267796	Sequence 1267796,
61	12	63.2	25	US-11-348-413-1268372	Sequence 1268372,
62	12	63.2	25	US-11-348-413-1268373	Sequence 1268373,
63	12	63.2	25	US-11-348-413-1268374	Sequence 1268374,
64	12	63.2	25	US-11-348-413-820167	Sequence 820167,
65	12	63.2	25	US-11-348-413-1085116	Sequence 1085116,
66	12	63.2	25	US-11-348-413-1267795	Sequence 1267795,
67	12	63.2	25	US-11-348-413-1267796	Sequence 1267796,
68	12	63.2	25	US-11-348-413-1268372	Sequence 1268372,
69	12	63.2	25	US-11-348-413-1268373	Sequence 1268373,
70	12	63.2	25	US-11-348-413-1268374	Sequence 1268374,
71	11.8	62.1	25	US-11-217-529-145056	Sequence 145056, A
72	11.8	62.1	25	US-11-217-529-141477	Sequence 141477,
73	11.8	62.1	25	US-11-217-529-145207	Sequence 145207,
74	11.8	62.1	25	US-11-217-529-147920	Sequence 147920,
75	11.8	62.1	25	US-11-217-529-160598	Sequence 160598,
76	11.8	62.1	25	US-11-217-529-186459	Sequence 186459,
77	11.8	62.1	25	US-11-348-413-101807	Sequence 101807,
78	11.8	62.1	25	US-11-348-413-238982	Sequence 238982,
79	11.8	62.1	25	US-11-348-413-238983	Sequence 238983,
80	11.8	62.1	25	US-11-348-413-238984	Sequence 238984,
81	11.8	62.1	25	US-11-348-413-238985	Sequence 238985,
82	11.8	62.1	25	US-11-348-413-251717	Sequence 251717,
83	11.8	62.1	25	US-11-348-413-449916	Sequence 449916,
84	11.8	62.1	25	US-11-348-413-449917	Sequence 449917,
85	11.8	62.1	25	US-11-348-413-449918	Sequence 449918,
86	11.8	62.1	25	US-11-348-413-449919	Sequence 449919,
87	11.8	62.1	25	US-11-348-413-449920	Sequence 449920,
88	11.8	62.1	25	US-11-348-413-615337	Sequence 615337,
89	11.8	62.1	25	US-11-348-413-615338	Sequence 615338,
90	11.8	62.1	25	US-11-348-413-636337	Sequence 636337,
91	11.8	62.1	25	US-11-348-413-693357	Sequence 693357,
92	11.8	62.1	25	US-11-348-413-791363	Sequence 791363,
93	11.8	62.1	25	US-11-348-413-794460	Sequence 794460,
94	11.8	62.1	25	US-11-348-413-831294	Sequence 831294,
95	11.8	62.1	25	US-11-348-413-851672	Sequence 851672,
96	11.8	62.1	25	US-11-348-413-851673	Sequence 851673,

C	97	11.8	62.1	25	9	US-11-348-413-851674
c	98	11.8	62.1	25	9	US-11-348-413-877430
c	99	11.8	62.1	25	9	US-11-348-413-1035845
c	100	11.8	62.1	25	9	US-11-348-413-1091924

## ALIGNMENTS

RESULT 1  
US-11-348-413-698648/c

```

; Sequence 698648, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 698648
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc.feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2598; WANO1UNSL_at; Start 163; Stop 187;
; OTHER INFORMATION: 11111100000000
US-11-348-413-698648

```

Query Match 70.5%; Score 13.4; DB 9; Length 25;  
Best Local Similarity 93.3%; Pred. No. 6.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACGTAATCTCCTT 16  
Db 25 GCACGTAATCTCCTT 11

RESULT 2  
US-11-348-413-698649/c

```

; Sequence 698649, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 698649
; LENGTH: 25

```

```

; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc.feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2598; WANO1UNSL_at; Start 164; Stop 188;
US-11-348-413-698649

```

US-11-348-413-698649

Query Match 70.5%; Score 13.4; DB 9; Length 25;  
Best Local Similarity 93.3%; Pred. No. 6.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACGTAATCTCCTT 16  
Db 24 GCACGTAATCTCCTT 10

RESULT 3

```

US-11-348-413-698650/c
; Sequence 698650, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 698650
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc.feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2598; WANO1UNSL_at; Start 167; Stop 191;
; OTHER INFORMATION: 11111100000000
US-11-348-413-698650

```

Query Match 70.5%; Score 13.4; DB 9; Length 25;  
Best Local Similarity 93.3%; Pred. No. 6.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACGTAATCTCCTT 16  
Db 21 GCACGTAATCTCCTT 7

RESULT 4

```

US-11-217-529-106544/c
; Sequence 106544, Application US/11217529
; Publication No. US2006099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

```



TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: S-38-285  
CURRENT APPLICATION NUMBER: US/11/217,529  
CURRENT FILING DATE: 2005-09-02  
PRIOR APPLICATION NUMBER: US 10/932,182  
PRIOR FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 106544  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Saccharomyces pastorianus  
US-11-217-529-106544

Query Match 69.5%; Score 13.2; DB 8; Length 25;  
Best Local Similarity 83.3%; Pred. No. 8.1e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCCTTCA 18  
Db 25 CTCACGGTACTCCTTGA 8

RESULT 5  
US-11-348-413-45911/c  
Sequence 45911, Application US/11348413  
Publication No. US20060160121A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
APPLICANT: Murphy, Ellen  
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
FILE REFERENCE: 031896-084100 (AM 101724)  
CURRENT APPLICATION NUMBER: US/11/348,413  
CURRENT FILING DATE: 2006-02-07  
PRIOR APPLICATION NUMBER: PCT/US05/035471  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 11/243,445  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 60/615,573  
PRIOR FILING DATE: 2004-10-05  
NUMBER OF SEQ ID NOS: 1276209  
SEQ ID NO 45911  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: probe  
NAME/KEY: misc feature  
LOCATION: (1)-(25)  
OTHER INFORMATION: SEQ ID NO: 779; WAN01UJNW; Start 469; Stop 493;  
US-11-348-413-45911

Query Match 69.5%; Score 13.2; DB 9; Length 25;  
Best Local Similarity 83.3%; Pred. No. 8.1e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCCTTCA 18  
Db 20 CGCAGGTATCTMAATCA 3

RESULT 6  
US-11-348-413-45912/c  
Sequence 45912, Application US/11348413  
Publication No. US20060160121A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
APPLICANT: Murphy, Ellen

APPLICANT: Olmsted, Stephen  
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
FILE REFERENCE: 031896-084100 (AM 101724)  
CURRENT APPLICATION NUMBER: US/11/348,413  
CURRENT FILING DATE: 2006-02-07  
PRIOR APPLICATION NUMBER: PCT/US05/035471  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 11/243,445  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 60/615,573  
PRIOR FILING DATE: 2004-10-05  
NUMBER OF SEQ ID NOS: 1276209  
SEQ ID NO 45912  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: probe  
NAME/KEY: misc feature  
LOCATION: (1)-(25)  
OTHER INFORMATION: SEQ ID NO: 779; WAN01UJNW; Start 470; Stop 494;  
US-11-348-413-45912

Query Match 69.5%; Score 13.2; DB 9; Length 25;  
Best Local Similarity 83.3%; Pred. No. 8.1e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCCTTCA 18  
Db 19 CGCAGGTATCTMAATCA 2

RESULT 7  
US-11-348-413-634497/c  
Sequence 634497, Application US/11348413  
Publication No. US20060160121A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
APPLICANT: Murphy, Ellen  
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
FILE REFERENCE: 031896-084100 (AM 101724)  
CURRENT APPLICATION NUMBER: US/11/348,413  
CURRENT FILING DATE: 2006-02-07  
PRIOR APPLICATION NUMBER: PCT/US05/035471  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 11/243,445  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 60/615,573  
PRIOR FILING DATE: 2004-10-05  
NUMBER OF SEQ ID NOS: 1276209  
SEQ ID NO 634497  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: probe  
NAME/KEY: misc feature  
LOCATION: (1)-(25)  
OTHER INFORMATION: SEQ ID NO: 779; WAN01UJNW; Start 467; Stop 491;  
US-11-348-413-634497

Query Match 69.5%; Score 13.2; DB 9; Length 25;  
Best Local Similarity 83.3%; Pred. No. 8.1e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCCTTCA 18

Db 22 CGCAGCATCTTAATCA 5

## RESULT 8

US-11-281-495-4  
; Sequence 4, Application US/11281495  
; Publication No. US20060115878A1  
; GENERAL INFORMATION:  
; APPLICANT: HARA, YOSHIHIKO  
; APPLICANT: IZUI, HIROSHI  
; APPLICANT: ASANO, TAKAHIRO  
; APPLICANT: WATANABE, YASUYUKI  
; APPLICANT: NAKAMATSU, TSUYOSHI  
; TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACID  
; FILE REFERENCE: 235806US0  
; CURRENT APPLICATION NUMBER: US/11/281,495  
; PRIOR FILING DATE: 2005-11-18  
; PRIOR APPLICATION NUMBER: US/10/396,488  
; PRIOR FILING DATE: 2003-03-26  
; PRIOR APPLICATION NUMBER: JP 2002-088668  
; PRIOR FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 42  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-281-495-4

## Query Match

Best Local Similarity 69.5%; Score 13.2; DB 8; Length 42;  
Best Local Similarity 83.3%; Pred. No. 8.e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGCATCTCTCTTCA 18  
Db 2 CGCAGCATCTCTCTTCA 19

## RESULT 9

US-11-348-413-684532/C  
; Sequence 684532, Application US/11348413  
; Publication No. US20060160121A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; APPLICANT: Murphy, Ellen  
; APPLICANT: Olmsted, Stephen  
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
; FILE REFERENCE: 031896-084100 (AM 101724)  
; CURRENT APPLICATION NUMBER: US/11/348,413  
; CURRENT FILING DATE: 2006-02-07  
; PRIOR APPLICATION NUMBER: PCT/US05/035471  
; PRIOR FILING DATE: 2005-10-05  
; PRIOR APPLICATION NUMBER: US 11/243,445  
; PRIOR FILING DATE: 2005-10-05  
; PRIOR APPLICATION NUMBER: US 60/615,573  
; PRIOR FILING DATE: 2004-10-05  
; NUMBER OF SEQ ID NOS: 1276209  
; SEQ ID NO 684532  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: probe  
; NAME/KEY: misc feature  
; LOCATION: (1)..(25)  
; OTHER INFORMATION: SEQ ID NO: 2204; WANO1UXA\_at; Start 652; Stop 676;  
US-11-348-413-684532

Query Match 68.4%; Score 13; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CACGGTATCTCCT 15  
Db 18 CACGGTATCTCCT 6

## RESULT 10

US-11-217-529-164386  
; Sequence 164386, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: KODAMA, YUKIO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 164386  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-164386

## Query Match

Best Local Similarity 67.4%; Score 12.8; DB 8; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTTC 17  
Db 4 GCACGGTATCTCCTTC 19

## RESULT 11

US-11-348-413-251718  
; Sequence 251718, Application US/11348413  
; Publication No. US20060160121A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; APPLICANT: Murphy, Ellen  
; APPLICANT: Olmsted, Stephen  
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
; FILE REFERENCE: 031896-084100 (AM 101724)  
; CURRENT APPLICATION NUMBER: US/11/348,413  
; CURRENT FILING DATE: 2006-02-07  
; PRIOR APPLICATION NUMBER: PCT/US05/035471  
; PRIOR FILING DATE: 2005-10-05  
; PRIOR APPLICATION NUMBER: US 11/243,445  
; PRIOR FILING DATE: 2005-10-05  
; PRIOR APPLICATION NUMBER: US 60/615,573  
; PRIOR FILING DATE: 2004-10-05  
; NUMBER OF SEQ ID NOS: 1276209  
; SEQ ID NO 251718  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: probe  
; NAME/KEY: misc feature  
; LOCATION: (1)..(25)  
; OTHER INFORMATION: SEQ ID NO: 7331; WANO1UM6N; Start 11; Stop 35;  
US-11-348-413-251718

OTHER INFORMATION: 00000001100000  
US-11-348-413-251718

Query Match 67.4%; Score 12.8; DB 9; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CACGATCTCTCTCA 18  
DB 10 CACGATCTCTCTCA 25

## RESULT 12

US-11-348-413-251719  
Sequence 251719, Application US/11348413  
Publication No. US20060160121A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
APPLICANT: Murphy, Ellen  
APPLICANT: Olmsted, Stephen  
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
FILE REFERENCE: 031896-084100 (AM 101724)  
CURRENT FILING DATE: 2006-02-07  
PCT/US05/035471  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 11/243,445  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 60/615,573  
PRIOR FILING DATE: 2004-10-05  
NUMBER OF SEQ ID NOS: 1276209  
SEQ ID NO 251719  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: probe  
NAME/KEY: misc\_feature  
LOCATION: (1..(25))  
OTHER INFORMATION: SEQ ID NO: 7331; WANO1UM6N; Start 12; Stop 36;  
US-11-348-413-251719

Query Match 67.4%; Score 12.8; DB 9; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CACGATCTCTCTCA 18  
DB 9 CACGATCTCTCTCA 24

## RESULT 13

US-11-348-413-865498  
Sequence 865498, Application US/11348413  
Publication No. US20060160121A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
APPLICANT: Murphy, Ellen  
APPLICANT: Olmsted, Stephen  
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
FILE REFERENCE: 031896-084100 (AM 101724)  
CURRENT FILING DATE: 2006-02-07  
PCT/US05/035471  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 11/243,445  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 60/615,573  
PRIOR FILING DATE: 2004-10-05

NUMBER OF SEQ ID NOS: 1276209  
SEQ ID NO 865498  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: probe

NAME/KEY: misc\_feature  
LOCATION: (1..(25))  
OTHER INFORMATION: SEQ ID NO: 7331; WANO1UM6N\_at; Start 12; Stop 36;  
OTHER INFORMATION: 00000001100000  
US-11-348-413-865498

Query Match 67.4%; Score 12.8; DB 9; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CACGATCTCTCTCA 18  
DB 9 CACGATCTCTCTCA 24

## RESULT 14

US-11-297-810-26/C  
Sequence 26, Application US/11297810  
Publication No. US2006012037A1  
GENERAL INFORMATION:  
APPLICANT: Le, Junming  
APPLICANT: Valcek, Jan  
APPLICANT: Daddona, Peter  
APPLICANT: Chrayeb, John  
APPLICANT: Knight, David  
APPLICANT: Siegel, Scott  
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of Human  
FILE REFERENCE: 0975, 1005-049  
CURRENT APPLICATION NUMBER: US/11/297, 810  
CURRENT FILING DATE: 2005-12-08  
PRIOR APPLICATION NUMBER: U.S. 09/927, 703  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: U.S. 09/756, 398  
PRIOR FILING DATE: 2001-01-08  
PRIOR APPLICATION NUMBER: U.S. 09/133, 119  
PRIOR FILING DATE: 1998-08-12  
PRIOR APPLICATION NUMBER: U.S. 08/570, 674  
PRIOR FILING DATE: 1995-12-11  
PRIOR APPLICATION NUMBER: U.S. 08/324, 799  
PRIOR FILING DATE: 1994-10-18  
PRIOR APPLICATION NUMBER: U.S. 08/192, 102  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/192, 861  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/192, 093  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/010, 406  
PRIOR FILING DATE: 1993-01-29  
PRIOR APPLICATION NUMBER: U.S. 08/013, 413  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26  
LENGTH: 52  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Partial sequence of pLC871  
US-11-297-810-26

Query Match 67.4%; Score 12.8; DB 8; Length 52;  
Best Local Similarity 87.5%; Pred. No. 1.5e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CACGGTATCTCTTCA 18  
| | | | | | | | | |  
Db 27 CCGGATATCTCTTCA 12

## RESULT 15

US-11-314-941-26/c  
; Sequence 26, Application US/11314941  
; Publication No. US20060140949A1

## GENERAL INFORMATION:

APPLICANT: Le, Junning  
APPLICANT: Vilcek, Jan  
APPLICANT: Daddona, Peter  
APPLICANT: Ghayeb, John  
APPLICANT: Knight, David  
APPLICANT: Siegel, Scott  
TITLE OF INVENTION: Human Anti-TNF Antibodies and Peptides  
FILE REFERENCE: 0975.1005-059  
CURRENT APPLICATION NUMBER: US/11/314, 941  
CURRENT FILING DATE: 2005-12-20  
PRIOR APPLICATION NUMBER: U.S. 10/198, 845  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: U.S. 09/756, 398  
PRIOR FILING DATE: 2001-01-08  
PRIOR APPLICATION NUMBER: U.S. 09/133, 119  
PRIOR FILING DATE: 1998-08-12  
PRIOR APPLICATION NUMBER: U.S. 08/570, 674  
PRIOR FILING DATE: 1995-12-11  
PRIOR APPLICATION NUMBER: U.S. 08/324, 799  
PRIOR FILING DATE: 1994-10-18  
PRIOR APPLICATION NUMBER: U.S. 08/192, 102  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/192, 861  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/192, 093  
PRIOR FILING DATE: 1994-02-04  
PRIOR APPLICATION NUMBER: U.S. 08/010, 406  
PRIOR FILING DATE: 1993-01-29  
PRIOR APPLICATION NUMBER: U.S. 08/013, 413  
PRIOR FILING DATE: 1993-02-02  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: FastSeq for windows Version 4.0  
SEQ ID NO 26

LENGTH: 52  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Partial sequence of pLC871  
US-11-314-941-26

Query Match 67.4%; Score 12.8; DB 9; Length 52;  
Best Local Similarity 87.5%; Pred. No. 1.5e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CACGGTATCTCTTCA 18  
| | | | | | | | | |  
Db 27 CCGGATATCTCTTCA 12

## RESULT 16

US-11-217-529-141152  
; Sequence 14152, Application US/11217529  
; Publication No. US20060099612A1

## GENERAL INFORMATION:

APPLICANT: SUNTORY LIMITED  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHIISA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: S-38-285  
CURRENT APPLICATION NUMBER: US/11/217, 529  
CURRENT FILING DATE: 2005-09-02  
PRIOR APPLICATION NUMBER: US 10/932, 182  
PRIOR FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 141152  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Saccharomyces pastorianus  
US-11-217-529-141152

Query Match 66.3%; Score 12.6; DB 8; Length 25;  
Best Local Similarity 78.9%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCGACGGTATCTCTTAC 19  
| | | | | | | | | |  
Db 3 CGTACGTATTTCTTAC 21

RESULT 17  
US-11-348-413-198939/c  
; Sequence 198939, Application US/11348413  
; Publication No. US20060160121A1

## GENERAL INFORMATION:

APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
APPLICANT: Murphy, Ellen  
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
FILE REFERENCE: 031896-084100 (AM 101724)  
CURRENT APPLICATION NUMBER: US/11/348, 413  
CURRENT FILING DATE: 2006-02-07  
PRIOR APPLICATION NUMBER: PCT/US05/035471  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 11/243, 445  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 60/615, 573  
PRIOR FILING DATE: 2004-10-05  
NUMBER OF SEQ ID NOS: 1276209  
SEQ ID NO 198939  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: probe  
NAME/KEY: misc.feature  
LOCATION: (1)-(25)  
OTHER INFORMATION: SEQ ID NO: 5880; WAN01U05C; Start 707; Stop 731;  
US-11-348-413-198939

Query Match 66.3%; Score 12.6; DB 9; Length 25;  
Best Local Similarity 78.9%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCGACGGTATCTCTTAC 19  
| | | | | | | | | |  
Db 19 CGCTCGTATCTCTTAC 1

## RESULT 18

US-11-348-413-810033/c  
; Sequence 810033, Application US/11348413  
; Publication No. US20060160121A1

## GENERAL INFORMATION:

APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
APPLICANT: Murphy, Ellen  
APPLICANT: Olmsted, Stephen

;; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
;; FILE REFERENCE: 031896-084100 (AM 101724)  
;; CURRENT APPLICATION NUMBER: US/11/348,413  
;; CURRENT FILING DATE: 2006-02-07  
;; PRIOR APPLICATION NUMBER: PCT/US05/035471  
;; PRIOR FILING DATE: 2005-10-05  
;; PRIOR APPLICATION NUMBER: US 11/243,445  
;; PRIOR FILING DATE: 2005-10-05  
;; PRIOR APPLICATION NUMBER: US 60/615,573  
;; PRIOR FILING DATE: 2004-10-05  
;; NUMBER OF SEQ ID NOS: 1276209  
;; SEQ ID NO 810033  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: Artificial  
;; FEATURE:  
;; OTHER INFORMATION: probe  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)..(25)  
;; OTHER INFORMATION: SEQ ID NO: 5880; WAN01U5C\_at; Start 701; Stop 725;  
;; US-11-348-413-810033

Query Match 66.3%; Score 12.6; DB 9; Length 25;  
Best Local Similarity 78.9%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACGGTATCTCTTCAC 19  
Db 25 CGCTCGGTATCTCTCTAC 7

RESULT 19  
US-10-511-937-136/c  
;; Sequence 136, Application US/10511937  
;; Publication No. US20060088836A1  
;; GENERAL INFORMATION:  
;; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
;; APPLICANT: Wollgemuth, Jay  
;; APPLICANT: Fry, Kirk  
;; APPLICANT: Woodward, Robert  
;; APPLICANT: Ly, Ngoc  
;; APPLICANT: Prentice, James  
;; APPLICANT: Morris, MacDonald  
;; APPLICANT: Rosenberg, Steven  
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
;; FILE REFERENCE: 506612000104  
;; CURRENT APPLICATION NUMBER: US/10/511,937  
;; CURRENT FILING DATE: 2004-10-19  
;; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
;; PRIOR FILING DATE: 2003-04-24  
;; PRIOR APPLICATION NUMBER: US 10/131,831  
;; PRIOR FILING DATE: 2002-04-24  
;; PRIOR APPLICATION NUMBER: US 10/325,899  
;; PRIOR FILING DATE: 2002-12-20  
;; NUMBER OF SEQ ID NOS: 3117  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 136  
;; LENGTH: 50  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; US-10-511-937-136

Query Match 66.3%; Score 12.6; DB 6; Length 50;  
Best Local Similarity 78.9%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACGGTATCTCTTCAC 19  
Db 49 CTCACGTCTCTCTCTGAC 31

RESULT 20  
US-10-554-711-392  
;; Sequence 392, Application US/10554711  
;; Publication No. US20060115806A1  
;; GENERAL INFORMATION:  
;; APPLICANT: University of Georgia Research Foundation  
;; APPLICANT: McDonald, John F.  
;; TITLE OF INVENTION: Global Analysis of Transposable Elements  
;; FILE REFERENCE: 21099.0075P1  
;; CURRENT APPLICATION NUMBER: US/10/554,711  
;; CURRENT FILING DATE: 2005-10-28  
;; PRIOR APPLICATION NUMBER: 60/466,798  
;; PRIOR FILING DATE: 2003-04-29  
;; NUMBER OF SEQ ID NOS: 778  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 392  
;; LENGTH: 50  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:/note =  
;; US-10-554-711-392

Query Match 66.3%; Score 12.6; DB 6; Length 50;  
Best Local Similarity 78.9%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACGGTATCTCTTCAC 19  
Db 31 CTCACGATCTCTCTTCAC 49

RESULT 21  
US-11-348-413-257483/c  
;; Sequence 257483, Application US/11348413  
;; Publication No. US20060160121A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wyeth  
;; APPLICANT: Mounts, William M  
;; APPLICANT: Murphy, Ellen  
;; APPLICANT: Olmsted, Stephen  
;; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
;; FILE REFERENCE: 031896-084100 (AM 101724)  
;; CURRENT APPLICATION NUMBER: US/11/348,413  
;; CURRENT FILING DATE: 2006-02-07  
;; PRIOR APPLICATION NUMBER: PCT/US05/035471  
;; PRIOR FILING DATE: 2005-10-05  
;; PRIOR APPLICATION NUMBER: US 11/243,445  
;; PRIOR FILING DATE: 2005-10-05  
;; PRIOR APPLICATION NUMBER: US 60/615,573  
;; PRIOR FILING DATE: 2004-10-05  
;; NUMBER OF SEQ ID NOS: 1276209  
;; SEQ ID NO 257483  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: Artificial  
;; FEATURE:  
;; OTHER INFORMATION: probe  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)..(25)  
;; OTHER INFORMATION: SEQ ID NO: 7489; WAN01UWCZ; Start 373; Stop 397;  
;; US-11-348-413-257483

Query Match 65.3%; Score 12.4; DB 9; Length 25;  
Best Local Similarity 92.9%; Pred. No. 2.3e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ACGGTATCTCTTC 17

Db 17 ACGGTCTCTCTTC 4

## RESULT 22

US-11-348-413-257484/c  
 ; Sequence 257484, Application US/11348413  
 ; Publication No. US20060160121A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; APPLICANT: Murphy, Ellen  
 ; APPLICANT: Olmsted, Stephen  
 ; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
 ; FILE REFERENCE: 031896-084100 (AM 101724)  
 ; CURRENT APPLICATION NUMBER: US/11/348,413  
 ; CURRENT FILING DATE: 2006-02-07  
 ; PRIOR APPLICATION NUMBER: PCT/US05/035471  
 ; PRIOR FILING DATE: 2005-10-05  
 ; PRIOR APPLICATION NUMBER: US 11/243,445  
 ; PRIOR FILING DATE: 2005-10-05  
 ; PRIOR APPLICATION NUMBER: US 60/615,573  
 ; PRIOR FILING DATE: 2004-10-05  
 ; NUMBER OF SEQ ID NOS: 1276209  
 ; SEQ ID NO 257484  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: probe  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)-(125)  
 ; OTHER INFORMATION: SEQ ID NO: 7489; WANO1UMCZ; Start 374; Stop 398;  
 ; OTHER INFORMATION: 000000011100000  
 ; US-11-348-413-257484

Query Match 65.3%; Score 12.4; DB 9; Length 25;

Best Local Similarity 92.9%; Pred. No. 2.3e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACGGTATCTCTTC 17  
 Db 16 ACGGTCTCTCTTC 3

## RESULT 23

US-11-348-413-257485/c  
 ; Sequence 257485, Application US/11348413  
 ; Publication No. US20060160121A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; APPLICANT: Murphy, Ellen  
 ; APPLICANT: Olmsted, Stephen  
 ; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
 ; FILE REFERENCE: 031896-084100 (AM 101724)  
 ; CURRENT APPLICATION NUMBER: US/11/348,413  
 ; CURRENT FILING DATE: 2006-02-07  
 ; PRIOR APPLICATION NUMBER: PCT/US05/035471  
 ; PRIOR FILING DATE: 2005-10-05  
 ; PRIOR APPLICATION NUMBER: US 11/243,445  
 ; PRIOR FILING DATE: 2005-10-05  
 ; PRIOR APPLICATION NUMBER: US 60/615,573  
 ; PRIOR FILING DATE: 2004-10-05  
 ; NUMBER OF SEQ ID NOS: 1276209  
 ; SEQ ID NO 257485

LENGTH: 25

TYPE: DNA

ORGANISM: Artificial

FEATURE:  
 OTHER INFORMATION: probe

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)-(125)

OTHER INFORMATION: SEQ ID NO: 7489; WANO1UMCZ; Start 375; Stop 399;  
 ; OTHER INFORMATION: 000000011100000  
 ; US-11-348-413-257485

Query Match 65.3%; Score 12.4; DB 9; Length 25;

Best Local Similarity 92.9%; Pred. No. 2.3e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACGGTATCTCTTC 17  
 Db 15 ACGGTCTCTCTTC 2

## RESULT 24

US-11-348-413-257486/c  
 ; Sequence 257486, Application US/11348413  
 ; Publication No. US20060160121A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; APPLICANT: Murphy, Ellen  
 ; APPLICANT: Olmsted, Stephen  
 ; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
 ; FILE REFERENCE: 031896-084100 (AM 101724)  
 ; CURRENT APPLICATION NUMBER: US/11/348,413  
 ; CURRENT FILING DATE: 2006-02-07  
 ; PRIOR APPLICATION NUMBER: PCT/US05/035471  
 ; PRIOR FILING DATE: 2005-10-05  
 ; PRIOR APPLICATION NUMBER: US 11/243,445  
 ; PRIOR FILING DATE: 2005-10-05  
 ; PRIOR APPLICATION NUMBER: US 60/615,573  
 ; PRIOR FILING DATE: 2004-10-05  
 ; NUMBER OF SEQ ID NOS: 1276209  
 ; SEQ ID NO 257486  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: probe  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)-(125)  
 ; OTHER INFORMATION: SEQ ID NO: 7489; WANO1UMCZ; Start 376; Stop 400;  
 ; OTHER INFORMATION: 000000011100000  
 ; US-11-348-413-257486

Query Match 65.3%; Score 12.4; DB 9; Length 25;

Best Local Similarity 92.9%; Pred. No. 2.3e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACGGTATCTCTTC 17  
 Db 14 ACGGTCTCTCTTC 1

## RESULT 25

US-11-348-413-857440  
 ; Sequence 857440, Application US/11348413  
 ; Publication No. US20060160121A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; APPLICANT: Murphy, Ellen  
 ; APPLICANT: Olmsted, Stephen  
 ; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
 ; FILE REFERENCE: 031896-084100 (AM 101724)  
 ; CURRENT APPLICATION NUMBER: US/11/348,413  
 ; CURRENT FILING DATE: 2006-02-07  
 ; PRIOR APPLICATION NUMBER: PCT/US05/035471  
 ; PRIOR FILING DATE: 2005-10-05  
 ; PRIOR APPLICATION NUMBER: US 11/243,445

```

; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 857440
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7111; WANO1UMK2_at; Start 619; Stop 643;
; OTHER INFORMATION: 000000011100000
US-11-348-413-857440
```

```

Query Match      65.3%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3  CACGATCTCTCCTT 16
          |||||
          1  CACGATCTCTCCTT 14
```

```

RESULT 26
US-11-348-413-871598/c
; Sequence 871598, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounte, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 871598
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7489; WANO1UMK2_at; Start 366; Stop 390;
; OTHER INFORMATION: 000000011100000
US-11-348-413-871598
```

```

Query Match      65.3%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4  ACGGTATCTCTTC 17
          |||||
          24  ACGGTCTCTCTTC 11
```

```

RESULT 27
US-11-348-413-871599/c
; Sequence 871599, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Wyeth
; APPLICANT: Mounte, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 871599
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 7489; WANO1UMK2_at; Start 371; Stop 395;
; OTHER INFORMATION: 000000011100000
US-11-348-413-871599
```

```

Query Match      65.3%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4  ACGGTATCTCTTC 17
          |||||
          19  ACGGTCTCTCTTC 6
```

```

RESULT 28
US-11-240-651-32
; Sequence 32, Application US/11240651
; Publication No. US20060110788A1
; GENERAL INFORMATION:
; APPLICANT: Kudlicki, Welslaw A.
; APPLICANT: Kerpelipola, Shrantchi
; APPLICANT: Fletcher, Julia
; APPLICANT: Getbehead, Ashley E.
; APPLICANT: Katzen, Federico
; APPLICANT: Voza-Brown, Laura
; TITLE OF INVENTION: Feeding Buffers, Systems, and Methods for In Vitro Synthesis of
; FILE REFERENCE: 0942.6660004
; CURRENT APPLICATION NUMBER: US/11/240,651
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: 60/614,590
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/642,094
; PRIOR FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/656,534
; PRIOR FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: Provisional Appl. No. To Be Assigned (Atty. Dkt. No. 0942.66
; 2005-09-27
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BSATA
; OTHER INFORMATION: Chemically synthesized
US-11-240-651-32
```

Query Match	65.3%	Score 12.4;	DB 8;	Length 31;
Best Local Similarity	92.9%;	Pred. No. 2.3e+03;		
Matches 13;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

```

QY      4 ACGGATCTCCTTC 17
         | |||||
Db      18 AGGTATCTCCTTC 31

```

RESULT 29  
US-11-240

US-11-240-651-14/c  
Sequence 14. Application US/11240651  
Publication NO. US20060110788A1  
GENERAL INFORMATION:  
APPLICANT: Kudlicki, Weislaw A.  
APPLICANT: Keppelcicola, Shitrantchi  
APPLICANT: Fletcher, Julia  
APPLICANT: Getbehead, Ashley E.  
APPLICANT: Katzen, Federico  
APPLICANT: Voza-Brown, Laura  
TITLE OF INVENTION: Feeding Buffers, Systems, and Methods for In Vitro Synthesis of  
TITLE OF INVENTION: Biomolecules  
FILE REFERENCE: 0942.666004  
CURRENT APPLICATION NUMBER: US/11/240,651  
CURRENT FILING DATE: 2005-10-03  
PRIOR APPLICATION NUMBER: 60/614,590  
PRIOR FILING DATE: 2004-10-01  
PRIOR APPLICATION NUMBER: 60/642,094  
PRIOR FILING DATE: 2005-01-10  
PRIOR APPLICATION NUMBER: 60/656,534  
PRIOR FILING DATE: 2005-02-28  
PRIOR APPLICATION NUMBER: Provisional Appl. No. To Be Assigned (Atty. Dkt. No. 0942.6-  
2005-09-27  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 14  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: C-Topo2 T7 Promoter  
FEATURE:  
OTHER INFORMATION: Chemically synthesized  
US-11-240-651-14

Query Match	65.3%	Score 12.4;	DB 8;	Length 60;
Best Local Similarity	92.9%;	Pred. No. 2.6e+03;		
Matches 13;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	4	ACGGTATCTCCTTC	17
Db	56	AGGGTATCTCCTTC	43

RESULT 30  
US-11-348

```

1 Sequence 429142, Application US/11348413
2 Publication No. US20060160121A1
3 GENERAL INFORMATION:
4 APPLICANT: Wyeth
5 APPLICANT: Mounts, William M
6 APPLICANT: Murphy, Ellen
7 APPLICANT: Olmsted, Stephen
8 TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
9 FILE REFERENCE: 031896-084100 (AM 101724)
10 CURRENT APPLICATION NUMBER: US/11/348,413
11 PCT FILING DATE: 2006-02-07
12 PRIOR APPLICATION NUMBER: PCT/US05/035471
13 PRIOR FILING DATE: 2005-10-05
14 PRIOR APPLICATION NUMBER: US 11/243,445
15 PRIOR FILING DATE: 2005-10-05
16 PRIOR APPLICATION NUMBER: US 60/615,573
17 PRIOR FILING DATE: 2004-10-05

```

```

; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 429142
; LENGTH: 25
;

```

Query Match	64.2%	Score	12.2	DB	9	Length	25
Best Local Similarity	82.4%	Pred. No.	2.9e+03				
Matches 14; Conservative	0	Mismatches	3	Indels	0	Gaps	0

QY	2	GCACGGTATCTCCTTCA	18
Db	1	GCAGATGTTCTCCTTCA	17

RESULT 31  
US-11-348

```

Sequence 636110, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIORITY APPLICATION NUMBER: PCT/US05/035471
PRIORITY FILING DATE: 2005-10-05
PRIORITY APPLICATION NUMBER: US 11/243,445
PRIORITY FILING DATE: 2005-10-05
PRIORITY APPLICATION NUMBER: US 60/615,573
PRIORITY FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 636110
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(25)
OTHER INFORMATION: SEQ ID NO: 822; WANO1UDD_at; Start 908; Stop 932;
US-11-348-413-636110

```

Query Match	64.2%	Score 12.2;	DB 9;	Length 25;
Best Local Similarity	82.4%;	Pred. No. 2.9e+03;		
Matches 14; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

OY	1	CGCAGGTATCTCCTTC	17
Dd	4	CGCAGGTATCAACAAC	20

RESULT 32  
US-11-348

Sequence 661408, Application US/113484113  
Publication No. US2006016012A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
APPLICANT: Murphy, Ellen



APPLICANT: Olmsted, Stephen  
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
FILE REFERENCE: 031896-084100 (AM 101724)  
CURRENT APPLICATION NUMBER: US/11/348,413  
CURRENT FILING DATE: 2006-02-07  
PRIOR APPLICATION NUMBER: PCT/US05/035471  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 11/243,445  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 60/615,573  
PRIOR FILING DATE: 2004-10-05  
NUMBER OF SEQ ID NOS: 1276209  
SEQ ID NO 661408  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: probe  
NAME/KEY: misc feature  
LOCATION: (1)-(25)  
OTHER INFORMATION: SEQ ID NO: 1509; WANOIUM2\_at; Start 160; Stop 184;  
US-11-348-413-661408

Query Match 64.2%; Score 12.2; DB 9; Length 25;  
Best Local Similarity 82.4%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGACGGTATCTCCTTC 17  
Db 23 CGAACGATATCGCCTTC 7

RESULT 33  
US-11-348-413-661409/c  
Sequence 661409, Application US/11348413  
Publication No. US20060160121A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
APPLICANT: Murphy, Ellen  
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
FILE REFERENCE: 031896-084100 (AM 101724)  
CURRENT APPLICATION NUMBER: US/11/348,413  
CURRENT FILING DATE: 2006-02-07  
PRIOR APPLICATION NUMBER: US 11/243,445  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: PCT/US05/035471  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 60/615,573  
PRIOR FILING DATE: 2004-10-05  
NUMBER OF SEQ ID NOS: 1276209  
SEQ ID NO 661409  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: probe  
NAME/KEY: misc feature  
LOCATION: (1)-(25)  
OTHER INFORMATION: SEQ ID NO: 1509; WANOIUM2\_at; Start 162; Stop 186;  
US-11-348-413-661409

Query Match 64.2%; Score 12.2; DB 9; Length 25;  
Best Local Similarity 82.4%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGACGGTATCTCCTTC 17  
|| ||| |||| |||||

Db 21 CGAACGATATCGCCTTC 5

RESULT 34  
US-11-348-413-661410/c  
Sequence 661410, Application US/11348413  
Publication No. US20060160121A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
APPLICANT: Murphy, Ellen  
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
FILE REFERENCE: 031896-084100 (AM 101724)  
CURRENT APPLICATION NUMBER: US/11/348,413  
CURRENT FILING DATE: 2006-02-07  
PRIOR APPLICATION NUMBER: PCT/US05/035471  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 11/243,445  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 60/615,573  
PRIOR FILING DATE: 2004-10-05  
NUMBER OF SEQ ID NOS: 1276209  
SEQ ID NO 661410  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: probe  
NAME/KEY: misc feature  
LOCATION: (1)-(25)  
OTHER INFORMATION: SEQ ID NO: 1509; WANOIUM2\_at; Start 166; Stop 190;  
US-11-348-413-661410

Query Match 64.2%; Score 12.2; DB 9; Length 25;  
Best Local Similarity 82.4%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGACGGTATCTCCTTC 17  
Db 17 CGAACGATATCGCCTTC 1

RESULT 35  
US-11-348-413-701530  
Sequence 701530, Application US/11348413  
Publication No. US20060160121A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
APPLICANT: Murphy, Ellen  
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
FILE REFERENCE: 031896-084100 (AM 101724)  
CURRENT APPLICATION NUMBER: US/11/348,413  
CURRENT FILING DATE: 2006-02-07  
PRIOR APPLICATION NUMBER: PCT/US05/035471  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 11/243,445  
PRIOR FILING DATE: 2005-10-05  
PRIOR APPLICATION NUMBER: US 60/615,573  
PRIOR FILING DATE: 2004-10-05  
NUMBER OF SEQ ID NOS: 1276209  
SEQ ID NO 701530  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: probe  
NAME/KEY: misc feature

```
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2675; WANO1UN86_at; Start 552; Stop 576;
; OTHER INFORMATION: 11111100000000
US-11-348-413-701530
```

```
Query Match          64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 CACGATATCTCCTTCA 19
         |||||
Db       1 CACGTAAGCTCTCAAC 17
```

```
RESULT 36
US-11-348-413-812478
; Sequence 812478, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 812478
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 5945; WANO1UUJ4_at; Start 499; Stop 523;
; OTHER INFORMATION: 000000011100000
US-11-348-413-812478
```

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Query Match          64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 GCACGATATCTCCTTCA 18
         |||||
Db       1 GCATGTATGTCTCTTCA 17
```

```
RESULT 37
US-11-348-413-90099
; Sequence 90099, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
```

```
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 90099
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
```

```
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2105; WANO1ULANR; Start 922; Stop 946;
; OTHER INFORMATION: 111111000000000
US-11-348-413-90099
```

```
Query Match          63.2%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 TATCTCCTTCAAC 19
         |||||
Db       5 TATCTCCTTCAAC 16
```

```
RESULT 38
US-11-348-413-90100
; Sequence 90100, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 90100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2105; WANO1ULANR; Start 923; Stop 947;
; OTHER INFORMATION: 111111000000000
US-11-348-413-90100
```

```
Query Match          63.2%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 TATCTCCTTCAAC 19
         |||||
Db       4 TATCTCCTTCAAC 15
```

```
RESULT 39
US-11-348-413-90101
; Sequence 90101, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

```

; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 90101
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2105; WANOIULNR; Start 924; Stop 948;
; OTHER INFORMATION: 1111110000000
US-11-348-413-90101

```

```

Query Match      63.2%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      8 TATCTCCTCACC 19
        |||||
Db      3 TATCTCCTCACC 14

```

```

RESULT 40
US-11-348-413-208705
; Sequence 208705, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 208705
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 6148; WANOIUKBT; Start 386; Stop 410;
; OTHER INFORMATION: 000000011100000
US-11-348-413-208705

```

```

Query Match      63.2%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      5 CGGATCTCCTT 16
        |||||
Db      8 CGGATCTCCTT 19

```

```

Search completed: August 10, 2006, 08:41:55
Job time : 87.6667 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 07:10:03 ; Search time 1821.33 Seconds  
(without alignments)  
583.346 Million cell updates/sec

Title: US-10-636-065-29  
Perfect score: 19  
Sequence: 1 cgcacgcatcccttcac 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 429206

Minimum DB seq length: 0  
Maximum DB seq length: 70

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est3: \*  
3: gb\_est4: \*  
4: gb\_est5: \*  
5: gb\_est6: \*  
6: gb\_hic: \*  
7: gb\_est2: \*  
8: gb\_est7: \*  
9: gb\_est8: \*  
10: gb\_est9: \*  
11: gb\_gsa1: \*  
12: gb\_gsa2: \*  
13: gb\_gsa3: \*  
14: gb\_gsa4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.2	74.7	51	14	LBAP012G02
C 2	13.8	72.6	66	2	BI218136
C 3	13.2	69.5	55	1	AA050107
C 4	13.2	69.5	55	14	AL767252
C 5	13.2	69.5	68	7	AV833333
C 6	12.6	66.3	40	11	AZ489384
C 7	12.6	66.3	62	11	BH000447
C 8	12.6	66.3	63	2	BI547302
C 9	12.4	65.3	31	1	AI032171
C 10	12.4	65.3	54	11	BZ384637
C 11	12.4	65.3	66	14	CR132014
C 12	12.4	65.3	70	14	BX946570
C 13	12.2	64.2	40	1	AA592106
C 14	12.2	64.2	41	2	BJ031518
C 15	12.2	64.2	54	6	AK219947
C 16	12.2	64.2	55	1	AA566958
C 17	12.2	64.2	56	13	CM048735
C 18	12.2	64.2	57	13	CL280533
C 19	12.2	64.2	57	14	CR156504

20	12.2	64.2	58	1	AA466227	AA466227 vgr6h09.x
21	12.2	64.2	62	4	CA913895	CA913895 PCS04370
22	12.2	64.2	67	1	AA270302	AA270302 v558e05.x
23	12.2	64.2	67	1	AA548218	AA548218 n199d10.8
24	12.2	64.2	67	10	W36489	W36489 mb71f10.r1
25	12	63.2	69	7	BE872737	BE872737 601450859
C 26	11.8	62.1	32	13	CZ489694	CZ489694 E06954-3P
C 27	11.8	62.1	34	1	AJ662253	AJ662253 AJ662253
C 28	11.8	62.1	34	14	AT796977	AT796977 Arabidops
C 29	11.8	62.1	52	14	ATH526844	ATH526844 Arabidops
C 30	11.8	62.1	53	8	CN655993	CN655993 LCM003K_B
C 31	11.8	62.1	55	4	CB006039	CB006039 VWC028H12
C 32	11.8	62.1	62	11	AZ459394	AZ459394 IM0264N10
C 33	11.8	62.1	63	1	AA453052	AA453052 z36f11.x
C 34	11.8	62.1	63	5	CD533428	CD533428 31M20_Ara
C 35	11.8	62.1	65	8	CV305631	CV305631 t164b04.g
C 36	11.8	62.1	65	14	FR0053439	AL689718 Fugu rubr
C 37	11.8	62.1	66	11	BH811036	BH811036 SALK_0571
C 38	11.8	62.1	66	11	BH811037	BH811037 SALK_0571
C 39	11.8	62.1	66	13	CZ012701	CZ012701 BGR574_Ba
C 40	11.8	62.1	68	8	CV305709	CV305709 t164g04.g
C 41	11.8	62.1	68	12	CG538067	CG538067 OST127647
C 42	11.8	62.1	69	11	BH790467	BH790467 SALK_0571
C 43	11.6	61.1	24	5	CF308728	CF308728 ABF--02-K
C 44	11.6	61.1	38	11	BH861410	BH861410 SALK_0815
C 45	11.6	61.1	50	1	AU105011	AU105011 AU105011
C 46	11.6	61.1	50	1	AU105012	AU105012 AU105012
C 47	11.6	61.1	50	1	AU105013	AU105013 AU105013
C 48	11.6	61.1	50	1	AU105014	AU105014 AU105014
C 49	11.6	61.1	50	1	AU105016	AU105016 AU105016
C 50	11.6	61.1	50	1	AU105019	AU105019 AU105019
C 51	11.6	61.1	50	1	AU105021	AU105021 AU105021
C 52	11.6	61.1	50	1	AU105022	AU105022 AU105022
C 53	11.6	61.1	50	1	AU105023	AU105023 AU105023
C 54	11.6	61.1	50	1	AU105024	AU105024 AU105024
C 55	11.6	61.1	50	1	AU105025	AU105025 AU105025
C 56	11.6	61.1	50	1	AU105026	AU105026 AU105026
C 57	11.6	61.1	50	1	AU105028	AU105028 AU105028
C 58	11.6	61.1	50	1	AU105030	AU105030 AU105030
C 59	11.6	61.1	50	1	AU105031	AU105031 AU105031
C 60	11.6	61.1	50	1	AU105032	AU105032 AU105032
C 61	11.6	61.1	50	1	AU105033	AU105033 AU105033
C 62	11.6	61.1	50	1	AU105035	AU105035 AU105035
C 63	11.6	61.1	50	1	AU105036	AU105036 AU105036
C 64	11.6	61.1	50	1	AU105037	AU105037 AU105037
C 65	11.6	61.1	50	1	AU105038	AU105038 AU105038
C 66	11.6	61.1	50	1	AU105039	AU105039 AU105039
C 67	11.6	61.1	50	1	AU105040	AU105040 AU105040
C 68	11.6	61.1	50	1	AU105041	AU105041 AU105041
C 69	11.6	61.1	50	1	AU105042	AU105042 AU105042
C 70	11.6	61.1	50	1	AU105043	AU105043 AU105043
C 71	11.6	61.1	50	1	AU105044	AU105044 AU105044
C 72	11.6	61.1	50	1	AU105047	AU105047 AU105047
C 73	11.6	61.1	50	1	AU105048	AU105048 AU105048
C 74	11.6	61.1	50	1	AU105050	AU105050 AU105050
C 75	11.6	61.1	50	1	AU105052	AU105052 AU105052
C 76	11.6	61.1	50	1	AU105054	AU105054 AU105054
C 77	11.6	61.1	50	1	AU105055	AU105055 AU105055
C 78	11.6	61.1	50	1	AU105059	AU105059 AU105059
C 79	11.6	61.1	50	1	AU105060	AU105060 AU105060
C 80	11.6	61.1	50	1	AU105064	AU105064 AU105064
C 81	11.6	61.1	50	1	AU105068	AU105068 AU105068
C 82	11.6	61.1	50	1	AU105069	AU105069 AU105069
C 83	11.6	61.1	50	1	AU105071	AU105071 AU105071
C 84	11.6	61.1	50	1	AU105072	AU105072 AU105072
C 85	11.6	61.1	50	1	AU105076	AU105076 AU105076
C 86	11.6	61.1	50	1	AU105077	AU105077 AU105077
C 87	11.6	61.1	50	1	AU105080	AU105080 AU105080
C 88	11.6	61.1	50	1	AU105085	AU105085 AU105085
C 89	11.6	61.1	50	1	AU105087	AU105087 AU105087
C 90	11.6	61.1	50	1	AU105088	AU105088 AU105088
C 91	11.6	61.1	50	1	AU105089	AU105089 AU105089
C 92	11.6	61.1	50	1	AU105090	AU105090 AU105090

c 93 11.6 61.1 50 1 AUI05092 AUI05092 AUI05092  
 c 94 11.6 61.1 50 1 AUI05093 AUI05093 AUI05093  
 c 95 11.6 61.1 50 1 AUI05094 AUI05094 AUI05094  
 c 96 11.6 61.1 50 3 BP132714 BP132714 BP132714  
 c 97 11.6 61.1 55 10 T57237 T57237 yb21h06.t1  
 c 98 11.6 61.1 62 10 DR368321 DR368321 6630667 C  
 c 99 11.6 61.1 64 1 A1149176 A1149176 qc76d08.x  
 c 100 11.6 61.1 64 11 B07692 B07692 CDC9f10 C-1

## ALIGNMENTS

RESULT 1  
 LBAF012G02/c  
 LOCUS LBAF012G02 51 bp DNA linear GSS 20-JUN-2003  
 DEFINITION Leishmania braziliensis GSS, clone LBAF012G02, genomic survey  
 sequence.

ACCESSION BX540068 GI:32135483  
 VERSION BX540068.1 GI:32135483  
 KEYWORDS GSS; genomic survey sequence.  
 SOURCE Leishmania braziliensis  
 ORGANISM Leishmania braziliensis  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
 Leishmania; Leishmania braziliensis species complex.

REFERENCE 1  
 AUTHORS Laurentino,E.C., Ruiz,J.C. and Cruz,A.K.  
 TITLE GSS analysis of the Leishmania braziliensis genome  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 51)  
 AUTHORS Cruz,A.K.  
 TITLE Direct Submission

COMMENT Submitted (17-JUN-2003) Cruz A.K., University of Sao Paulo,  
 Department of Molecular and Cell Biology, FMRP, Avenida  
 Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL

FEATURES  
 Location: akcruz@mp.usp.br.  
 source

1. 51  
 /organism="Leishmania braziliensis"  
 /mol\_type="genomic DNA"  
 /strain="MHOM/BR/75/M2904"  
 /db\_xref="taxon:5660"  
 /clone="LBAF012G02"

## ORIGIN

Query Match 74.7%; Score 14.2; DB 14; Length 51;  
 Best Local Similarity 84.2%; Pred. No. 1.4e+04;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCCTTCAC 19  
 |||||  
 32 CGCAGCGTATCTCCTTCAC 14

Db 32 CGCAGCGTATCTCCTTCAC 14

RESULT 2  
 BI218136/c  
 LOCUS BI218136 66 bp mRNA linear EST 11-JUL-2001  
 DEFINITION 602934250F1 NCI\_CGAP\_Li9 Mus musculus cDNA clone IMAGE:5097541 5',  
 mRNA sequence.

ACCESSION BI218136 GI:14671580  
 VERSION BI218136.1 GI:14671580  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 66)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.llnl.gov  
 plate: LLM11234 row: c column: 14  
 High quality sequence stop: 64.

## FEATURES

source

1. 66  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5097541"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_11b="NCI CGAP\_Li9"  
 /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.9 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP library."

## ORIGIN

Query Match 72.6%; Score 13.8; DB 2; Length 66;  
 Best Local Similarity 88.2%; Pred. No. 2.3e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCCTTC 17  
 |||||  
 24 CGCAGCGTATCTCCTTC 8

Db 24 CGCAGCGTATCTCCTTC 8

RESULT 3  
 AA050107 55 bp mRNA linear EST 09-SEP-1996  
 LOCUS AA050107  
 DEFINITION mJ10904.t1 Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA  
 clone IMAGE:475734 5' similar to SW:WPS1\_HUMAN P42677  
 MERTLOPAN-STIMULIN 1, mRNA sequence.

ACCESSION AA050107 GI:1529795  
 VERSION AA050107.1 GI:1529795  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 55)  
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
 Waterston,R.  
 TITLE The WashU-HMNI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HMNI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: mouseest@wustl.wustl.edu  
 This clone is available royalty-free through LNLN; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:286478

Trice considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seg primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 1.

## FEATURES

source

1. 55  
 /organism="Mus musculus"  
 /mol\_type="mRNA"



Best Local Similarity 83.3%; Pred. No. 4.8e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GCACGGATCTCTTCAC 19  
30 GCGCGATATCCTTCAC 13

RESULT 6  
AZ489384/c 40 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0321171F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
DEFINITION clone UUGCIM0321121 F, genomic survey sequence.  
ACCESSION AZ489384  
VERSION AZ489384.1 GI:10659081  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 40)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0321 row: 1 column: 21  
Seq primer: CGTTGTAAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 40.  
Location/Qualifiers

FEATURES  
source 1..40  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCIM0321121"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 66.3%; Score 12.6; DB 11; Length 40;  
Best Local Similarity 78.9%; Pred. No. 9.6e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCGACGGATCTCTTCAC 19  
33 CACAGGATATCCTTCAC 15

RESULT 7  
BH000447/c 62 bp DNA linear GSS 27-APR-2001  
LOCUS 2M0288K14F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
DEFINITION clone UUGC2M0288K14 F, genomic survey sequence.  
ACCESSION BH000447  
VERSION BH000447.1 GI:13871673  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 62)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0288 row: K column: 14  
Seq primer: CGTTGTAAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 62.  
Location/Qualifiers

FEATURES  
source 1..62  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0288K14"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN



Query Match 66.3%; Score 12.6; DB 11; Length 62;  
 Best Local Similarity 78.9%; Pred. No. 1e+05; Mismatches 4; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCCTTCAC 19  
 |||||  
 45 CACCCAGTCTCTCCTTCAC 27

RESULT 8  
 B1547302/c 63 bp mRNA linear EST 05-SEP-2001  
 LOCUS 603197180P1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5276803 5';  
 DEFINITION mRNA sequence.

ACCESSION B1547302  
 VERSION B1547302  
 KEYWORDS B1547302.1 GI:15434614  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 63)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Straubeberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NMGRI), Shitaki  
 Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: LLM1698 row: p column: 20  
 High quality sequence stop: 9.  
 Location/Qualifiers  
 1. 63  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5276803"  
 /rname\_type="hippocampus"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH MGC\_95"  
 /note="Organ: brain; Vector: pBluescriptR (modified  
 pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI  
 (gtagag); Oligo-dT primed using primer  
 5'-TTTTTTTTTTTTTAA-3', size-selected for average  
 insert size 2.5 kb and normalized to R0T 5. This is a  
 primary library enriched for full-length clones and  
 constructed using the Cap-trapper method (Carninci, in  
 preparation). Library constructed by M. Brownstein  
 (NMGRI/NMGRI, National Institutes of Health). Note: this  
 is a NIH\_MGC library."

ORIGIN

Query Match 66.3%; Score 12.6; DB 2; Length 63;  
 Best Local Similarity 78.9%; Pred. No. 1e+05; Mismatches 4; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCCTTCAC 19  
 |||||  
 43 CGCAGCTAGGCCCTTCAC 25

RESULT 9  
 A1032171 31 bp mRNA linear EST 27-AUG-1998  
 LOCUS 0094c11.01 NCI\_CGAP\_k1d3 Homo sapiens cDNA clone IMAGE:1635476 3';  
 DEFINITION

similar to SW:PROX\_HUMAN P50336 PROTOPORPHYRINOGEN OXIDASE ;, mRNA  
 sequence.  
 A1032171  
 A1032171.1 GI:3250383  
 EST.  
 VERSION A1032171.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 31)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Straubeberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www-bio.lnl.gov/bdrip/image/image.html

Trace considered overall poor quality  
 Insert Length: 1676 Std Error: 0.00  
 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 31  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1635476"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP\_k1d3"  
 /note="Organ: Kidney; Vector: pT7TD-PacI; Site\_1: Not I;  
 Site\_2: Eco RI; 1st strand cDNA was primed with a Not I -  
 oligo(dT) primer, double-stranded cDNA was ligated to Eco  
 RI adaptors (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of the modified pT773  
 vector. mRNA source: 2 pooled kidneys. Library went  
 through one round of normalization. Library constructed by  
 Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 65.3%; Score 12.4; DB 1; Length 31;  
 Best Local Similarity 92.9%; Pred. No. 1.2e+05; Mismatches 1; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCA 18  
 |||||  
 2 CGGATCTCCTTCA 15

RESULT 10  
 B2384637/c 54 bp DNA linear GSS 26-NOV-2002  
 LOCUS B2384637  
 DEFINITION Arabidopsis thaliana TDNA insertion lines  
 Arabidopsis thaliana genomic clone SALK\_135814.20.40.x, genomic  
 survey sequence.  
 B2384637  
 B2384637.1 GI:25482257  
 GSS.  
 ACCESSION B2384637  
 VERSION B2384637  
 KEYWORDS Arabidopsis thaliana (thale cress)  
 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 1 (bases 1 to 54)  
 Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shim, P., Zimmerman, J., and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5g06840.  
Class: TDNA tagged.

## FEATURES

source  
Location/Qualifiers

1..54  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_135814.20.40.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 65.3%; Score 12.4; DB 11; Length 54;  
Best Local Similarity 92.9%; Pred. No. 1.3e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGATCTCCTT 16  
Db 50 CACGGTATCACCTT 37

RESULT 11  
LOCUS CR132014 66 bp DNA linear GSS 06-JUL-2004  
DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN363121, genomic survey sequence.  
ACCESSION CR132014  
KEYWORDS GSS; genome survey sequence; MICR.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 66)  
AUTHORS Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J., and Bradley, A.  
TITLE Direct Substitution  
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <http://www.sanger.ac.uk/MICR>  
Location/Qualifiers

## FEATURES

source  
1..66  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPN363121"  
/clone\_lib="MHPN"

## ORIGIN

Query Match 65.3%; Score 12.4; DB 14; Length 66;  
Best Local Similarity 92.9%; Pred. No. 1.3e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGTATCTCTTCAC 19  
Db 21 GGTATCTCTTCAC 34

RESULT 12  
LOCUS BX946520/c 70 bp DNA linear GSS 05-APR-2004  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GR-767D03-024595, genomic survey sequence.  
ACCESSION BX946520  
KEYWORDS BX946520.1 GI:42596206  
SOURCE GSS.  
ORGANISM Arabidopsis thaliana (thale cress)

## REFERENCE

AUTHORS  
TITLE

JOURNAL Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., and Weishaar, B.  
PUBMED GABI-Kat Simplesearch: a flanking sequence tag (PST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
BIOINFORMATICS 19 (11), 1441-1442 (2003)  
12874060

## REFERENCE

AUTHORS  
TITLE

JOURNAL An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
PLANT MOL. BIOL. 53 (1-2), 247-259 (2003)  
14756321

## REFERENCE

AUTHORS  
TITLE

JOURNAL Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weishaar, B.  
PUBMED High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
BIOTECHNIQUES 35 (6), 1164-1168 (2003)  
14682050

## REFERENCE

AUTHORS  
TITLE

JOURNAL Rosso, M.G., Strizhov, N., Li, Y. and Weishaar, B.  
PUBMED Direct Substitution  
Submitted (31-MAR-2004) Weishaar, B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone fib18. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

## FEATURES

source  
Location/Qualifiers

1..70  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="GK-767D03-024595"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

## ORIGIN

Query Match 65.3%; Score 12.4; DB 14; Length 70;  
Best Local Similarity 92.9%; Pred. No. 1.3e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db	OY
30 CGCAGGATCTTC 14	1 CGCAGGATCTTC 14       
Query Match	64.2% Score 12.2; DB 1; Length 40;
Best Local Similarity	82.4%; Pred. No. 1.6e+05;
Matches 14; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
1 CGCAGGATCTTCCTTC 17	       
CGCAGGATCTTC 14	

```

RESULT 14
B0031518/c 41 bp mRNA linear EST 26-SEP-2003
LOCUS
DEFINITION B0031518 NIBB Mochii normalized Xenopus neurola library Xenopus
laevis cDNA clone XL007109 5', mRNA sequence.
ACCESSION B0031518
VERSION B0031518.1 GI:17409726
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 41)
1 Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and
Kohara,Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@gene.nig.ac.jp
The information of this clone is available through the following
URL.
http://xenopus.nibb.ac.jp.
location/qualifiers
1..41
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL007109"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/clone_id="NIBB Mochii normalized Xenopus neurola
library"
ORIGIN
Query Match 64.2% Score 12.2; DB 2; Length 41;
Best Local Similarity 77.8%; Pred. NO.1.6e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGCAGCGTATCTCCTCA 18
|||||
24 CGCCTATATCTCTCCA 7
RESULT 15
AK219947 54 bp mRNA linear HTC 23-NOV-2004
LOCUS AK219947
DEFINITION Mus musculus cDNA, clone:Y2G0150D19, strand:unspecified.
ACCESSION AK219947
VERSION AK219947.1 GI:56044338
KEYWORDS HTC; ASSETS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
1 Warahiki,A., Waki,K., Hayatsu,N., Shiraki,T., Kondo,S.,
Nakamura,M., Sasaki,D., Arahawa,T., Kawai,J., Harbers,M.,
Hayashizaki,Y. and Carninci,P.
Libraries enriched for alternatively spliced exons reveal splicing
patterns in melanocytes and melanomas
Nat. Methods 1, 233-239 (2004)
2 (bases 1 to 54)
2 Arakawa,T., Carninci,P., Fukuda,S., Harbers,M., Hayatsu,N.,
Hoti,F., Imotani,K., Kawai,J., Kondo,S., Murata,M., Nakamura,M.,
Nomura,K., Ono,M., Sasaki,D., Shiraki,T., Waki,K., Watahiki,A. and
Hayashizaki,Y.

```

**TITLE**  
JOURNAL

**COMMENT**  
Direct Submission  
Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
Alternative Splicing Libraries (ASLs) are prepared by: Preparing of single-stranded DNA using a RNA template from full length cDNA libraries, hybridizing of single-stranded DNAs, removing of remaining single-stranded DNA, digesting of regions comprising double-stranded DNA by a set of 4 bp-cutters, capturing of DNA hybrids with loop structures (alternative spliced exon), ligating of Y-shaped primers to isolated DNA hybrids with loop structures, PCR amplification of ligation products and their cloning into pFLC1 vector. (Reference).  
Location/Qualifiers  
1. 54  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="Y2G0150D19"  
/cell\_line="mixture of B16-F10Y and melan-c"  
/cell\_type="mixture of melanoma cell and melanocyte cell"  
/clone\_lib="Alternative Splicing Library L3"  
/note="strand:unspecified"

**ORIGIN**

**Query Match**  
Best Local Similarity 64.2%; Score 12.2; DB 6; Length 54;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY**  
1 CGCAGGTATCTCTTC 17  
21 CCGAGATATCTCTTC 37

**Db**  
1012 Loblolly pine C Pinus taeda CDNA clone 5c6g, mRNA sequence.  
AA566958 55 bp mRNA linear EST 28-AUG-1998  
AA566958  
AA566958.1 GI:3366171  
EST.  
Pinus taeda (loblolly pine)  
Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 55)  
Allona, I., Ouhm, M., Shoop, E., Swope, R., St Cyr, S., Carlis, J., Riedl, J., Retzel, E., Campbell, M.M., Sedoreff, R. and Whetten, R.W. Analysis of xylem formation in pine by cDNA sequencing  
Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9693-9698 (1998)  
9689143  
Contact: Ross Whetten  
Forest Biotechnology Group  
North Carolina State University  
Dept. of Forestry, NC State University, 6113 Jordan Hall,  
Raleigh, NC, 27695-8008  
Tel: 919-515-7800  
Fax: 919-515-7801  
Email: rosewhet@unity.ncsu.edu  
Seq primer: T3.  
Location/Qualifiers  
1. 55  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/db\_xref="taxon:3352"  
/clone="5c6g"  
/issue\_type="Xylem"  
/lab\_host="SOLR"

**FEATURES**  
source

**TITLE**  
JOURNAL

**COMMENT**  
/clone\_lib="Loblolly pine C"  
/note="Vector: lambda-ZAP; Site 1: EcoRI; Site 2: XhoI;  
The library was made from immature xylem from the underside of inclined stems of differentiating wood. A mixture of four genotypes were used. Oligo-dT prime cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms"

**ORIGIN**

**Query Match**  
Best Local Similarity 77.8%; Score 12.2; DB 1; Length 55;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

**QY**  
2 GCACGTATCTCTTCAC 19  
36 GCAGGGATTTCCTCAC 53

**Db**  
104\_287\_10513599\_115\_30213 Sorghum bicolor genomic clone 10513599, genomic survey sequence.  
CM048735 56 bp DNA linear GSS 28-OCT-2004  
104\_287\_10513599\_115\_30213 Sorghum bicolor genomic clone 10513599, genomic survey sequence.  
CM048735  
CM048735.1 GI:54725465  
GSS.  
Sorghum bicolor (sorghum)  
Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum. 1 (bases 1 to 56)  
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, B., Kohling, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holman, H., Roe, B.A., Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddalo, J.A. and Martienssen, R.A.  
Sorghum genome sequencing by methylation filtration  
PLoS Biol. 3 (1), e13 (2005)  
15660154  
Contact: Bedell JA  
Orion Genomics, LLC  
4041 Forest Park Ave, St. Louis, MO 63108, USA  
Tel: 314 615 6979  
Fax: 314 615 5975  
Email: jbedell@oriongenomics.com  
Plate: 287 row: j column: 13  
Seq primer: M13/BUC Reverse  
Class: methylation filtered  
High quality sequence stop: 56.  
Location/Qualifiers  
1. 56  
/organism="Sorghum bicolor"  
/mol\_type="genomic DNA"  
/cultivar="ATx623"  
/db\_xref="taxon:4558"  
/clone="10513599"  
/clone\_lib="Sorghum methylation filtered library (libid: 104)"  
/note="Organ: leaf; Vector: pBSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

**ORIGIN**

**Query Match**  
Best Local Similarity 64.2%; Score 12.2; DB 13; Length 56;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY**  
1 CGCAGGTATCTCTTC 17



## ORIGIN

3'] ; double-stranded cDNA was ligated to Eco RI adaptors [GTGATTCGGTACC], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed by Bob Barstead."

Query Match 64.2%; Score 12.2; DB 1; Length 58;  
Best Local Similarity 82.4%; Pred. No. 1.7e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Db 31 GCACGATCTCCTTCA 18  
31 GCACGATCTCCTTCA 47

RESULT 21  
CA913895  
LOCUS  
DEFINITION CA913895 62 bp mRNA linear EST 27-DEC-2002  
PCS04370 Scarlet Runner Bean Susensor Region Triplex2 Phaseolus  
coccineus cDNA 5' similar to sc07b11.y1 Gm-c1035 Glycine max cDNA,  
mRNA sequence.  
ACCESSION CA913895 GI:27400887  
VERSION  
KEYWORDS EST.  
SOURCE Phaseolus coccineus  
ORGANISM Phaseolus coccineus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Phaseolus.  
1 (bases 1 to 62)  
Bul,A.O., Le,B.H., Weterings,K., Bi,Y.-P., Choi,J.-S.,  
McElroy,K.E., Choi,P.S., Harada,J.J., Fischer,R.L. and  
Goldberg,R.B.  
Gene Activity in Different Regions of a Post-Fertilization Plant  
Embryo by EST Analysis  
Unpublished (2002)  
CONTACT: Goldberg, R.B.  
Department of Molecular, Cell, & Developmental Biology  
University of California, Los Angeles  
621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA  
Tel: 310 825 3270  
Fax: 310 825 8201  
Email: bobg@ucla.edu  
Seq primer: 5' Triplex  
POLYA=No.

## FEATURES

## source

1..62 Location/Qualifiers  
/organism="Phaseolus coccineus"  
/mol\_type="mRNA"  
/cultivar="Hammond's Dwarf Scarlet"  
/db\_xref="taxon:3886"  
/dev\_stage="6-days post-pollination"  
/clone\_lib="Scarlet Runner Bean Susensor Region Triplex2"  
/note="Organ: Susensor Region of Globular-Stage Embryos;  
Vector: Triplex2; Site 1: SfiIA; Site 2: SfiIB; Susensor  
regions were micro-dissected from globular-stage embryos  
six days after pollination from greenhouse-grown plants  
[Weterings et al., Plant Cell 13, 2409-2425 (2001)].  
Double-stranded cDNA was synthesized from susensor mRNA  
using the SMART cDNA Library Construction Kit according to  
the manufacturer (Clontech). The susensor cDNA fragments  
were directionally ligated into the SfiI restriction site  
of the lambda Triplex2 vector (Clontech), and the  
recombinant cDNAs were transformed into E. coli XL1-Blue  
cells (Clontech). Susensor cDNA plasmids used for  
directional sequencing were obtained by in vivo excision  
from the lambda Triplex2 recombinants in E. coli BM25.8  
cells (Clontech)."

## ORIGIN

Query Match 64.2%; Score 12.2; DB 4; Length 62;  
Best Local Similarity 82.4%; Pred. No. 1.7e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Query 3 CACGGATCTCCTTCA 19  
12 CACGATCTCCTTCA 28

RESULT 22  
AA270302  
LOCUS  
DEFINITION AA270302 67 bp mRNA linear EST 26-MAR-1997  
vase005.r1 Soares mouse 3NME12.5 Mus musculus cDNA clone  
IMAGE:735584 5', similar to SW:UCRO BOVIN P13271  
UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN  
QP-C ; mRNA sequence.  
ACCESSION AA270302 GI:1908666  
VERSION  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
1 (bases 1 to 67)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Stepcoe,M., Tan,F., Underwood,K., Moore,B.,  
Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
CONTACT: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watsn.wustl.edu  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MG1:452632  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28m13 rev2 ET from Amersham  
High quality sequence stop: 1.

## FEATURES

## source

1..67 Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_lib="IMAGE:735584"  
/sex="unknown"  
/tissue\_type="fetus"  
/dev\_stage="12.5dpc total fetus"  
/lab\_host="DH10B"  
/clone\_lib="Soares mouse 3NME12.5"  
/note="Organ: whole fetus; Vector: pT73D-PacI; Site 1:  
Not I; Site 2: Eco RI; 1st strand cDNA was primed with a  
Not I - oligo(dT) primer [5'  
TGTTCACATCTGAAGTGGAGCGCGCCCTTATTTTTTTTTTTTTTTT 3'] ,  
on total mouse RNA [provided by Minoru Ko, Wayne State  
Univ.]; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT73 vector.  
Library went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 64.2%; Score 12.2; DB 1; Length 67;  
Best Local Similarity 82.4%; Pred. No. 1.7e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Query 2 GCACGATCTCCTTCA 18

Db 31 GCACGATCTCTCTACA 47

RESULT 23  
AA548218/c  
LOCUS  
DEFINITION  
AA548218 67 bp mRNA linear EST 05-SEP-1997  
n399d10.61 NCI CGAP Pril Homo sapiens cDNA clone IMAGE:1000627  
similar to GB:M2125 TROPOMYOSIN, FIBROBLAST AND EPITHELIAL  
MUSCLE-TYPE (HUMAN);, mRNA sequence.

ACCESSION  
AA548218  
VERSION  
AA548218.1 GI:2318500  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
REFERENCE  
AUTHORS  
TITLE  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL  
COMMENT  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapdb-remail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.  
Chuacui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html

FEATURES  
source  
Trace considered overall poor quality  
Insert Length: 585 Std Error: 0.00  
Seq primer: -40m13 fwd. 5' from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..67  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1000627"  
/sex="male"  
/tissue\_type="normal prostatic epithelial cells"  
/lab\_host="DH10B"  
/clone\_id="NCI CGAP Pril"  
/note="Organ: prostate; Vector: pAMP10; mRNA made from  
normal prostatic epithelial cells, cDNA made by oligo-dT  
priming. Non-directionally cloned. Size-selected on  
agarose gel, average insert size 600 bp. Library made by  
D. Krizman, NIH."

ORIGIN  
Query Match 64.2%; Score 12.2; DB 1; Length 67;  
Best Local Similarity 82.4%; Pred. No. 1.7e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGCATCTCTCTTC 17  
Db 38 GCACGACGATCTCTTC 22

RESULT 24  
W36489  
LOCUS  
DEFINITION  
W36489 67 bp mRNA linear EST 12-SEP-1996  
m571f10.r1 Soares mouse p3MNP19.5 Mus musculus cDNA clone  
IMAGE:334891.5, similar to SW:UCR7 BOVIN P13271  
UBQUINOL-CYTOKROME C REDUCTASE 9.5 KD PROTEIN ;, mRNA sequence.  
W36489  
VERSION  
W36489.1 GI:1318394  
KEYWORDS  
EST.

SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
TITLE  
Marr, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,  
Trelis, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waters, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marr, M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:216291

FEATURES  
source  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..67  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:334891"  
/dev\_stage="19.5 dpc total fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Vector: pT73D (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5'  
TGTTCACCAATCTAGAGTGGAGCGCGCATTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M. Patricia Bonaldo. RNA was kindly provided by  
Dr. Minoru Ko (Wayne State University)."

ORIGIN  
Query Match 64.2%; Score 12.2; DB 10; Length 67;  
Best Local Similarity 82.4%; Pred. No. 1.7e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCACGATCTCTCTCA 18  
Db 31 GCACGATCTCTCTACA 47

RESULT 25  
BE872737  
LOCUS  
DEFINITION  
BE872737 69 bp mRNA linear EST 20-OCT-2000  
601450859F1 NIH\_MGC\_65 Homo sapiens cDNA clone IMAGE:3854607.5,  
mRNA sequence.  
BE872737  
VERSION  
BE872737.1 GI:10321513  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
REFERENCE  
AUTHORS  
NIH-MGC http://mgi.nci.nih.gov/.

**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLAM9580 row: f column: 16  
 High quality sequence stop: 69.

#### FEATURES

source

```
1..69
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAG:3854607"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH1_MGC_65"
/note="Organ: colon; Vector: PCMV-SPORT6; Site_1: NotI, Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."
```

#### ORIGIN

Query Match 63.2%; Score 12; DB 7; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GATCTCTCTCA 18  
 |||||  
 23 GATCTCTCTCA 34

**RESULT 26** 32 bp DNA linear GSS 29-APR-2005  
**CZ489694/c**  
**LOCUS** melanosaster genomic Sequence recovered from 3' end of piggybac,  
**DEFINITION** genomic survey sequence.  
**ACCESSION** CZ489694  
**VERSION** CZ489694.1 GI:62987132  
**KEYWORDS** GSS.  
**SOURCE** Drosophila melanogaster (fruit fly)  
**ORGANISM** Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 32)  
 Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.D., Rymer,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W., Greer,K., Hartouni,S.R., Howie,B., Jakkula,L., Joo,D., Kilpatrick,K., Lauffer,A., Mazotta,J., Smith,R.D., Stevens,L.M., Stuber,C., Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F., Swimmer,C., Koczynski,C., Dwyk,G., Winberg,M.L. and Margolis,J. A complementary transposon tool kit for Drosophila melanogaster using P and piggybac  
 Nat. Genet. 36 (3), 283-287 (2004)  
 14981521

**REFERENCE** Contact: Roger A Hoskins  
**AUTHORS** Berkeley Drosophila Genome Project  
**TITLE** Lawrence Berkeley National Laboratory  
**JOURNAL** Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA  
**PUBMED** Tel: 510 486 4015  
**COMMENT** Fax: 510 486 6798  
 Email: [RHoskins@lbl.gov](mailto:RHoskins@lbl.gov)  
 Sequence recovery method was inverse PCR.  
 Sequence orientation is forward strand relative to 5' end of piggyBac element.

The piggyBac insertion position is 1 in the 32 bases. This insertion position refers to the first base of the 4 base TAA target recognition sequence.  
 Class: transposon insertion site.  
 Location/Qualifiers

#### FEATURES

source

```
1..32
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac WH insertions"
/note="Vector: piggyBac WH (GenBank accession number AY515148); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the WH element using the constitutive alpha-1 tubulin-piggyBac transposase source. We remobilized the WH element from a single amputation element on the Binsncy balancer chromosome in dysgenic females. We outcrossed dysgenic virgin females in vials to the isogenic w- strain and selected new hops in the following generation. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."
```

#### ORIGIN

Query Match 62.1%; Score 11.8; DB 13; Length 32;  
 Best Local Similarity 86.7%; Pred. No. 2.5e+05;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGGTATCTCTTCA 18  
 |||||  
 Db 31 ACGGTATTTCTTCA 17

**RESULT 27** 34 bp mRNA linear EST 28-JUN-2004  
**AJ662253**  
**LOCUS** CSEQRAN09 Sus scrofa cDNA clone C0000023\_F16, mRNA  
**DEFINITION** sequence.  
**ACCESSION** AJ662253  
**VERSION** AJ662253.1 GI:49346376  
**KEYWORDS** EST.  
**SOURCE** Sus scrofa (pig)  
**ORGANISM** Sus scrofa

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Sus.  
 1 (bases 1 to 34)  
 Anderson,S.I., Finlayson,H.A. and Archibald,A.L. Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
 Unpublished (2004)  
 Contact: Anderson SI  
 Genomics and Bioinformatics  
 Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector:pBluescriptII(KS+). R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentae. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, [www.arkgenomics.org](http://www.arkgenomics.org).  
 Location/Qualifiers

#### FEATURES

source

```
1..34
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000023_F16"
/tissue_type="Placenta"
/clone_lib="CSEQRAN09"
/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2:
```



NotI; Single pass sequencing. Normalised library  
constructed from pooled tissue from day 30 placentas."

to determine the genomic sequence flanking the insertion.  
T-DNA derived sequences were removed."

Query Match 62.1%; Score 11.8; DB 1; Length 34;  
Best Local Similarity 86.7%; Pred. No. 2.6e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 62.1%; Score 11.8; DB 14; Length 34;  
Best Local Similarity 86.7%; Pred. No. 2.6e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 CGGTATCTCCTTAC 19  
|||||  
Db 10 CGGTTCCTTCC 24

OY 5 CGGTATCTCCTTAC 19  
|||||  
Db 13 CGGTTCCTTCCC 27

#### RESULT 28

AL769677 34 bp DNA linear GSS 01-APR-2004  
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-091A08-011956,  
DEFINITION genomic survey sequence.  
AL769677  
AL769677.1 GI:21531879

RESULT 29  
ATH526844/c 52 bp DNA linear GSS 08-FEB-2006  
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
DEFINITION 127H07, genomic survey sequence.  
ATH526844  
ATH526844.1 GI:26795104

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
ATH526844.1 GI:26795104  
GSS; left border; T-DNA flanking sequence.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE  
AUTHORS  
TITLE  
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weishaar, B.  
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for  
the identification of T-DNA insertion mutants in Arabidopsis  
thaliana  
Bioinformatics 19 (11), 1441-1442 (2003)

REFERENCE  
AUTHORS  
TITLE  
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, P.,  
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,  
Lepoint, L., Gachebo, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL  
PUBMED  
12874060  
2  
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and  
Weishaar, B.  
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for  
flanking sequence tag-based reverse genetics  
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

JOURNAL  
PUBMED  
1246565  
2 (bases 1 to 52)  
Balzerque, S.  
Direct Submission  
Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (http://www.genoplante.com and  
http://genoplante-info.infobiogen.fr).

REFERENCE  
AUTHORS  
TITLE  
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and  
Weishaar, B.  
High-throughput generation of sequence indexes from T-DNA  
mutagenized Arabidopsis thaliana lines  
Biotechniques 35 (6), 1164-1168 (2003)

COMMENT  
Submitted (21-MAR-2004) Weishaar B., Max-Planck-Institut fuer  
Zoechungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence has been recovered from the left border of the T-DNA.  
It indicates an insertion within the locus defined by BAC clone  
K19E1. Details on the protocols used for generation of the sequence  
are described in references 1-3. The sequences are generated at the  
MPI for Plant Breeding Research in the context of the GABI-Kat  
project. GABI-Kat is part of the German Plant Genomics program  
designated 'GABI'. Information on line availability can be found  
at: http://www.mpi-koein.mpg.de/GABI-Kat/.

JOURNAL  
PUBMED  
14682050  
4 (bases 1 to 34)  
Rosso, M.G., Li, Y., Strizhov, N. and Weishaar, B.  
Direct Submission  
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer  
Zoechungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence has been recovered from the left border of the T-DNA.  
It indicates an insertion within the locus defined by BAC clone  
K19E1. Details on the protocols used for generation of the sequence  
are described in references 1-3. The sequences are generated at the  
MPI for Plant Breeding Research in the context of the GABI-Kat  
project. GABI-Kat is part of the German Plant Genomics program  
designated 'GABI'. Information on line availability can be found  
at: http://www.mpi-koein.mpg.de/GABI-Kat/.

FEATURES  
source  
1..52  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Massillaewekija"  
/db\_xref="taxon:3702"  
/clone\_1ib="127H07"  
/clone\_1ib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Massillaewekija"  
1..52  
/notes="T-DNA flanking sequence  
left border"

COMMENT  
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer  
Zoechungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence has been recovered from the left border of the T-DNA.  
It indicates an insertion within the locus defined by BAC clone  
K19E1. Details on the protocols used for generation of the sequence  
are described in references 1-3. The sequences are generated at the  
MPI for Plant Breeding Research in the context of the GABI-Kat  
project. GABI-Kat is part of the German Plant Genomics program  
designated 'GABI'. Information on line availability can be found  
at: http://www.mpi-koein.mpg.de/GABI-Kat/.

FEATURES  
source  
1..52  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Massillaewekija"  
/db\_xref="taxon:3702"  
/clone\_1ib="127H07"  
/clone\_1ib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Massillaewekija"  
1..52  
/notes="T-DNA flanking sequence  
left border"

#### FEATURES

source  
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/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="GK-091A08-011956"  
/clone\_1ib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/notes="PCR was performed on DNA from Arabidopsis thaliana  
plants (T1) which were transformed with the T-DNA from  
vector pACT161 (Genbank accession number: A537514). The  
lines contain one or more T-DNA insertions. The DNA  
fragment(s) resulting from the PCR were directly sequenced

misc\_feature  
1..52  
/notes="T-DNA flanking sequence  
left border"

Query Match 62.1%; Score 11.8; DB 1; Length 34;  
Best Local Similarity 86.7%; Pred. No. 2.6e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 62.1%; Score 11.8; DB 14; Length 52;  
Best Local Similarity 86.7%; Pred. No. 2.7e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 ACGTATCTCCTTCA 18  
|||||  
Db 28 ACTGATCTGCTTCA 14

OY 4 ACGTATCTCCTTCA 18  
|||||  
Db 28 ACTGATCTGCTTCA 14

fragment(s) resulting from the PCR were directly sequenced

```

RESULT 30
CN655993
LOCUS
DEFINITION LCM003K_B04_T3_D04_04 LCM003 library Glycine max cDNA 5', mRNA
sequence.
ACCESSION CN655993
VERSION
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 53)
Klink,V.P., Alharouf,N.W., Macdonald,M. and Matthews,B.F.
Laser Capture Microdissection (LCM) and Expression Analyses of
Glycine max (Soybean) Syncytium Containing Root Regions Formed by
the Plant Pathogen Heterodera glycines (Soybean Cyst Nematode)
Plant Mol Biol. 59 (6), 965-979 (2005)
16307369
JOURNAL
PUBMED
COMMENT Contact: Alharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alharouf@ars.usda.gov.

FEATURES
source
1..53
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Kent"
/db_xref="taxon:3847"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="LCM003 library"
/notes="Vector: PCR4 TOPO; cDNA clones from mRNA extracted
from syncytium of soybean roots cv. Kent after infection
by SCN race 3."

ORIGIN
Query Match 62.1%; Score 11.8; DB 8; Length 53;
Best Local Similarity 81.2%; Pred. No. 2.7e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGCATCTCTCTT 16
Db 7 CGCAGCATCTCTCTT 22

RESULT 31
CB006039/C 55 bp mRNA linear EST 10-JAN-2003
LOCUS
DEFINITION VVC028H12_138248 An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera
cDNA clone VVC028H12 5, mRNA sequence.
ACCESSION CB006039
VERSION
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 55)
Cushman,J.C.
REFERENCE An expressed sequence tag database for abiotic stressed berries of
AUTHORS Vitis vinifera var. Chardonnay
TITLE Unpublished (2002)
JOURNAL Contact: Cushman JC
COMMENT Department of Biochemistry

```

```

University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 028 row: H column: 12
Seq primer: T3 20mer
High quality sequence stop: 55.
Location/Qualifiers
1..55
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVC028H12"
/tissue_type="berries"
/dev_stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
/clone_lib="An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay"
/notes="Vector: lambda Uni-zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

ORIGIN
Query Match 62.1%; Score 11.8; DB 4; Length 55;
Best Local Similarity 86.7%; Pred. No. 2.7e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CACGGTATCTCTTCC 17
Db 38 CACGGTATCTCTTCC 24

RESULT 32
AZ459394 62 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION 1M0264N10P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0264N10 F, genomic survey sequence.
ACCESSION AZ459394
VERSION
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 62)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiser,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: N column: 10
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 62.
Location/Qualifiers
1..62
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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Db 22 CGAGCTGATCTCT 8

RESULT 35  
LOCUS CV305631  
DEFINITION t16db04.g7 Mouse 5' RACE clones Mus musculus cDNA 5', mRNA  
ACCESSION CV305631  
VERSION CV305631  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 65)  
Dike,S., Ballija,V.S., Nascimento,L.U., Xuan,Z., Ou,J., Zutavern,T., Palmer,L.E., Hannon,G., Zhang,W.Q. and McCombie,W.R.  
The mouse genome: Experimental examination of gene predictions and transcriptional start sites  
Genome Res. 14 (12), 2424-2429 (2004)  
JOURNAL 15574821  
PUBMED  
COMMENT Contact: Ballija VS  
McCombie Laboratory  
Cold Spring Harbor Laboratory  
500 Sunnyside Blvd, Woodbury, NY 11797, USA  
Fax: 516 422 4109  
Email: ballija@cshl.org.  
FEATURES  
source 1..65  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone\_lib="Mouse 5' RACE clones"  
/note="Vector: PCR-TOP02.1; Cloned 5' RACE fragments amplified from 5' RACE cDNA generated from 15 pooled mouse tissues and stages: 7, 11, 15, & 17-day total embryo, whole brain, eye, kidney, liver, lung, prostate, submaxillary gland, smooth muscle, spleen, testes and uterus."

ORIGIN

Query Match 62.1%; Score 11.8; DB 8; Length 65;  
Best Local Similarity 86.7%; Pred. No. 2.8e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCACGGTATCTCCTT 16  
|||||  
28 GCAGGCTATCTGCTT 42

Db 28 GCAGGCTATCTGCTT 42

RESULT 36  
PRO053439/c  
LOCUS FR0053439 65 bp DNA linear GSS 31-JUL-2002  
DEFINITION Fugu rubripes GSS sequence, clone B214J13dH1, genomic survey  
sequence.  
ACCESSION AL689718  
VERSION AL689718.1 GI:22079147  
KEYWORDS GSS; genome survey sequence.  
SOURCE Takifugu rubripes (Fugu rubripes)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Takifugu.  
1 (bases 1 to 65)  
Smith,S.F.  
Direct Submission  
Submitted (08-MAR-2002) MRC Human Genome Mapping Project Resource  
Centre Hinxton, Cambridge, CB10 1SB. UK Email: dione1p@hgmpr.mrc.ac.uk

COMMENT Vector: pBluescript II KS  
V type: phagemid  
PRIMER: KS  
DESCR: One pass dye-terminator sequencing of BAC (pBelosBAC11) cloned genomic sequence  
The BACs can be obtained from [www.hgmpr.mrc.ac.uk](http://www.hgmpr.mrc.ac.uk).  
FEATURES  
source 1..65  
/organism="Takifugu rubripes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:31033"  
/clone\_lib="B214J13dH1"  
/clone\_1ib="BAC B214J13"

ORIGIN

Query Match 62.1%; Score 11.8; DB 14; Length 65;  
Best Local Similarity 86.7%; Pred. No. 2.8e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGTATCTCCTTCAC 19  
|||||  
Db 65 CGGTATCTCCTTCAC 51

RESULT 37  
BH811036 66 bp DNA linear GSS 02-MAY-2002  
LOCUS BH811036  
DEFINITION SALK\_057115 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_057115, genomic survey sequence.  
ACCESSION BH811036  
VERSION BH811036.1 GI:20388854  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 66)  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinb,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Becker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Becker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckers@salk.edu  
This is single pass sequence recovered from the left border of TDNA.  
Class: TDNA tagged.  
FEATURES  
source 1..66  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone\_lib="SALK\_057115"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)"

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 66;  
Best Local Similarity 86.7%; Pred. No. 2.8e+05;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGATCTCTTCAC 19  
|||  
13 CGATATCTCTTCAC 27

RESULT 38  
BH811037 66 bp DNA linear GSS 02-MAY-2002  
LOCUS  
DEFINITION SALK\_057118 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
thaliana genomic clone SALK\_057118, genomic survey sequence.  
ACCESSION BH811037  
VERSION BH811037.1 GI:20388855  
KEYWORDS  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurooids II; Brassicales; Brassicaceae; Arabidopsie.  
REFERENCE  
Alonso, J.M., Leisbe, T.J., Barajas, P., Chen, H., Cheuk, R.,  
Gadrihab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
Shim, P., Zimmerman, J. and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
JOURNAL  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
FEATURES  
source location/Qualifiers  
1..66  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_057118"  
/note="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)"

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 66;  
Best Local Similarity 86.7%; Pred. No. 2.8e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGATCTCTTCAC 19  
|||  
13 CGATATCTCTTCAC 27

RESULT 39  
CZ012701/c 66 bp mRNA linear GSS 05-JAN-2005  
LOCUS  
DEFINITION B0B524 BayGenomics Gene Trap Library pGTL1xf Mus musculus cDNA,  
mRNA sequence.  
ACCESSION CZ012701  
VERSION CZ012701.1 GI:57118300  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Bay Area Functional Genomics Consortium (BayGenomics)  
Contact: BayGenomics  
Email: info@baygenomics.ucsf.edu  
Sequence tag generated by 5' RACE of total RNA from gene trap ES  
cell line. ES cell lines harboring insertion mutation of target  
gene are available upon request from BayGenomics. Annotation  
information available from  
[http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPT=ON-EXACT&TYPE=CELL\\_LINE&KEY=B0B524](http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPT=ON-EXACT&TYPE=CELL_LINE&KEY=B0B524).  
Class: Gene trap.

FEATURES  
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/mol\_type="mRNA"  
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/db\_xref="taxon:10090"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
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/note="Vector: pGTL1xf"

ORIGIN

Query Match 62.1%; Score 11.8; DB 13; Length 66;  
Best Local Similarity 86.7%; Pred. No. 2.8e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGGATCTCTTCA 18  
|||  
31 AAGGATCTCTTCA 17

RESULT 40  
CV305709 68 bp mRNA linear EST 23-SEP-2004  
LOCUS  
DEFINITION t164904.g7 Mouse 5' RACE clones Mus musculus cDNA 5', mRNA  
sequence.  
ACCESSION CV305709  
VERSION CV305709.1 GI:52623042  
KEYWORDS  
SOURCE EST.  
ORGANISM Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
REFERENCE  
Dike, S., Ballja, V.S., Nascimento, L.U., Xuan, Z., Ou, J., Zutavern, T.,  
Palmer, L.E., Hannon, G., Zhang, M.Q. and McCombie, W.R.  
The mouse genome: Experimental examination of gene predictions and  
transcriptional start sites  
Genome Res. 14 (12), 2424-2429 (2004)  
JOURNAL  
PUBMED  
15574821  
Contact: Ballja VS  
McCombie Laboratory  
Cold Spring Harbor Laboratory  
500 Sunnyside Blvd, Woodbury, NY 11797, USA  
Fax: 516 422 4109  
Email: ballja@cshl.org.  
Location/Qualifiers  
1..68  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone\_lib="Mouse 5' RACE clones"  
/note="Vector: PCR-TOPO2.1; Cloned 5' RACE fragments  
amplified from 5' RACE cDNA generated from 15 pooled mouse  
tissues and stages: 7, 11, 15, & 17-day total embryo,  
whole brain, eye, kidney, liver, lung, prostate,

submaxillary gland, smooth muscle, spleen, testes and  
uterus."

Query Match 62.1%; Score 11.8; DB 8; Length 68;  
Best Local Similarity 86.7%; Pred. No. 2.8e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCACGGTATCTCCTT 16  
Db 28 GCATGGTATCTCCTT 42

Search completed: August 10, 2006, 08:47:18  
Job time : 1827.33 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model1

Run on: August 10, 2006, 07:16:15 ; Search time 69.6667 Seconds  
(without alignments)  
510.302 Million cell updates/sec

Title: US-10-636-065-29

Perfect score: 19

Sequence: 1 cgcacgctatctcttcac 19

Scoring table: IDENTITY NUC

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1503076

Minimum DB seq length: 0

Maximum DB seq length: 70

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents NA:\*

1: /EMC\_Celerra\_SIDS3/prodata/2/ina/1/COMB.seq:\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/ina/5/COMB.seq:\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/ina/6A/COMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/ina/6B/COMB.seq:\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/ina/7/COMB.seq:\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/ina/H/COMB.seq:\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/ina/H/COMB.seq:\*  
8: /EMC\_Celerra\_SIDS3/prodata/2/ina/HP/COMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/prodata/2/ina/RE/COMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/prodata/2/ina/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	100.0	19	US-09-672-717-29	Sequence 29, Appl
2	94.7	23	US-09-392-580-3	Sequence 3, Appl
3	81.1	54	US-09-121-211-5	Sequence 5, Appl
4	72.6	59	US-08-956-171E-2496	Sequence 2496, Ap
5	72.6	59	US-08-781-986A-2496	Sequence 2496, Ap
6	70.5	37	US-08-245-754A-15	Sequence 15, Appl
7	70.5	37	US-08-557-731-15	Sequence 15, Appl
8	69.5	20	US-09-198-452A-2460	Sequence 2460, Ap
9	69.5	29	US-10-345-599B-9	Sequence 9, Appl
10	69.5	56	US-09-270-767-31190	Sequence 31190, A
11	67.4	22	US-09-485-529-27	Sequence 27, Appl
12	67.4	23	US-09-485-529-29	Sequence 29, Appl
13	67.4	52	US-09-756-301B-26	Sequence 26, Appl
14	67.4	70	US-08-392-771-2	Sequence 2, Appl
15	66.3	39	US-09-108-006C-33	Sequence 33, Appl
16	66.3	50	US-10-131-827-2096	Sequence 2096, Ap
17	66.3	50	US-10-131-831-2096	Sequence 2096, Ap
18	65.3	21	US-09-432-978-8933	Sequence 8933, Ap
19	65.3	29	US-10-007-010-6	Sequence 6, Appl
20	65.3	35	US-09-485-529-25	Sequence 25, Appl
21	65.3	47	US-09-422-978-316	Sequence 316, Appl
22	64.2	21	US-08-811-682-32	Sequence 32, Appl
23	64.2	24	US-08-697-610-4	Sequence 4, Appl

24	12.2	64.2	24	3	US-08-349-357-4	Sequence 4, Appl
25	12.2	64.2	25	3	US-09-396-1966-18978	Sequence 18978, A
26	12.2	64.2	25	3	US-09-396-1966-77184	Sequence 77184, A
27	12.2	64.2	25	3	US-09-396-1966-77195	Sequence 77195, A
28	12.2	64.2	50	3	US-10-131-827-840	Sequence 840, App
29	12.2	64.2	50	3	US-10-131-831-840	Sequence 840, App
30	12.2	64.2	67	3	US-09-270-767-27961	Sequence 27961, A
31	12.2	64.2	68	2	US-08-553-339-1	Sequence 1, Appl
32	12.2	64.2	68	2	US-09-051-542-1	Sequence 1, Appl
33	12.2	64.2	68	2	US-08-450-274-1	Sequence 1, Appl
34	12.2	64.2	68	7	PCT-US94-05285A-1	Sequence 1, Appl
35	12.2	63.2	29	3	US-09-470-767-7	Sequence 7, Appl
36	12	63.2	41	3	US-08-813-507-46	Sequence 46, Appl
37	12	63.2	41	3	US-09-464-453-46	Sequence 46, Appl
38	12	63.2	53	3	US-09-695-437A-48	Sequence 48, Appl
39	11.8	62.1	16	4	US-09-137-822A-3	Sequence 3, Appl
40	11.8	62.1	20	3	US-09-917-963-122	Sequence 122, App
41	11.8	62.1	25	3	US-09-396-1966-49834	Sequence 49834, A
42	11.8	62.1	26	2	US-09-156-425-3	Sequence 3, Appl
43	11.8	62.1	26	3	US-08-643-704A-40	Sequence 40, Appl
44	11.8	62.1	27	3	US-09-253-396A-103	Sequence 103, App
45	11.8	62.1	27	3	US-09-555-166-47	Sequence 47, Appl
46	11.8	62.1	31	3	US-08-445-463B-48	Sequence 48, Appl
47	11.8	62.1	31	3	US-08-445-464C-48	Sequence 48, Appl
48	11.8	62.1	31	3	US-08-044-857D-48	Sequence 48, Appl
49	11.8	62.1	31	7	PCT-US94-03437-48	Sequence 48, Appl
50	11.8	62.1	60	3	US-08-643-704A-6	Sequence 6, Appl
51	11.6	61.1	20	3	US-09-735-567-21	Sequence 21, Appl
52	11.6	61.1	22	3	US-08-990-571-54	Sequence 54, Appl
53	11.6	61.1	22	3	US-09-528-784A-54	Sequence 54, Appl
54	11.6	61.1	22	3	US-09-569-098B-54	Sequence 54, Appl
55	11.6	61.1	25	2	US-08-174-144-19	Sequence 19, Appl
56	11.6	61.1	25	2	US-08-775-164-19	Sequence 19, Appl
57	11.6	61.1	25	2	US-08-775-607-19	Sequence 19, Appl
58	11.6	61.1	25	2	US-08-775-607-19	Sequence 19, Appl
59	11.6	61.1	25	3	US-09-396-1966-8394	Sequence 8394, Ap
60	11.6	61.1	25	3	US-09-396-1966-14580	Sequence 14580, A
61	11.6	61.1	25	3	US-09-396-1966-75153	Sequence 75153, A
62	11.6	61.1	25	3	US-09-396-1966-75153	Sequence 75153, A
63	11.6	61.1	25	3	US-09-396-1966-87092	Sequence 87092, A
64	11.6	61.1	25	7	PCT-US93-06828-19	Sequence 19, Appl
65	11.6	61.1	26	3	US-09-550-605B-2	Sequence 2, Appl
66	11.6	61.1	26	3	US-09-550-605B-5	Sequence 5, Appl
67	11.6	61.1	27	3	US-08-926-842B-39	Sequence 39, Appl
68	11.6	61.1	27	3	US-09-818-780-11	Sequence 11, Appl
69	11.6	61.1	29	3	US-09-807-897-20	Sequence 20, Appl
70	11.6	61.1	46	3	US-09-354-664-7	Sequence 7, Appl
71	11.6	61.1	50	3	US-10-131-827-2429	Sequence 2429, Ap
72	11.6	61.1	50	5	US-10-131-831-2429	Sequence 2429, Ap
73	11.6	61.1	52	2	US-08-447-173A-56	Sequence 56, Appl
74	11.4	60.0	20	2	US-08-466-265-15	Sequence 15, Appl
75	11.4	60.0	25	3	US-09-396-1966-99034	Sequence 99034, A
76	11.4	60.0	25	3	US-09-396-1966-99050	Sequence 99050, A
77	11.4	60.0	25	3	US-09-396-1966-99051	Sequence 99051, A
78	11.4	60.0	25	3	US-09-396-1966-103409	Sequence 103409, A
79	11.4	60.0	27	2	US-08-192-102-10	Sequence 10, Appl
80	11.4	60.0	27	2	US-08-324-799-10	Sequence 10, Appl
81	11.4	60.0	27	2	US-08-192-861A-10	Sequence 10, Appl
82	11.4	60.0	27	3	US-09-133-119-10	Sequence 10, Appl
83	11.4	60.0	27	3	US-08-192-093A-10	Sequence 10, Appl
84	11.4	60.0	27	3	US-09-756-398B-10	Sequence 10, Appl
85	11.4	60.0	27	3	US-09-756-398B-10	Sequence 10, Appl
86	11.4	60.0	27	4	US-09-766-535A-10	Sequence 10, Appl
87	11.4	60.0	28	2	US-08-827-845-14	Sequence 14, Appl
88	11.4	60.0	28	2	US-08-827-845-14	Sequence 14, Appl
89	11.4	60.0	30	2	US-07-884-811-11	Sequence 11, Appl
90	11.4	60.0	30	2	US-07-885-971-11	Sequence 11, Appl
91	11.4	60.0	30	2	US-08-087-783A-11	Sequence 11, Appl
92	11.4	60.0	30	2	US-08-194-088B-11	Sequence 11, Appl
93	11.4	60.0	30	2	US-08-435-501-10	Sequence 10, Appl
94	11.4	60.0	30	2	US-08-435-501-10	Sequence 10, Appl
95	11.4	60.0	30	2	US-08-792-078-10	Sequence 10, Appl
96	11.4	60.0	30	2	US-08-194-087-11	Sequence 11, Appl

97 11.4 60.0 30 7 PCT-US93-04648-11  
98 11.4 60.0 30 7 PCT-US93-04717-10  
99 11.4 60.0 37 2 US-08-264-115-5  
100 11.4 60.0 39 10 5256648-37

Sequence 11, Appl  
Sequence 10, Appl  
Sequence 5, Appl  
Patent No. 5256648

## ALIGNMENTS

## RESULT 1

US-09-672-717-29  
; Sequence 29, Application US/09672717  
; Patent No. 6673917  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Lacasse, Eric  
; APPLICANT: Baird, Stephen  
; APPLICANT: Holcik, Martin  
; APPLICANT: Young, Sean  
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses  
; FILE REFERENCE: 07891/025001  
; CURRENT APPLICATION NUMBER: US/09/672,717  
; NUMBER OF SEQ ID NOS: 231  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: based on Homo sapiens  
US-09-672-717-29

Query Match 100.0%; Score 19; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCTCTTCCAC 19  
DB 1 CGCAGGTATCTCTCTTCCAC 19

## RESULT 2

US-09-392-580-3  
; Sequence 3, Application US/09392580  
; Patent No. 6087173  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Elizabeth J. Ackermann  
; APPLICANT: Lex M. Cowsett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION  
; FILE REFERENCE: RTS-0072  
; CURRENT APPLICATION NUMBER: US/09/392,580  
; CURRENT FILING DATE: 1999-09-09  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 3  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
US-09-392-580-3

Query Match 94.7%; Score 18; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCTCTTCCAC 19  
DB 1 GCACGGTATCTCTCTTCCAC 18

## RESULT 3

US-09-121-211-5/c  
; Sequence 5, Application US/09121211  
; Patent No. 6750052  
; GENERAL INFORMATION:  
; APPLICANT: Shinohara, Toshimichi  
; APPLICANT: Shingh, Dharendra P.  
; APPLICANT: Chylack, Leo T.  
; TITLE OF INVENTION: Lens Epithelial Cell Derived Growth  
; FILE REFERENCE: B0801/7116  
; CURRENT APPLICATION NUMBER: US/09/121,211  
; CURRENT FILING DATE: 1998-07-23  
; EARLIER APPLICATION NUMBER: U.S. 60/053,549  
; EARLIER FILING DATE: 1997-07-23  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; NAME/KEY: CDS  
; LOCATION: (1)...(54)  
US-09-121-211-5

Query Match 81.1%; Score 15.4; DB 3; Length 54;  
Best Local Similarity 94.1%; Pred. No. 1.4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGTATCTCTCTTCCAC 19  
DB 48 CACGGTATCTCTCTTCCAC 32

## RESULT 4

US-08-956-171E-2496  
; Sequence 2496, Application US/08956171E  
; Patent No. 6593114  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunach  
; APPLICANT: Gail H. Choi  
; APPLICANT: Patrick S. Dillon  
; APPLICANT: Craig A. Rosen  
; APPLICANT: Steven C. Barash  
; APPLICANT: Michael R. Fannon  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5256  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/956,171E  
; FILING DATE: 20-Oct-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/009,861  
; FILING DATE: January 5, 1996  
; APPLICATION NUMBER: 08/781,986  
; FILING DATE: January 3, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark J. Hyman  
; REGISTRATION NUMBER: 46,789  
; REFERENCE/DOCKET NUMBER: PB248P1



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 2496:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 2496:  
US-08-956-171E-2496

Query Match 72.6%; Score 13.8; DB 3; Length 59;  
Best Local Similarity 88.2%; Pred. No. 9.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCCTTC 17  
DB 14 CGCAGGAMTTCTTC 30

## RESULT 5

US-08-781-986A-2496  
Sequence 2496, Application US/08781986A  
Patent No. 6737248  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5255  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,986A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Bob  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET NUMBER: PB248PP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 2496:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-781-986A-2496

Query Match 72.6%; Score 13.8; DB 3; Length 59;  
Best Local Similarity 88.2%; Pred. No. 9.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCCTTC 17  
DB 14 CGCAGGAMTTCTTC 30

## RESULT 6

US-08-245-754A-15  
Sequence 15, Application US/08245754A  
Patent No. 5541110  
GENERAL INFORMATION:  
APPLICANT: Siegall, Clay B.  
TITLE OF INVENTION: Cloning and Expression of a Gene  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bristol-Myers Squibb Company  
STREET: 3005 First Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/245,754A

FILING DATE: 06-MAY-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Poor, Brian W.

REGISTRATION NUMBER: 32,928

REFERENCE/DOCKET NUMBER: ON0124

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 728-4800

TELEFAX: (206) 727-3601

INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-245-754A-15

Query Match 70.5%; Score 13.4; DB 2; Length 37;  
Best Local Similarity 93.3%; Pred. No. 1.5e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CAGGTATCTCCTTC 17  
DB 1 CAGGTATCTCCTTC 15

## RESULT 7

US-08-597-731-15  
Sequence 15, Application US/08597731  
Patent No. 5932447  
GENERAL INFORMATION:  
APPLICANT: Siegall, Clay B.  
TITLE OF INVENTION: Cloning and Expression of a Gene  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bristol-Myers Squibb Company  
STREET: 3005 First Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/597,731  
FILING DATE: 07-FEB-1996

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/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/245,754
/ FILING DATE: 06-MAY-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Poor, Brian W.
/ REGISTRATION NUMBER: 32,928
/ REFERENCE/DOCKET NUMBER: ON0124
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 728-4800
/ TELEFAX: (206) 727-3601
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 37 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-597-731-15
```

```
Query Match 70.5%; Score 13.4; DB 2; Length 37;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 GCACGATCTCTCTTC 17
Db 1 CATGATCTCTCTTC 15
```

```
RESULT 8
US-09-198-452A-2460/C
/ Sequence 2460, Application US/09198452A
/ Patent No. 6559294
/ GENERAL INFORMATION:
/ APPLICANT: Grifflais, R.
/ TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
/ TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
/ FILE REFERENCE: 9710-003-999
/ CURRENT APPLICATION NUMBER: US/09/198,452A
/ CURRENT FILING DATE: 1998-11-24
/ NUMBER OF SEQ ID NOS: 6849
/ SEQ ID NO 2460
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Chlamydia pneumoniae
/ US-09-198-452A-2460
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Query Match 69.5%; Score 13.2; DB 3; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 2 GCACGATCTCTCTTC 19
Db 18 GGACGATCTCTCTTC 1
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```
RESULT 9
US-10-345-599B-9
/ Sequence 9, Application US/10345599B
/ Patent No. 6946294
/ GENERAL INFORMATION:
/ APPLICANT: KANG, JCONG-GU
/ TITLE OF INVENTION: TRANSGENIC PLANT TRANSFORMED WITH A TRANSLATIONALLY
/ TITLE OF INVENTION: CONTROLLED TUMOR PROTEIN (TCTP) GENE
/ FILE REFERENCE: 4469-114.10S
/ CURRENT APPLICATION NUMBER: US/10/345,599B
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: Patentin Ver. 3.2
/ SEQ ID NO 9
/ LENGTH: 29
/ TYPE: DNA
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/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Primer
/ US-10-345-599B-9
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```
Query Match 69.5%; Score 13.2; DB 3; Length 29;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1 CGCAGGATCTCTCTTCA 18
Db 9 CGCAGGATCTCTCTTCA 26
```

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RESULT 10
US-09-270-767-31190
/ Sequence 31190, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 31190
/ LENGTH: 56
/ TYPE: DNA
/ ORGANISM: Drosophila melanogaster
/ US-09-270-767-31190
```

```
Query Match 69.5%; Score 13.2; DB 3; Length 56;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 CGCAGGATCTCTCTTCA 18
Db 4 CGCAGGATCTCTCTTCA 21
```

```
RESULT 11
US-09-485-529-27/C
/ Sequence 27, Application US/09485529
/ Patent No. 6762348
/ GENERAL INFORMATION:
/ APPLICANT: Harberd, Nicholas P
/ APPLICANT: Richards, Donald B
/ APPLICANT: Peng, Junrong
/ TITLE OF INVENTION: Genetic Control of Plant Growth and Development
/ FILE REFERENCE: 620-91
/ CURRENT APPLICATION NUMBER: US/09/485,529
/ CURRENT FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: PCT/GB98/02383
/ PRIOR FILING DATE: 1998-08-07
/ PRIOR APPLICATION NUMBER: GB 9717192.0
/ PRIOR FILING DATE: 1997-08-13
/ NUMBER OF SEQ ID NOS: 108
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 27
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
/ US-09-485-529-27
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```
Query Match 67.4%; Score 12.8; DB 3; Length 22;
Best Local Similarity 87.5%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 4 ACGGATCTCTCTTCA 19
```

Db 19 AGCGTATCTGCTTCAAC 4

## RESULT 12

US-09-485-529-29  
; Sequence 29, Application US/09485529  
; Patent No. 6762348  
; GENERAL INFORMATION:  
; APPLICANT: Harberd, Nicholas P  
; APPLICANT: Richards, Donald E  
; APPLICANT: Peng, Jintong  
; TITLE OF INVENTION: Genetic Control of Plant Growth and Development  
; FILE REFERENCE: 620-91  
; CURRENT APPLICATION NUMBER: US/09/485,529  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: PCT/GB98/02383  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: GB 9717192.0  
; PRIOR FILING DATE: 1997-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-485-529-29

Query Match 67.4%; Score 12.8; DB 3; Length 23;  
Best Local Similarity 87.5%; Pred. No. 2.9e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACAGTATCTGCTTCAAC 19  
Db 4 AGCGTATCTGCTTCAAC 19

RESULT 13  
US-09-756-301B-26/c  
; Sequence 26, Application US/09756301B  
; Patent No. 6790444  
; GENERAL INFORMATION:  
; APPLICANT: Le, Junming  
; APPLICANT: Vilecek, Jan  
; APPLICANT: Daddona, Peter  
; APPLICANT: Ghayeb, John  
; APPLICANT: Knight, David M.  
; APPLICANT: Siegel, Scott  
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of  
; TITLE OF INVENTION: Human Tumor Necrosis Factor  
; FILE REFERENCE: 0975.1005-008  
; CURRENT APPLICATION NUMBER: US/09/756,301B  
; CURRENT FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: U.S. 09/133,119  
; PRIOR FILING DATE: 1998-08-12  
; PRIOR APPLICATION NUMBER: U.S. 08/570,674  
; PRIOR FILING DATE: 1995-12-11  
; PRIOR APPLICATION NUMBER: U.S. 08/324,799  
; PRIOR FILING DATE: 1994-10-18  
; PRIOR APPLICATION NUMBER: U.S. 08/192,102  
; PRIOR FILING DATE: 1994-02-04  
; PRIOR APPLICATION NUMBER: U.S. 08/192,861  
; PRIOR FILING DATE: 1994-02-04  
; PRIOR APPLICATION NUMBER: U.S. 08/192,093  
; PRIOR FILING DATE: 1994-02-04  
; PRIOR APPLICATION NUMBER: U.S. 08/010,406  
; PRIOR FILING DATE: 1993-01-29  
; PRIOR APPLICATION NUMBER: U.S. 08/013,413  
; PRIOR FILING DATE: 1993-02-02  
; PRIOR APPLICATION NUMBER: U.S. 07/943,852  
; PRIOR FILING DATE: 1992-09-11

; PRIOR APPLICATION NUMBER: U.S. 07/853,606  
; PRIOR FILING DATE: 1992-03-18  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Partial sequence of pLC871  
US-09-756-301B-26

Query Match 67.4%; Score 12.8; DB 3; Length 52;  
Best Local Similarity 87.5%; Pred. No. 3.2e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CACGATATCTGCTTCA 18  
Db 27 CCGATATCTGCTTCA 12

RESULT 14  
US-08-392-771-2/c  
; Sequence 2, Application US/08392771  
; Patent No. 5917122  
; GENERAL INFORMATION:  
; APPLICANT: Byrnie, Guenard  
; TITLE OF INVENTION: TETRACYCLINE REPRESSOR-MEDIATED BINARY  
; TITLE OF INVENTION: REGULATION SYSTEM FOR CONTROL OF GENE EXPRESSION IN  
; TITLE OF INVENTION: TRANSGENIC ANIMALS  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BAXTER INTERNATIONAL INC.  
; ADDRESSEE: LAW DEPARTMENT, MPR-A25  
; STREET: 1620 N. MAUEGAN ROAD  
; CITY: MCGRAW PARK  
; STATE: ILLINOIS  
; COUNTRY: USA  
; ZIP: 60085

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/392,771  
; FILING DATE: 24-FEB-1995  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MATTEWSON, CHARLES R.  
; REGISTRATION NUMBER: 30,660  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847-473-6693  
; TELEFAX: 847-473-6933

; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 70 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-392-771-2

Query Match 67.4%; Score 12.8; DB 2; Length 70;  
Best Local Similarity 87.5%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACAGTATCTGCTTCAAC 19  
Db 63 ACAGTATCTGCTTCAAC 48

```
RESULT 15
US-09-108-006C-33/c
; Sequence 33, Application US/09108006C
; Patent No. 6524613
; GENERAL INFORMATION:
; APPLICANT: Steer, Clifford J.
; Krenn, Betsy T.
; Bandyopadhyay, Paramita
; Roy-Chowdhury, Jayanta
; TITLE OF INVENTION: Hepatocellular Chimeraplasty
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kimeragen, Inc.
; STREET: 300 Pleasant Run
; CITY: Newtown
; STATE: PA
; COUNTRY: USA
; ZIP: 18940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,006C
; FILING DATE: 30-Jun-1992
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,288
; FILING DATE: 30-Apr-1997
; APPLICATION NUMBER: 60/054,837
; FILING DATE: 05-AUG-1997
; APPLICATION NUMBER: 60/064,996
; FILING DATE: 10-NOV-1997
; APPLICATION NUMBER: 60/074,497
; FILING DATE: 12-FEB-1998
; APPLICATION NUMBER: PCT US 98/08834
; FILING DATE: 30-APR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebe, Thomas
; REGISTRATION NUMBER: 29258
; REFERENCE/DOCKET NUMBER: 7991-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-504-4444
; TELEFAX: 215-504-4545
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-108-006C-33

Query Match      66.3%; Score 12.6; DB 3; Length 39;
Best Local Similarity 78.9%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CGCAGCGTATCTCTCTTAC 19
Db      29 CCCCACATATCTCTTCTTAC 11

RESULT 16
US-10-131-827-2096/c
; Sequence 2096, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; Fry, Kirk
; APPLICANT: Woodward, Robert
```

```
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2096
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-2096

Query Match      66.3%; Score 12.6; DB 3; Length 50;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CGCAGCGTATCTCTCTTAC 19
Db      49 CTCACGTCTCTCTGAC 31

RESULT 17
US-10-131-831-2096/c
; Sequence 2096, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2096
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-2096

Query Match      66.3%; Score 12.6; DB 5; Length 50;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CGCAGCGTATCTCTCTTAC 19
Db      49 CTCACGTCTCTCTGAC 31

RESULT 18
US-09-422-978-8933
; Sequence 8933, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Ballelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
```

```

; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8933
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-20198 for SEQ 1068, in compl
US-09-422-978-8933
```

```

Query Match          65.3%; Score 12.4; DB 3; Length 21;
Best Local Similarity 92.9%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY          4 ACGGTAATCTCCTTC 17
Db          7 ACTGTAATCTCCTTC 20
```

```

RESULT 19
US-10-007-010-6/c
; Sequence 6, Application US/10007010
; Patent No. 6828151
; GENERAL INFORMATION:
; APPLICANT: Alexander H. Borchers
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
; FILE REFERENCE: RTS-0345
; CURRENT APPLICATION NUMBER: US/10/007,010
; CURRENT FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 6
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-007-010-6
```

```

Query Match          65.3%; Score 12.4; DB 3; Length 29;
Best Local Similarity 92.9%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY          3 CACGGTAATCTCCTT 16
Db          20 CACGGTAATCTCCTT 7
```

```

RESULT 20
US-09-485-529-25
; Sequence 25, Application US/09485529
; Patent No. 6762348
; GENERAL INFORMATION:
; APPLICANT: Harberd, Nicholas P
; APPLICANT: Richards, Donald E
; APPLICANT: Peng, Jinhong
; TITLE OF INVENTION: Genetic Control of Plant Growth and Development
; FILE REFERENCE: 620-91
; CURRENT APPLICATION NUMBER: US/09/485,529
; CURRENT FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/GB98/02383
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: GB 9717192.0
; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 108
```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-485-529-25
```

```

Query Match          65.3%; Score 12.4; DB 3; Length 35;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY          6 GGTATCTCTTCAC 19
Db          1 GGTATCTCTTCAC 14
```

```

RESULT 21
US-09-422-978-316/c
; Sequence 316, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSRT.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 316
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-14179-191 : polymorphic base A or G
US-09-422-978-316
```

```

Query Match          65.3%; Score 12.4; DB 3; Length 47;
Best Local Similarity 81.2%; Pred. No. 5.1e+03;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY          4 ACGGTAATCTCTTCAC 19
Db          39 ACGGTAATCTCTTCAY 24
```

```

RESULT 22
US-08-811-682-32/c
; Sequence 32, Application US/08811682
; Patent No. 6331616
; GENERAL INFORMATION:
; APPLICANT: Tompkins, Wayne A.F.
; APPLICANT: Tompkins, Mary B.
; APPLICANT: Yang, Joo-Sung
; TITLE OF INVENTION: Feline Immunodeficiency Virus Clone
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Bell Seitzer Park & Gibson
; STREET: PO Drawer 34009
; CITY: Charlotte
; STATE: No. 6331616th Carolina
; COUNTRY: USA
; ZIP: 28234
```

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/811,662  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Virginia C.  
REGISTRATION NUMBER: 37,092  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-420-2200  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-811-682-32

Query Match 64.2%; Score 12.2; DB 3; Length 21;  
Best Local Similarity 82.4%; Pred. No. 6e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTTCA 18  
DB 18 GCACGATATCTCCTTA 2

RESULT 23  
US-08-697-610-4  
Sequence 4, Application US/08697610  
Patent No. 6172187  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Sato, Takaki  
TITLE OF INVENTION: CD40 Associated Proteins  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/697,610  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/349,357  
FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-697-610-4

Query Match 64.2%; Score 12.2; DB 3; Length 24;  
Best Local Similarity 82.4%; Pred. No. 6e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CACGGTATCTCCTTCA 19  
DB 8 CACTGTCTCTCTGCAC 24

RESULT 24  
US-08-349-357-4  
Sequence 4, Application US/08349357  
Patent No. 6265556

GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Sato, Takaki  
TITLE OF INVENTION: CD40 Associated Proteins  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/349,357  
FILING DATE: 02-DEC-1994

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 1203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-349-357-4

Query Match 64.2%; Score 12.2; DB 3; Length 24;  
Best Local Similarity 82.4%; Pred. No. 6e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CACGGTATCTCCTTCA 19  
DB 8 CACTGTCTCTCTGCAC 24

RESULT 25  
US-09-396-18978  
Sequence 18978, Application US/0939618978  
Patent No. 6821724

GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1

;; CURRENT APPLICATION NUMBER: US/09/396,196G  
;; CURRENT FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: 60/100,678  
;; PRIOR FILING DATE: 1998-09-17  
;; NUMBER OF SEQ ID NOS: 127806  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 18978  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: Mus musculus  
US-09-396-196G-18978

Query Match 64.2%; Score 12.2; DB 3; Length 25;  
Best Local Similarity 82.4%; Pred. No. 6.1e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CACGGTATCTCCTTCAC 19  
Db 7 CACGGCATCTACTCCAC 23

RESULT 26  
US-09-396-196G-77184  
;; Sequence 77184, Application US/09396196G  
;; Patent No. 6821724  
;; GENERAL INFORMATION:  
;; APPLICANT: Michael Miltmann  
;; APPLICANT: David Lockhart  
;; APPLICANT: Affymetrix, Inc.  
;; TITLE OF INVENTION: Methods of Genetic Analysis  
;; FILE REFERENCE: 3101.1  
;; CURRENT APPLICATION NUMBER: US/09/396,196G  
;; CURRENT FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: 60/100,678  
;; PRIOR FILING DATE: 1998-09-17  
;; NUMBER OF SEQ ID NOS: 127806  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 77184  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: mus musculus  
US-09-396-196G-77184

Query Match 64.2%; Score 12.2; DB 3; Length 25;  
Best Local Similarity 82.4%; Pred. No. 6.1e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCCTTC 17  
Db 9 CGCAGTATCATCTTC 25

RESULT 27  
US-09-396-196G-77195  
;; Sequence 77195, Application US/09396196G  
;; Patent No. 6821724  
;; GENERAL INFORMATION:  
;; APPLICANT: Michael Miltmann  
;; APPLICANT: David Mack  
;; APPLICANT: David Lockhart  
;; APPLICANT: Affymetrix, Inc.  
;; TITLE OF INVENTION: Methods of Genetic Analysis  
;; FILE REFERENCE: 3101.1  
;; CURRENT APPLICATION NUMBER: US/09/396,196G  
;; CURRENT FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: 60/100,678  
;; PRIOR FILING DATE: 1998-09-17  
;; NUMBER OF SEQ ID NOS: 127806  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 77195  
;; LENGTH: 25  
;; TYPE: DNA

;; ORGANISM: mus musculus  
US-09-396-196G-77195

Query Match 64.2%; Score 12.2; DB 3; Length 25;  
Best Local Similarity 82.4%; Pred. No. 6.1e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCCTTC 17  
Db 3 CGCAGTATCATCTTC 19

RESULT 28  
US-10-131-827-840  
;; Sequence 840, Application US/10131827  
;; Patent No. 6905827  
;; GENERAL INFORMATION:  
;; APPLICANT: Wohlgenuth, Jay  
;; APPLICANT: Fry, Kirk  
;; APPLICANT: Woodward, Robert  
;; APPLICANT: Ly, Ngoc  
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
;; FILE REFERENCE: 506612000120  
;; CURRENT APPLICATION NUMBER: US/10/131,827  
;; CURRENT FILING DATE: 2002-09-06  
;; PRIOR APPLICATION NUMBER: US 10/006,290  
;; PRIOR FILING DATE: 2001-10-22  
;; PRIOR APPLICATION NUMBER: US 60/296,764  
;; PRIOR FILING DATE: 2001-06-08  
;; NUMBER OF SEQ ID NOS: 9090  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 840  
;; LENGTH: 50  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-131-827-840

Query Match 64.2%; Score 12.2; DB 3; Length 50;  
Best Local Similarity 82.4%; Pred. No. 6.1e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCACGGTATCTCCTTCA 18  
Db 26 GCCCGGTACGTCTTCA 42

RESULT 29  
US-10-131-831-840  
;; Sequence 840, Application US/10131831  
;; Patent No. 7026121  
;; GENERAL INFORMATION:  
;; APPLICANT: Wohlgenuth, Jay  
;; APPLICANT: Fry, Kirk  
;; APPLICANT: Woodward, Robert  
;; APPLICANT: Ly, Ngoc  
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING  
;; FILE REFERENCE: 506612000121  
;; CURRENT APPLICATION NUMBER: US/10/131,831  
;; CURRENT FILING DATE: 2002-08-05  
;; PRIOR APPLICATION NUMBER: US 10/006,290  
;; PRIOR FILING DATE: 2001-10-22  
;; PRIOR APPLICATION NUMBER: US 60/296,764  
;; PRIOR FILING DATE: 2001-06-08  
;; NUMBER OF SEQ ID NOS: 9190  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 840  
;; LENGTH: 50  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-131-831-840

Query Match 64.2%; Score 12.2; DB 5; Length 50;  
Best Local Similarity 82.4%; Pred. No. 6.6e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTTCA 18  
Db 26 GCCCGGTAGCTCCTTCA 42

## RESULT 30

US-09-270-767-27961/C  
; Sequence 27961, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; NUMBER OF SEQ ID NOS: 1999-03-17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27961  
; LENGTH: 67  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-27961

Query Match 64.2%; Score 12.2; DB 3; Length 67;  
Best Local Similarity 82.4%; Pred. No. 6.8e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCCTTC 17  
Db 58 CGCAGGTATCTCCTTC 42

## RESULT 31

US-08-553-339-1  
; Sequence 1, Application US/08553339A  
; Patent No. 5856300  
; GENERAL INFORMATION:  
; APPLICANT: Rittershaus, Charles W  
; APPLICANT: Carol, Toth A  
; TITLE OF INVENTION: COMPOSITIONS COMPRISING COMPLEMENT RELATED PROTEINS AND  
; TITLE OF INVENTION: CARBOHYDRATES, AND METHODS FOR PRODUCING AND USING  
; FILE REFERENCE: TCS-409, 1P US sequence 11st  
; CURRENT APPLICATION NUMBER: US/08/553,339A  
; EARLIER FILING DATE: 1995-11-13  
; EARLIER APPLICATION NUMBER: US 08/061,982  
; EARLIER FILING DATE: 1993-05-17  
; EARLIER APPLICATION NUMBER: PCT/US94/05285  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 68  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: commercial  
US-08-553-339-1

Query Match 64.2%; Score 12.2; DB 2; Length 68;  
Best Local Similarity 82.4%; Pred. No. 6.8e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCCTTC 17  
Db 1 CGCCGGTCTCCCTTC 17

RESULT 32  
US-09-061-542-1  
; Sequence 1, Application US/09061542  
; Patent No. 5976540  
; GENERAL INFORMATION:  
; APPLICANT: Rittershaus, Charles W  
; APPLICANT: Carol, Toth A  
; TITLE OF INVENTION: COMPOSITIONS COMPRISING COMPLEMENT RELATED PROTEINS AND  
; TITLE OF INVENTION: CARBOHYDRATES, AND METHODS FOR PRODUCING AND USING  
; FILE REFERENCE: TCS-409, 1P US-2 sequence 11st  
; CURRENT APPLICATION NUMBER: US/09/061,542  
; EARLIER FILING DATE: 1998-04-16  
; EARLIER APPLICATION NUMBER: US 08/553,339  
; EARLIER FILING DATE: 1995-11-13  
; EARLIER APPLICATION NUMBER: US 08/061,982  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 68  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: commercial  
US-09-061-542-1

Query Match 64.2%; Score 12.2; DB 2; Length 68;  
Best Local Similarity 82.4%; Pred. No. 6.8e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCCTTC 17  
Db 1 CGCCGGTCTCCCTTC 17

## RESULT 33

US-08-450-274-1  
; Sequence 1, Application US/08450274  
; Patent No. 6193979  
; GENERAL INFORMATION:  
; APPLICANT: Rittershaus, Charles W.  
; APPLICANT: Toth, Carol A.  
; TITLE OF INVENTION: Compositions comprising complement  
; TITLE OF INVENTION: related proteins and carbohydrates and methods for producing ar  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Banner & Allegretti, Ltd.  
; STREET: 10 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-7407  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: wordperfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,274  
; FILING DATE: (concurrently herewith)  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; FILING DATE: 12-May-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Leon R. Yankwich  
; REGISTRATION NUMBER: 30,237  
; REFERENCE/DOCKET NUMBER: TCS-101-PCON  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-9100  
; TELEFAX: 617-345-9111



; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 68 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; US-08-450-274-1

Query Match 64.2%; Score 12.2; DB 3; Length 68;  
 Best Local Similarity 82.4%; Pred. No. 6.8e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGGATCTCTCCCTTC 17  
 DB 1 CGCCCGGTCTCCCTTC 17

RESULT 34  
 PCT-US94-05285A-1  
 ; Sequence 1, Application PC/TUS9405285A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rittershaus, Charles W.  
 ; APPLICANT: Roth, Carol A.  
 ; TITLE OF INVENTION: Compositions comprising complement  
 ; TITLE OF INVENTION: related proteins and carbohydrates, and methods for producing  
 ; TITLE OF INVENTION: using said compositions  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: T Cell Sciences, Inc.  
 ; STREET: 38 Sidney Street  
 ; CITY: Cambridge  
 ; STATE: Massachusetts  
 ; COUNTRY: United States of America  
 ; ZIP: 02139  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage  
 ; COMPUTER: IBM PC Compatible  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: WordPerfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/05285A  
 ; FILING DATE: 12-MAY-1994  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/061,982  
 ; FILING DATE: 17-MAY-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Matchew, Gale F.  
 ; REGISTRATION NUMBER: 32,269  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-621-1400  
 ; TELEFAX: 617-621-0627  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 68 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE:  
 ; DESCRIPTION: DNA  
 ; PCT-US94-05285A-1

Query Match 64.2%; Score 12.2; DB 7; Length 68;  
 Best Local Similarity 82.4%; Pred. No. 6.8e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGGATCTCTCCCTTC 17  
 DB 1 CGCCCGGTCTCCCTTC 17

RESULT 35  
 US-09-470-276-7  
 ; Sequence 7, Application US/09470276  
 ; Patent No. 6670460  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.  
 ; APPLICANT: KOLODNER, Richard  
 ; APPLICANT: WINAND, Nena  
 ; TITLE OF INVENTION: A METHOD OF DETECTION OF ALTERATIONS IN MSH5  
 ; FILE REFERENCE: 700157/47483C  
 ; CURRENT APPLICATION NUMBER: US/09/470,276  
 ; CURRENT FILING DATE: 1999-12-22  
 ; PRIOR APPLICATION NUMBER: 60/051,686  
 ; PRIOR FILING DATE: 1997-07-03  
 ; PRIOR APPLICATION NUMBER: PCT/US98/13850  
 ; PRIOR FILING DATE: 1998-07-02  
 ; NUMBER OF SEQ ID NOS: 104  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 7  
 ; LENGTH: 29  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-470-276-7

Query Match 63.2%; Score 12; DB 3; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGTATCTCTCTTC 17  
 DB 9 GGTATCTCTCTTC 20

RESULT 36  
 US-08-813-507-46/c  
 ; Sequence 46, Application US/08813507  
 ; Patent No. 6114116  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lemieux, Bertrand  
 ; APPLICANT: Landry, Benoit S.  
 ; APPLICANT: Sapolsky, Ronald J.  
 ; TITLE OF INVENTION: Brascica Polymorphisms  
 ; NUMBER OF SEQUENCES: 173  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/813,507  
 ; FILING DATE: 07-MAR-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/032,069  
 ; FILING DATE: 02-DEC-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Liebeschuetz, Joe  
 ; REGISTRATION NUMBER: 37,505  
 ; REFERENCE/DOCKET NUMBER: 018547-030100US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415 576-0200  
 ; TELEFAX: 415 576-0200  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 46:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 41 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-813-507-46

Query Match 63.2%; Score 12; DB 3; Length 41;  
Best Local Similarity 85.7%; Pred. No. 8.2e+03;  
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCA 18  
DB 21 YGGTCTCTCCTTCA 8

RESULT 37  
US-09-464-453-46/c  
Sequence 46, Application US/09464453  
Patent No. 635866  
GENERAL INFORMATION:  
APPLICANT: Lemieux, Bertrand  
Landry, Benoit S.  
Sapolsky, Ronald J.  
TITLE OF INVENTION: Brassica Polymorphisms  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/464,453  
FILING DATE: 14-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/813,507  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschuetz, Joe  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 018547-030100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415 576-0200  
TELEFAX: 415 576-0200  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
US-09-464-453-46

Query Match 63.2%; Score 12; DB 3; Length 41;  
Best Local Similarity 85.7%; Pred. No. 8.2e+03;  
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCA 18  
DB 21 YGGTCTCTCCTTCA 8

RESULT 38  
US-09-695-437A-48/c  
Sequence 48, Application US/09695437A  
Patent No. 6803203

GENERAL INFORMATION:  
APPLICANT: Brookhaven Science Associates  
APPLICANT: Anderson, Carl W  
APPLICANT: Connolly, Margery A  
TITLE OF INVENTION: DNA-PK Assay  
FILE REFERENCE: BSA 01-02  
CURRENT APPLICATION NUMBER: US/09/695,437A  
CURRENT FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 08/398,139  
PRIOR FILING DATE: 1995-03-03  
PRIOR APPLICATION NUMBER: 08/132,284  
PRIOR FILING DATE: 1993-10-06  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 48  
LENGTH: 53  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Sense primer sequence  
US-09-695-437A-48

Query Match 63.2%; Score 12; DB 3; Length 53;  
Best Local Similarity 100.0%; Pred. No. 8.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGTATCTCCTTC 17  
DB 32 GGTATCTCCTTC 21

RESULT 39  
US-09-137-822A-3/c  
Sequence 3, Application US/09137822A  
Patent No. 6979536  
GENERAL INFORMATION:  
APPLICANT: NAESBY, MICHAEL  
TITLE OF INVENTION: SMALL TRIPLEX FORMING PNA OLIGOS  
FILE REFERENCE: 108382-08067  
CURRENT APPLICATION NUMBER: US/09/137,822A  
CURRENT FILING DATE: 1998-08-21  
PRIOR APPLICATION NUMBER: EP 97 114 512.3  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 3  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-137-822A-3

Query Match 62.1%; Score 11.8; DB 4; Length 16;  
Best Local Similarity 86.7%; Pred. No. 9.3e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCAC 19  
DB 16 CGGTATCTTCTGCAC 2

RESULT 40  
US-09-917-963-122/c  
Sequence 122, Application US/09917963  
Patent No. 6767739  
GENERAL INFORMATION:  
APPLICANT: Rosanne M. Crooke  
APPLICANT: Mark J. Graham  
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSMAL TRIGLYCERIDE TRANSFER PROTEIN  
TITLE OF INVENTION: EXPRESSION  
FILE REFERENCE: ISPH-0591

; CURRENT APPLICATION NUMBER: US/09/917,963  
; CURRENT FILING DATE: 2001-07-30  
; NUMBER OF SEQ ID NOS: 137  
; SEQ ID NO 122  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-917-963-122

Query Match 62.1%; Score 11.8; DB 3; length 20;  
Best Local Similarity 86.7%; Pred. No. 9.6e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGGTATCTCCTTCA 18  
||| |||||  
Db 15 ACGATGTCTCCTTCA 1

Search completed: August 10, 2006, 08:50:50  
Job time : 71.6667 secs

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 08:11:42 ; Search time 272.667 Seconds

(without alignments)  
485.841 Million cell updates/sec

Title: US-10-636-065-29

Perfect score: 19

Sequence: 1 cgcacgctactctcttcac 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 524920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 340112

Minimum DB seq length: 19

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :  
1: N Geneseq\_8:\*  
2: Geneseqn1980s:\*  
3: Geneseqn1990s:\*  
4: Geneseqn2000s:\*  
5: Geneseqn2001as:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*  
14: Geneseqn2005s:\*  
15: Geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	6	ABK93682 Human inh
2	19	100.0	19	14	AEAI0008 Antisense
3	19	100.0	19	14	AEAI0086 Antisense
4	15	78.9	19	14	ADK86146 XIAP targ
5	15	78.9	19	14	ADK86613 XIAP targ
6	14	73.7	19	10	ADP68184 Human ant
7	14	73.7	19	10	ADP68262 Human ant
8	14	73.7	19	14	AEAI0122 Antisense
9	14	73.7	19	14	AEAI0076 Antisense
10	14	73.7	19	14	AEAI0108 Antisense
11	14	73.7	19	14	AEAI09518 Antisense
12	14	73.7	19	14	AEAI0267 Antisense
13	14	73.7	19	14	AEAI09596 Antisense
14	13	68.4	19	14	AEAI0267 Antisense
15	13	68.4	19	14	AEAI09596 Antisense
16	12.6	65.3	19	12	AAK24944 Mouse oes
17	11.8	62.1	19	2	AAK33389 Murine MB
18	11.8	62.1	19	2	AAK33389 Murine MB

19	11.8	62.1	19	15	AEI14562 Human cho
20	11.4	60.0	19	10	ADP73037 DNA seque
21	11.4	60.0	19	10	ACD28194 Human rep
22	11.1	57.9	19	3	AAZ73203 Human bla
23	11.1	57.9	19	12	ADQ61051 Anti-HCK
24	11.1	57.9	19	14	ADY83894 Escherich
25	11.1	57.9	19	14	ADY83902 Escherich
26	11.1	57.9	19	14	AEAI02570 Cholester
27	11.1	57.9	19	14	AEAI02470 Cholester
28	11.1	57.9	19	14	AEAI02470 Cholester
29	11.1	57.9	19	14	AEAI02470 Cholester
30	10.8	56.8	19	3	AAAI5544 Cyclin A1
31	10.8	56.8	19	3	AAAI5544 Cyclin A1
32	10.8	56.8	19	3	AAAI5544 Cyclin A1
33	10.8	56.8	19	3	AAAI5544 Cyclin A1
34	10.8	56.8	19	3	AAAI5544 Cyclin A1
35	10.8	56.8	19	3	AAAI5544 Cyclin A1
36	10.8	56.8	19	3	AAAI5544 Cyclin A1
37	10.8	56.8	19	3	AAAI5544 Cyclin A1
38	10.8	56.8	19	3	AAAI5544 Cyclin A1
39	10.8	56.8	19	3	AAAI5544 Cyclin A1
40	10.8	56.8	19	3	AAAI5544 Cyclin A1
41	10.8	56.8	19	3	AAAI5544 Cyclin A1
42	10.8	56.8	19	3	AAAI5544 Cyclin A1
43	10.8	56.8	19	3	AAAI5544 Cyclin A1
44	10.8	56.8	19	3	AAAI5544 Cyclin A1
45	10.8	56.8	19	3	AAAI5544 Cyclin A1
46	10.8	56.8	19	3	AAAI5544 Cyclin A1
47	10.8	56.8	19	3	AAAI5544 Cyclin A1
48	10.8	56.8	19	3	AAAI5544 Cyclin A1
49	10.8	56.8	19	3	AAAI5544 Cyclin A1
50	10.8	56.8	19	3	AAAI5544 Cyclin A1
51	10.8	56.8	19	3	AAAI5544 Cyclin A1
52	10.8	56.8	19	3	AAAI5544 Cyclin A1
53	10.8	56.8	19	3	AAAI5544 Cyclin A1
54	10.8	56.8	19	3	AAAI5544 Cyclin A1
55	10.8	56.8	19	3	AAAI5544 Cyclin A1
56	10.8	56.8	19	3	AAAI5544 Cyclin A1
57	10.8	56.8	19	3	AAAI5544 Cyclin A1
58	10.8	56.8	19	3	AAAI5544 Cyclin A1
59	10.8	56.8	19	3	AAAI5544 Cyclin A1
60	10.8	56.8	19	3	AAAI5544 Cyclin A1
61	10.8	56.8	19	3	AAAI5544 Cyclin A1
62	10.8	56.8	19	3	AAAI5544 Cyclin A1
63	10.8	56.8	19	3	AAAI5544 Cyclin A1
64	10.8	56.8	19	3	AAAI5544 Cyclin A1
65	10.8	56.8	19	3	AAAI5544 Cyclin A1
66	10.8	56.8	19	3	AAAI5544 Cyclin A1
67	10.8	56.8	19	3	AAAI5544 Cyclin A1
68	10.8	56.8	19	3	AAAI5544 Cyclin A1
69	10.8	56.8	19	3	AAAI5544 Cyclin A1
70	10.8	56.8	19	3	AAAI5544 Cyclin A1
71	10.8	56.8	19	3	AAAI5544 Cyclin A1
72	10.8	56.8	19	3	AAAI5544 Cyclin A1
73	10.8	56.8	19	3	AAAI5544 Cyclin A1
74	10.8	56.8	19	3	AAAI5544 Cyclin A1
75	10.8	56.8	19	3	AAAI5544 Cyclin A1
76	10.8	56.8	19	3	AAAI5544 Cyclin A1
77	10.8	56.8	19	3	AAAI5544 Cyclin A1
78	10.8	56.8	19	3	AAAI5544 Cyclin A1
79	10.8	56.8	19	3	AAAI5544 Cyclin A1
80	10.8	56.8	19	3	AAAI5544 Cyclin A1
81	10.8	56.8	19	3	AAAI5544 Cyclin A1
82	10.8	56.8	19	3	AAAI5544 Cyclin A1
83	10.8	56.8	19	3	AAAI5544 Cyclin A1
84	10.8	56.8	19	3	AAAI5544 Cyclin A1
85	10.8	56.8	19	3	AAAI5544 Cyclin A1
86	10.8	56.8	19	3	AAAI5544 Cyclin A1
87	10.8	56.8	19	3	AAAI5544 Cyclin A1
88	10.8	56.8	19	3	AAAI5544 Cyclin A1
89	10.8	56.8	19	3	AAAI5544 Cyclin A1
90	10.8	56.8	19	3	AAAI5544 Cyclin A1
91	10.8	56.8	19	3	AAAI5544 Cyclin A1

92	10.4	54.7	19	3	AAZ70584	Human b1a	c 165	10	52.6	19	14	ADY87409	ADY87409 VEGFR s1R
93	10.4	54.7	19	3	AAZ71863	Human b1a	c 166	10	52.6	19	14	AEA34632	Aea34632 Human TRP
94	10.4	54.7	19	5	AAH60708	Cyclin A1	c 167	10	52.6	19	14	AEA44556	Aea44556 Human TRP
95	10.4	54.7	19	12	AD51075	Human NOV	c 168	10	52.6	19	14	AED36644	Aed36644 VEGF or V
96	10.4	54.7	19	12	ADM86592	Example n	c 169	10	52.6	19	14	AED36217	Aed36217 VEGF or V
97	10.4	54.7	19	12	ADQ27225	RNA Inter	c 170	10	52.6	19	14	AED64040	Aed64040 Human AVP
98	10.4	54.7	19	14	AEB05347	Human IL-	c 171	10	52.6	19	14	AEB03031	Aeo03031 Human AVP
99	10.4	54.7	19	14	AEB05124	Human IL-	c 172	10	52.6	19	14	AEB43431	Aee43431 Human hAI
100	10.4	54.7	19	14	AEC14961	Human IL-	c 173	10	52.6	19	14	AEB43432	Aee43432 Human hAI
101	10.4	54.7	19	14	AEC15184	Human IL-	c 174	10	52.6	19	14	AEP53635	Aef53635 Human BMP
102	10.4	54.7	19	15	AEB71863	Human K10	c 175	9.8	51.6	19	2	AAQ91357	AAq91357 Chemosom
103	10.2	53.7	19	2	AAQ06429	Oligonucle	c 176	9.8	51.6	19	2	AAH66907	AAh66907 Ab1-2 gen
104	10.2	53.7	19	3	AAA29755	Human g1a	c 177	9.8	51.6	19	2	AAZ06975	AaZ06975 Human GAB
105	10.2	53.7	19	6	ABK41152	Human obe	c 178	9.8	51.6	19	2	AAK61047	AAk61047 PCR prime
106	10.2	53.7	19	10	ADP84170	Human bre	c 179	9.8	51.6	19	2	AAZ70138	AaZ01238 PCR prime
107	10.2	53.7	19	10	ADP83907	Human bre	c 180	9.8	51.6	19	3	AAZ71637	AaZ71637 Human b1a
108	10.2	53.7	19	10	ADP83907	Human bre	c 181	9.8	51.6	19	3	AAZ71637	AaZ71637 Human b1a
109	10.2	53.7	19	11	ADN34338	Lower str	c 182	9.8	51.6	19	4	AAH42019	AAh42019 Disease t
110	10.2	53.7	19	11	ADN34099	Upper str	c 183	9.8	51.6	19	4	AAH42019	AAh42019 Disease t
111	10.2	53.7	19	12	ADQ61980	Anti-EDG7	c 184	9.8	51.6	19	4	AAH42018	AAh42018 Disease t
112	10.2	53.7	19	14	ADZ53940	Human b1a	c 185	9.8	51.6	19	4	AAH42018	AAh42018 Disease t
113	10.2	53.7	19	14	ADZ55692	Human b1a	c 186	9.8	51.6	19	10	ADP36724	ADp36724 Human VEG
114	10.2	53.7	19	14	ADZ53939	Human b1a	c 187	9.8	51.6	19	10	ADP37048	ADp37048 Human VEG
115	10.2	53.7	19	14	ADZ55693	Human b1a	c 188	9.8	51.6	19	10	ADP31507	ADp31507 Human IGF
116	10.2	53.7	19	14	ADZ55690	Human b1a	c 189	9.8	51.6	19	10	ADP31784	ADp31784 Human IGF
117	10.2	53.7	19	14	ADZ53938	Human b1a	c 190	9.8	51.6	19	10	ADP54265	ADp54265 Human GAB
118	10.2	53.7	19	14	ADZ55691	Human b1a	c 191	9.8	51.6	19	10	ADP53929	ADp53929 Human GAB
119	10.2	53.7	19	14	ADZ55694	Human b1a	c 192	9.8	51.6	19	10	ADP54214	ADp54214 Human GAB
120	10.2	53.7	19	14	ADZ53941	Human b1a	c 193	9.8	51.6	19	10	ADP54550	ADp54550 Human GAB
121	10.2	53.7	19	14	ADZ53942	Human b1a	c 194	9.8	51.6	19	11	ADL79673	ADl79673 Human HER
122	10.2	53.7	19	14	AEA44595	Human TRP	c 195	9.8	51.6	19	11	ADL79366	ADl79366 Human HER
123	10.2	53.7	19	14	AEA34671	Human TRP	c 196	9.8	51.6	19	12	ADK95375	ADk95375 Primer of
124	10.2	53.7	19	14	AEB29096	Human s1R	c 197	9.8	51.6	19	12	ADQ27824	Adq27824 RNA Inter
125	10.2	53.7	19	14	AEB54778	Human s1R	c 198	9.8	51.6	19	12	ADQ27826	Adq27826 RNA Inter
126	10.2	53.7	19	14	AEB26225	Human cyc	c 199	9.8	51.6	19	14	ADV14668	ADv14668 PPTA CDNA
127	10.2	53.7	19	14	AEB25986	Human cyc	c 200	9.8	51.6	19	14	ADV94023	ADv94023 Presentill
128	10.2	53.7	19	14	AED92125	Target/si	c 201	9.8	51.6	19	14	ADV93940	ADv93940 Presentill
129	10.2	53.7	19	14	AED93881	siRNA low	c 202	9.8	51.6	19	14	ADY50713	ADy50713 MAPK14 si
130	10.2	53.7	19	14	AED92128	Target/si	c 203	9.8	51.6	19	14	ADY87977	ADy87977 VEGFR s1R
131	10.2	53.7	19	14	AED93877	siRNA low	c 204	9.8	51.6	19	14	ADY88301	ADy88301 VEGFR s1R
132	10.2	53.7	19	14	AED93877	siRNA low	c 205	9.8	51.6	19	14	ADY88301	ADy88301 VEGFR s1R
133	10.2	53.7	19	14	AED92127	Target/si	c 206	9.8	51.6	19	14	ADZ82509	ADz82509 Method of
134	10.2	53.7	19	14	AED92129	Target/si	c 207	9.8	51.6	19	14	ADZ82935	ADz82935 VHL gene-
135	10.2	53.7	19	14	AED93880	siRNA low	c 208	9.8	51.6	19	14	AEA02525	Aea02525 Cholester
136	10.2	53.7	19	14	AED92126	Target/si	c 209	9.8	51.6	19	14	AEA34532	Aea34532 Human TRP
137	10.2	53.7	19	14	AED93878	siRNA low	c 210	9.8	51.6	19	14	AEA44456	Aea44456 Human TRP
138	10.2	53.7	19	15	AEE57146	Human h1n	c 211	9.8	51.6	19	14	AEB64332	Aeb64332 Human IGF
139	10.2	53.7	19	15	AEE57148	Human h1n	c 212	9.8	51.6	19	14	AEB64609	Aeb64609 Human IGF
140	10.2	53.7	19	15	AEE58901	Human h1n	c 213	9.8	51.6	19	14	AEB92257	Aeb92257 Human GAT
141	10.2	53.7	19	15	AEE58902	Human h1n	c 214	9.8	51.6	19	14	AEC33463	Aec33463 Human GAB
142	10.2	53.7	19	15	AEE58899	Human h1n	c 215	9.8	51.6	19	14	AEC33514	Aec33514 Human GAB
143	10.2	53.7	19	15	AEE57149	Human h1n	c 216	9.8	51.6	19	14	AEC33799	Aec33799 Human GAB
144	10.2	53.7	19	15	AEE58898	Human h1n	c 217	9.8	51.6	19	14	AEC33178	Aec33178 Human GAB
145	10.2	53.7	19	15	AEE57147	Human h1n	c 218	9.8	51.6	19	14	AEC58766	Aec58766 Human pre
146	10.2	53.7	19	15	AEE57150	Human h1n	c 219	9.8	51.6	19	14	AEC58683	Aec58683 Human pre
147	10.2	53.7	19	15	AEE58900	Human h1n	c 220	9.8	51.6	19	14	AEC95899	Aec95899 Human act
148	10.2	53.7	19	15	AEP93378	Human pPG	c 221	9.8	51.6	19	14	AED37212	Aed37212 VEGF or V
149	10	52.6	19	2	AAH62761	Murine bc	c 222	9.8	51.6	19	14	AED37536	Aed37536 VEGF or V
150	10	52.6	19	2	AAH93204	Primer us	c 223	9.8	51.6	19	14	AEE53633	Aee53633 Human hAI
151	10	52.6	19	3	AAA52297	PTT15b ve	c 224	9.8	51.6	19	14	AEE46724	Aee46724 Human hAI
152	10	52.6	19	3	AAA90497	Control o	c 225	9.8	51.6	19	14	AEE53628	Aee53628 Human hAI
153	10	52.6	19	8	ABX13462	Human NOV	c 226	9.8	51.6	19	14	AEE53629	Aee53629 Human hAI
154	10	52.6	19	8	ACD20499	Human NOV	c 227	9.8	51.6	19	14	AEE53636	Aee53636 Human hAI
155	10	52.6	19	10	ADR36156	Human VEG	c 228	9.8	51.6	19	14	AEE46709	Aee46709 Human hAI
156	10	52.6	19	10	ADR35729	Human VEG	c 229	9.8	51.6	19	14	AEE53637	Aee53637 Human hAI
157	10	52.6	19	10	ADR84176	Human bre	c 230	9.8	51.6	19	14	AEE53626	Aee53626 Human hAI
158	10	52.6	19	12	ADR83913	Human bre	c 231	9.8	51.6	19	14	AEE53634	Aee53634 Human hAI
159	10	52.6	19	12	ADK23679	Human bre	c 232	9.8	51.6	19	14	AEE53632	Aee53632 Human hAI
160	10	52.6	19	12	ADN62486	Human NOV	c 233	9.8	51.6	19	14	AEE53625	Aee53625 Human hAI
161	10	52.6	19	12	ADQ28304	UPET-UBI	c 234	9.8	51.6	19	14	AEE46723	Aee46723 Human hAI
162	10	52.6	19	14	ADY98354	Human H1A	c 235	9.8	51.6	19	14	AEE53624	Aee53624 Human hAI
163	10	52.6	19	14	ADY83910	Becherich	c 236	9.8	51.6	19	14	AEB46710	Aee46710 Human hAI
164	10	52.6	19	14	ADY86982	VEGFR s1R	c 237	9.8	51.6	19	14	AEE53627	Aee53627 Human hAI

238	9.8	51.6	19	14	AEBS3631	Aee53631 Human hai	311	9.4	49.5	19	13	ADU59910	Adu59910 Human pap
C 239	9.8	51.6	19	14	AEBS3630	Aee53630 Human hai	312	9.4	49.5	19	13	ADU59934	Adu59934 Human pap
C 240	9.8	51.6	19	14	AEBS3635	Aee53635 Human hai	313	9.4	49.5	19	13	ADT26142	Adt26142 Human pap
C 241	9.6	50.5	19	2	AAZ40531	Aaz40531 Human STE	C 314	9.4	49.5	19	14	ADY94081	Ady94081 Presentill
C 242	9.6	50.5	19	2	AAV72609	Aav72609 Human coa	C 315	9.4	49.5	19	14	ADY93998	Ady93998 Presentill
C 243	9.6	50.5	19	2	AAAX31877	S. aureus	C 316	9.4	49.5	19	14	ADY03176	Ady03176 Extend pr
C 244	9.6	50.5	19	3	AAZ72756	Human bla	C 317	9.4	49.5	19	14	ADY52838	Ady52838 Human CHR
C 245	9.6	50.5	19	4	AAAF82399	Mealworm	C 318	9.4	49.5	19	14	ADY83898	Ady83898 Escherich
C 246	9.6	50.5	19	5	ABAB82144	Zmaxi gen	C 319	9.4	49.5	19	14	ADY83874	Ady83874 Escherich
C 247	9.6	50.5	19	6	ABK41008	Human obe	C 320	9.4	49.5	19	14	ADY83882	Ady83882 Escherich
C 248	9.6	50.5	19	6	ABQ74049	SSO probe	C 321	9.4	49.5	19	14	ADY83906	Ady83906 Escherich
C 249	9.6	50.5	19	6	ABK22941	Human zma	C 322	9.4	49.5	19	14	ADY83901	Ady83901 Escherich
C 250	9.6	50.5	19	8	ACC45524	Human HBM	C 323	9.4	49.5	19	14	ADY83892	Ady83892 Escherich
C 251	9.6	50.5	19	10	ADB98222	Sequence	C 324	9.4	49.5	19	14	ADY83893	Ady83893 Escherich
C 252	9.6	50.5	19	10	ADB98713	Mitogen a	C 325	9.4	49.5	19	14	ADY83900	Ady83900 Escherich
C 253	9.6	50.5	19	10	ADB98818	Mitogen a	C 326	9.4	49.5	19	14	ADY83903	Ady83903 Escherich
C 254	9.6	50.5	19	10	ADP93656	Human TER	C 327	9.4	49.5	19	14	ADY83895	Ady83895 Escherich
C 255	9.6	50.5	19	10	ADP93402	Human TER	C 328	9.4	49.5	19	14	ADY88274	Ady88274 VEGFR b1R
C 256	9.6	50.5	19	11	ADL69874	Human GIP	C 329	9.4	49.5	19	14	ADY87950	Ady87950 VEGFR b1R
C 257	9.6	50.5	19	11	ADL69987	Human GIP	C 330	9.4	49.5	19	14	ADZ87959	Adz87959 Early gro
C 258	9.6	50.5	19	12	ADH68492	Rosa bp f	C 331	9.4	49.5	19	14	ADZ88133	Adz88133 Early gro
C 259	9.6	50.5	19	12	ADK40301	Human HNF	C 332	9.4	49.5	19	14	AEA06682	Aea06682 g protein
C 260	9.6	50.5	19	13	ADQ94230	Phosphola	C 333	9.4	49.5	19	14	AEA06595	Aea06595 g protein
C 261	9.6	50.5	19	13	ADR17087	Human chr	C 334	9.4	49.5	19	14	AEA32954	Aea32954 Human hML
C 262	9.6	50.5	19	13	ADR47738	Human chr	C 335	9.4	49.5	19	14	AEA42544	Aea42544 Human WNT
C 263	9.6	50.5	19	13	ADR81760	Hepaticitis	C 336	9.4	49.5	19	14	AEA42707	Aea42707 Human WNT
C 264	9.6	50.5	19	13	ADT86217	Hepaticitis	C 337	9.4	49.5	19	14	ABE24669	Aeb24669 Human MDR
C 265	9.6	50.5	19	14	ADU64854	Human MAP	C 338	9.4	49.5	19	14	ABE24927	Aeb24927 Human MDR
C 266	9.6	50.5	19	14	ADU64959	Human MAP	C 339	9.4	49.5	19	14	ABE43539	Aeb43539 Novel hum
C 267	9.6	50.5	19	14	ADU64959	Human MAP	C 340	9.4	49.5	19	14	ABE43713	Aeb43713 Novel hum
C 268	9.6	50.5	19	14	AEA31093	Hog chole	C 341	9.4	49.5	19	14	ABE89742	Aeb89742 CYP2C9 ge
C 269	9.6	50.5	19	14	ABE805470	Human IL-	C 342	9.4	49.5	19	14	ABE89874	Aeb89874 CYP2C9 ge
C 270	9.6	50.5	19	14	ABE805247	Human IL-	C 343	9.4	49.5	19	14	ABE89824	Aeb89824 Human pre
C 271	9.6	50.5	19	14	ABE899466	Human chr	C 344	9.4	49.5	19	14	ABE89741	Aeb89741 Human pre
C 272	9.6	50.5	19	14	ABE815659	Human tel	C 345	9.4	49.5	19	14	ABD31785	Aeb31785 VEGF or V
C 273	9.6	50.5	19	14	ABE815882	Human tel	C 346	9.4	49.5	19	14	ABD37509	Aeb37509 VEGF or V
C 274	9.6	50.5	19	14	ABE815882	Human tel	C 347	9.4	49.5	19	14	ABD64734	Aeb64734 Pseudobac
C 275	9.6	50.5	19	14	ABE854034	Human tra	C 348	9.4	49.5	19	14	ABE853639	Aeb853639 Human GAL
C 276	9.6	50.5	19	14	ABE854211	Human tra	C 349	9.4	49.5	19	14	ABE853657	Aeb853657 Human ADR
C 277	9.6	50.5	19	14	ABE854058	Human tra	C 350	9.4	49.5	19	15	ABE836999	Aeb836999 Human SDR
C 278	9.6	50.5	19	14	ABE854070	Human tra	C 351	9.4	49.5	19	15	ABE836820	Aeb836820 Human SDR
C 279	9.6	50.5	19	14	ABE854071	Human tra	C 352	9.2	48.4	19	2	AAQ12858	Aaq12858 Probe to
C 280	9.6	50.5	19	14	ABE854187	Human tra	C 353	9.2	48.4	19	2	AAQ12858	Aaq12858 Probe to
C 281	9.6	50.5	19	14	ABE854224	Human tra	C 354	9.2	48.4	19	3	AAZ36524	Aaz36524 Probe hyb
C 282	9.6	50.5	19	14	ABE854223	Human tra	C 355	9.2	48.4	19	3	AAZ36535	Aaz36535 Probe hyb
C 283	9.6	50.5	19	14	ABE854223	Human tra	C 356	9.2	48.4	19	3	AAZ38047	Aaz38047 Primer se
C 284	9.6	50.5	19	14	ABE854223	Human tra	C 357	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 285	9.6	50.5	19	14	ABE854223	Human tra	C 358	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 286	9.6	50.5	19	14	ABE854223	Human tra	C 359	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 287	9.6	50.5	19	14	ABE854223	Human tra	C 360	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 288	9.6	50.5	19	14	ABE854223	Human tra	C 361	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 289	9.6	50.5	19	14	ABE854223	Human tra	C 362	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 290	9.6	50.5	19	14	ABE854223	Human tra	C 363	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 291	9.6	50.5	19	14	ABE854223	Human tra	C 364	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 292	9.6	50.5	19	14	ABE854223	Human tra	C 365	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 293	9.6	50.5	19	14	ABE854223	Human tra	C 366	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 294	9.6	50.5	19	14	ABE854223	Human tra	C 367	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 295	9.6	50.5	19	14	ABE854223	Human tra	C 368	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 296	9.6	50.5	19	14	ABE854223	Human tra	C 369	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 297	9.6	50.5	19	14	ABE854223	Human tra	C 370	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 298	9.6	50.5	19	14	ABE854223	Human tra	C 371	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 299	9.6	50.5	19	14	ABE854223	Human tra	C 372	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 300	9.6	50.5	19	14	ABE854223	Human tra	C 373	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 301	9.6	50.5	19	14	ABE854223	Human tra	C 374	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 302	9.6	50.5	19	14	ABE854223	Human tra	C 375	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 303	9.6	50.5	19	14	ABE854223	Human tra	C 376	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 304	9.6	50.5	19	14	ABE854223	Human tra	C 377	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 305	9.6	50.5	19	14	ABE854223	Human tra	C 378	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 306	9.6	50.5	19	14	ABE854223	Human tra	C 379	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 307	9.6	50.5	19	14	ABE854223	Human tra	C 380	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 308	9.6	50.5	19	14	ABE854223	Human tra	C 381	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 309	9.6	50.5	19	14	ABE854223	Human tra	C 382	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon
C 310	9.6	50.5	19	14	ABE854223	Human tra	C 383	9.2	48.4	19	3	AAZ59005	Aaz59005 Pseudomon

C 384	9.2	48.4	19.0	ADP93477	Human	TER	C 457	9.2	48.4	19.14	AECl5023	AEcl15023	Human	IL
C 385	9.2	48.4	19.10	ADH16461	Human	BAC	C 458	9.2	48.4	19.19	AECl15246	AEcl15246	Human	IL
C 386	9.2	48.4	19.10	ADH16786	Human	BAC	C 459	9.2	48.4	19.14	AECl3456	AEcl3456	Human	GAS
C 387	9.2	48.4	19.11	ADL69781	Human	GIP	C 460	9.2	48.4	19.14	AECl3792	AEcl3792	Human	GAS
C 388	9.2	48.4	19.11	ADL69821	Human	GIP	C 461	9.2	48.4	19.14	AECS98589	AEcs98589	Human	bea
C 389	9.2	48.4	19.11	ADN34742	Human	GIP	C 462	9.2	48.4	19.14	AECS89264	AEcs89264	Human	bea
C 390	9.2	48.4	19.11	ADN35000	Human	GIP	C 463	9.2	48.4	19.14	AECS8755	AEcs8755	Human	bea
C 391	9.2	48.4	19.12	ADL91661	Human	lowe	C 464	9.2	48.4	19.14	AECS8672	AEcs8672	Human	pr
C 392	9.2	48.4	19.12	ADN35855	Human	NSC	C 465	9.2	48.4	19.14	AECD36232	AEcd36232	VEGF or	
C 393	9.2	48.4	19.12	ADN75454	Human	CD4	C 466	9.2	48.4	19.14	AECD36639	AEcd36639	VEGF or	
C 394	9.2	48.4	19.12	ADN75379	Human	CD4	C 467	9.2	48.4	19.14	AECS6844	AEcs6844	Human	os
C 395	9.2	48.4	19.12	ADN15882	Human	SA	C 468	9.2	48.4	19.14	AECS6410	AEcs6410	Human	os
C 396	9.2	48.4	19.12	ADG62467	Anti-OPR1		C 469	9.2	48.4	19.14	AECD93521	AEcd93521	siRNA	lo
C 397	9.2	48.4	19.12	ADQ14170	CAVpN3/DYS		C 470	9.2	48.4	19.14	AECD92130	AEcd92130	Target/s	
C 398	9.2	48.4	19.13	ADT00467	Novel	mut	C 471	9.2	48.4	19.14	AECD93882	AEcd93882	siRNA	lo
C 399	9.2	48.4	19.13	ADT64559	SARS	coro	C 472	9.2	48.4	19.14	AECD93876	AEcd93876	Target/s	
C 400	9.2	48.4	19.13	ADT66210	SARS	coro	C 473	9.2	48.4	19.14	AECD91767	AEcd91767	Target/s	
C 401	9.2	48.4	19.14	ADN84542	MAP3K9	ma	C 474	9.2	48.4	19.14	AECD91771	AEcd91771	Target/s	
C 402	9.2	48.4	19.14	ADV93846	Beta-secr		C 475	9.2	48.4	19.14	AECD91772	AEcd91772	Target/s	
C 403	9.2	48.4	19.14	ADV93929	Presentill		C 476	9.2	48.4	19.14	AECD93520	AEcd93520	siRNA	lo
C 404	9.2	48.4	19.14	ADV943521	Beta-secr		C 477	9.2	48.4	19.14	AECD91769	AEcd91769	Target/s	
C 405	9.2	48.4	19.14	ADV94012	Presentill		C 478	9.2	48.4	19.14	AECD92124	AEcd92124	Target/s	
C 406	9.2	48.4	19.14	ADW78928	Human	ace	C 479	9.2	48.4	19.14	AECD93519	AEcd93519	siRNA	lo
C 407	9.2	48.4	19.14	ADW79342	Human	ace	C 480	9.2	48.4	19.14	AECD93523	AEcd93523	siRNA	lo
C 408	9.2	48.4	19.14	ADY02646	Extend pr		C 481	9.2	48.4	19.14	AECD93524	AEcd93524	siRNA	lo
C 409	9.2	48.4	19.14	ADY57903	Human	hai	C 482	9.2	48.4	19.14	AECD93522	AEcd93522	siRNA	lo
C 410	9.2	48.4	19.14	ADY57596	Human	hai	C 483	9.2	48.4	19.14	AECD91770	AEcd91770	Target/s	
C 411	9.2	48.4	19.14	ADY50633	MAPK14	si	C 484	9.2	48.4	19.14	AECD91768	AEcd91768	Target/s	
C 412	9.2	48.4	19.14	ADY86997	VEGFR	g1R	C 485	9.2	48.4	19.14	AEED04613	AEed04613	Oligonuc	
C 413	9.2	48.4	19.14	ADY87424	VEGFR	g1R	C 486	9.2	48.4	19.14	AEES4510	AEes4510	Human	ha



530	9	47.4	19	3	AAZ70070	Human	bia	C 603	9	47.4	19	12	ADN96697	Adn96697	Human	NOV
C 531	9	47.4	19	3	AAZ29625	Forward P		C 604	9	47.4	19	12	ADN96493	Adn96493	Human	NOV
C 532	9	47.4	19	4	AAH40849	SNP spec		C 605	9	47.4	19	12	ADN96430	Adn96430	Human	NOV
C 533	9	47.4	19	4	AAE26247	B. megate		C 606	9	47.4	19	12	AD044682	Ad044682	Human	Oil
534	9	47.4	19	5	AAH23943	S. spiritit		C 607	9	47.4	19	12	AD018590	Ad018590	Analytica	
535	9	47.4	19	5	AAH60015	Cyclin F		C 608	9	47.4	19	12	AD018249	Ad018249	Analytica	
C 536	9	47.4	19	5	AAH60522	Cyclin H		C 609	9	47.4	19	12	AD018528	Ad018528	Analytica	
537	9	47.4	19	6	ABN88122	Caenorhab		C 610	9	47.4	19	12	AD018495	Ad018495	Analytica	
C 538	9	47.4	19	6	ABL43167	Human chr		C 611	9	47.4	19	12	AD048759	Ad048759	Human	neu
C 539	9	47.4	19	6	ABD22639	Sense PCR		C 612	9	47.4	19	12	AD062637	Ad062637	Human	ret
C 540	9	47.4	19	6	ABK82137	Novel fto		C 613	9	47.4	19	12	AD067690	Ad067690	Human	ret
C 541	9	47.4	19	8	ACC55340	Human ADA		C 614	9	47.4	19	13	AD082672	Ad082672	Beta-acti	
C 542	9	47.4	19	8	ABT32656	Microbial		C 615	9	47.4	19	13	ADR87856	Adr87856	Human	apo
C 543	9	47.4	19	8	ABQ80061	T. marit		C 616	9	47.4	19	13	ADR77667	Adr77667	Human	apo
C 544	9	47.4	19	8	ABZ26021	PCR prime		C 617	9	47.4	19	13	ADR78517	Adr78517	Human	apo
C 545	9	47.4	19	9	ACD06573	RT-PCR pr		C 618	9	47.4	19	13	ADR79302	Adr79302	Human	apo
C 546	9	47.4	19	9	ACD06663	RT-PCR pr		C 619	9	47.4	19	13	ADR76554	Adr76554	Human	apo
C 547	9	47.4	19	9	ACD06597	RT-PCR pr		C 620	9	47.4	19	13	ADR79498	Adr79498	Human	apo
C 548	9	47.4	19	9	ACD06513	RT-PCR pr		C 621	9	47.4	19	13	ADR75899	Adr75899	Human	apo
C 549	9	47.4	19	9	ACD06534	RT-PCR pr		C 622	9	47.4	19	13	ADR81487	Adr81487	Hepatic	
C 550	9	47.4	19	9	ACD06744	RT-PCR pr		C 623	9	47.4	19	13	ADR78958	Adr78958	Human	apo
C 551	9	47.4	19	9	ACD06558	RT-PCR pr		C 624	9	47.4	19	13	ADR78062	Adr78062	Human	apo
C 552	9	47.4	19	9	ACD06801	RT-PCR pr		C 625	9	47.4	19	13	ADR78490	Adr78490	Human	apo
C 553	9	47.4	19	10	ADD00571	HCV codin		C 626	9	47.4	19	13	ADR76138	Adr76138	Human	apo
C 554	9	47.4	19	10	ADD00570	HCV codin		C 627	9	47.4	19	13	ADR76340	Adr76340	Human	apo
C 555	9	47.4	19	10	ADD00457	HCV codin		C 628	9	47.4	19	13	ADR80720	Adr80720	Human	apo
C 556	9	47.4	19	10	ADD00569	HCV codin		C 629	9	47.4	19	13	ADR75872	Adr75872	Human	apo
C 557	9	47.4	19	10	ADDE5585	Human c-f		C 630	9	47.4	19	13	ADR766115	Adr766115	SARS	coro
C 558	9	47.4	19	10	ADDE5585	Human c-f		C 631	9	47.4	19	13	ADR76464	Adr76464	SARS	coro
C 559	9	47.4	19	10	ADDE5701	Human c-f		C 632	9	47.4	19	13	ADR82110	Adr82110	Apoli	
C 560	9	47.4	19	10	ADDE27194	Stearoyl-		C 633	9	47.4	19	13	ADR83941	Adr83941	Apoli	
C 561	9	47.4	19	10	ADDE37484	Stearoyl-		C 634	9	47.4	19	13	ADR80315	Adr80315	Apoli	
C 562	9	47.4	19	10	ADDE30433	Mitogen a		C 635	9	47.4	19	13	ADR80581	Adr80581	Apoli	
C 563	9	47.4	19	10	ADDE30224	Mitogen a		C 636	9	47.4	19	13	ADR80783	Adr80783	Apoli	
C 564	9	47.4	19	10	ADDE30405	Mitogen a		C 637	9	47.4	19	13	ADR80997	Adr80997	Apoli	
C 565	9	47.4	19	10	ADDF36673	Human VEG		C 638	9	47.4	19	13	ADR83745	Adr83745	Apoli	
C 566	9	47.4	19	10	ADDF36997	Human VEG		C 639	9	47.4	19	13	ADR85944	Adr85944	Hepatic	
C 567	9	47.4	19	10	ADDF52593	Hepatic		C 640	9	47.4	19	13	ADR82933	Adr82933	Apoli	
C 568	9	47.4	19	10	ADDF51897	Hepatic		C 641	9	47.4	19	13	ADR85163	Adr85163	Apoli	
C 569	9	47.4	19	10	ADDF52059	Hepatic		C 642	9	47.4	19	13	ADR82505	Adr82505	Apoli	
C 570	9	47.4	19	10	ADDF52597	Hepatic		C 643	9	47.4	19	13	ADR82960	Adr82960	Apoli	
C 571	9	47.4	19	10	ADDF51904	Hepatic		C 644	9	47.4	19	13	ADR80342	Adr80342	Apoli	
C 572	9	47.4	19	10	ADDF52755	Hepatic		C 645	9	47.4	19	13	ADR83401	Adr83401	Apoli	
C 573	9	47.4	19	10	ADDF52600	Hepatic		C 646	9	47.4	19	13	ADR83199	Adr83199	Apoli	
C 574	9	47.4	19	10	ADFE1901	Hepatic		C 647	9	47.4	19	13	ADV25298	Adv25298	Enterococ	
C 575	9	47.4	19	10	ADFE1901	Hepatic		C 648	9	47.4	19	13	ADX16147	Adx16147	Human	DNA
576	9	47.4	19	10	ADFE68284	Human ant		C 649	9	47.4	19	13	ACU79181	Acu79181	SARS	coro
577	9	47.4	19	10	ADFE68284	Human ant		C 650	9	47.4	19	14	ADU65546	Adu65546	Human	MAP
C 578	9	47.4	19	10	ADFE68252	Human ant		C 651	9	47.4	19	14	ADU65574	Adu65574	Human	MAP
C 579	9	47.4	19	10	ADFE4402	Human GAB		C 652	9	47.4	19	14	ADU65365	Adu65365	Human	MAP
C 580	9	47.4	19	10	ADFE4546	Human GAB		C 653	9	47.4	19	14	ADU65337	Adu65337	Human	MAP
581	9	47.4	19	10	ADFE4546	Human GAB		C 654	9	47.4	19	14	ADU944227	Adu944227	Present	
C 582	9	47.4	19	10	ADFE4210	Human GAB		C 655	9	47.4	19	14	ADU94103	Adu94103	Present	
C 583	9	47.4	19	10	ADFE5176	Human ERG		C 656	9	47.4	19	14	ADU50904	Adu50904	MAPK4	si
584	9	47.4	19	10	ADFE5000	Human ERG		C 657	9	47.4	19	14	ADY81927	Ady81927	Thale-crc	
585	9	47.4	19	10	ABZ297373	Human IL4		C 658	9	47.4	19	14	ADY88250	Ady88250	VEGFR	61R
C 586	9	47.4	19	10	ACG43711	PCR prime		C 659	9	47.4	19	14	ADY87926	Ady87926	VEGFR	61R
C 587	9	47.4	19	10	ADU66112	Human TGF		C 660	9	47.4	19	14	ADZ01380	Adz01380	Hepatic	
588	9	47.4	19	10	ADU66300	Human TGF		C 661	9	47.4	19	14	ADZ01921	Adz01921	Hepatic	
589	9	47.4	19	11	ADL59887	Arabidops		C 662	9	47.4	19	14	ADZ02076	Adz02076	Hepatic	
C 590	9	47.4	19	11	ADN34250	Lower str		C 663	9	47.4	19	14	ADZ02125	Adz02125	Hepatic	
C 591	9	47.4	19	11	ADN34011	Upper str		C 664	9	47.4	19	14	ADZ02128	Adz02128	Hepatic	
C 592	9	47.4	19	11	ADN34488	Human int		C 665	9	47.4	19	14	ADZ01914	Adz01914	Hepatic	
C 593	9	47.4	19	11	ADN34488	Human int		C 666	9	47.4	19	14	ADZ02122	Adz02122	Hepatic	
C 594	9	47.4	19	11	ABD30404	Human IL4		C 667	9	47.4	19	14	ADZ020918	Adz020918	Hepatic	
C 595	9	47.4	19	12	ADH76834	WCHR1 tra		C 668	9	47.4	19	14	ADZ20814	Adz20814	Human	c-f
C 596	9	47.4	19	12	ADU59192	Oligonuc		C 669	9	47.4	19	14	ADZ20698	Adz20698	Human	c-f
C 597	9	47.4	19	12	ADN66787	Human per		C 670	9	47.4	19	14	ADZ883100	Adz883100	MPHOSPH	
C 598	9	47.4	19	12	ADN86469	Human NOV		C 671	9	47.4	19	14	ADZ82700	Adz82700	Method of	
C 599	9	47.4	19	12	ADN86454	Human NOV		C 672	9	47.4	19	14	ADZ83233	Adz83233	RAB3D gen	
C 600	9	47.4	19	12	ADN96409	Human NOV		C 673	9	47.4	19	14	AEA09618	Aea09618	Antisense	
C 601	9	47.4	19	12	ADN96559	Human NOV		C 674	9	47.4	19	14	AEA09778	Aea09778	Antisense	
C 602	9	47.4	19	12	ADN96640	Human NOV		C 675	9	47.4	19	14	AEA09586	Aea09586	Antisense	

676	9	47.4	19	14	AEA096332	Aeo096332	Antisense	c 749	8.8	46.3	19	2	AAX09256	Aax09256	Human bia
c 677	9	47.4	19	14	AD254045	Ad254045	Huntngt1	c 750	8.8	46.3	19	2	AAV44654	Aav44654	Primer fo
c 678	9	47.4	19	14	AD254046	Ad254046	Huntngt1	c 751	8.8	46.3	19	2	AAV27773	Aav27773	Monamine
c 679	9	47.4	19	14	AD255797	Ad255797	Huntngt1	c 752	8.8	46.3	19	2	AAV81899	Aav81899	Chicken t
c 680	9	47.4	19	14	AD254044	Ad254044	Huntngt1	c 753	8.8	46.3	19	2	AAZ01338	Aaz01338	PCR prime
c 681	9	47.4	19	14	AD255798	Ad255798	Huntngt1	c 754	8.8	46.3	19	3	AAa83550	Aaa83550	cdk-we-hu
c 682	9	47.4	19	14	AD255796	Ad255796	Huntngt1	c 755	8.8	46.3	19	3	AAa84005	Aaa84005	Cyclin A2
c 683	9	47.4	19	14	AEA05099	Aeo05099	Human 5-a	c 756	8.8	46.3	19	3	AAa84006	Aaa84006	Cyclin A2
c 684	9	47.4	19	14	AEA05222	Aeo05222	Human 5-a	c 757	8.8	46.3	19	3	AAZ73270	Aaz73270	Human bia
c 685	9	47.4	19	14	AEA99083	Aeo99083	Human 5-a	c 758	8.8	46.3	19	3	AAZ70796	Aaz70796	Human bia
c 686	9	47.4	19	14	AEA98933	Aeo98933	Human Fas	c 759	8.8	46.3	19	3	AAA71512	Aaa71512	Neocorzin
c 687	9	47.4	19	14	AEA33624	Aea33624	18S DNA r	c 760	8.8	46.3	19	4	AAE59402	Aae59402	Human hos
c 688	9	47.4	19	14	AEb72024	Aeb72024	Human S-a	c 761	8.8	46.3	19	5	AAH59167	Aah59167	Cyclin A2
c 689	9	47.4	19	14	AEb72147	Aeb72147	Human 5-a	c 762	8.8	46.3	19	5	AAH58712	Aah58712	Cdk-we-hu
c 690	9	47.4	19	14	AEb29286	Aeb29286	Human s1R	c 763	8.8	46.3	19	5	AAH59168	Aah59168	Cyclin A2
c 691	9	47.4	19	14	AEb55101	Aeb55101	s1RNA tar	c 764	8.8	46.3	19	6	ABA95075	Aba95075	Mouse IDP
c 692	9	47.4	19	14	AEb54963	Aeb54963	s1RNA tar	c 765	8.8	46.3	19	6	ABK15585	Abk15585	Melanocor
c 693	9	47.4	19	14	AEb25898	Aeb25898	Human cyc	c 766	8.8	46.3	19	6	ABK15582	Abk15582	Melanocor
c 694	9	47.4	19	14	AEb26137	Aeb26137	Human cyc	c 767	8.8	46.3	19	6	AD38866	Ad38866	Rat sense
c 695	9	47.4	19	14	AEb33459	Aeb33459	Human GAB	c 768	8.8	46.3	19	6	ABQ74945	Abq74945	Medane re
c 696	9	47.4	19	14	AEb33795	Aeb33795	Human GAB	c 769	8.8	46.3	19	6	ABH89717	Abh89717	Human ABC
c 697	9	47.4	19	14	AEb33651	Aeb33651	Human GAB	c 770	8.8	46.3	19	6	ABH89721	Abh89721	Human ABC
c 698	9	47.4	19	14	AEb33315	Aeb33315	Human GAB	c 771	8.8	46.3	19	8	ACC49453	Acc49453	Beta-acti
c 699	9	47.4	19	14	AEb38970	Aeb38970	Human pre	c 772	8.8	46.3	19	9	ABE281567	Ab281567	Glia1 f1b
c 700	9	47.4	19	14	AEb58846	Aeb58846	Human pre	c 773	8.8	46.3	19	9	ACC84000	Acc84000	Beta-acti
c 701	9	47.4	19	14	AEb01394	Aeb01394	Salmonell	c 774	8.8	46.3	19	9	ADA25475	Ada25475	Human PKC
c 702	9	47.4	19	14	AEbC0853	AebC0853	Hepatit1s	c 775	8.8	46.3	19	9	ADA25350	Ada25350	Human PKC
c 703	9	47.4	19	14	AEbC61546	AebC61546	Hepatit1s	c 776	8.8	46.3	19	9	ADA27382	Ada27382	Human bet
c 704	9	47.4	19	14	AEbC61704	AebC61704	Hepatit1s	c 777	8.8	46.3	19	10	ADC46954	Adc46954	PCR prime
c 705	9	47.4	19	14	AEbC61008	AebC61008	Hepatit1s	c 778	8.8	46.3	19	10	ADC08984	Adc08984	Beta-acti
c 706	9	47.4	19	14	AEbC60850	AebC60850	Hepatit1s	c 779	8.8	46.3	19	10	ADD08997	Add08997	Human bet
c 707	9	47.4	19	14	AEbC61542	AebC61542	Hepatit1s	c 780	8.8	46.3	19	10	ADD42111	Add42111	Beta-acti
c 708	9	47.4	19	14	AEbC61549	AebC61549	Hepatit1s	c 781	8.8	46.3	19	10	ACF58143	Acf58143	Beta-acti
c 709	9	47.4	19	14	AEbC60846	AebC60846	Hepatit1s	c 782	8.8	46.3	19	10	ACF80610	Acf80610	Baculovir
c 710	9	47.4	19	14	AEb11516	Aeb11516	s1RNA use	c 783	8.8	46.3	19	10	ADE27361	Ade27361	Stearyl1-
c 711	9	47.4	19	14	AEb37485	Aeb37485	VEGF or V	c 784	8.8	46.3	19	10	ADE27071	Ade27071	Stearyl1-
c 712	9	47.4	19	14	AEb37161	Aeb37161	VEGF or V	c 785	8.8	46.3	19	10	ADE85902	Ade85902	Beta-acti
c 713	9	47.4	19	14	AEbD65950	AebD65950	Arabidops	c 786	8.8	46.3	19	10	ADE29481	Ade29481	Mitogen a
c 714	9	47.4	19	14	AEbD65625	AebD65625	Arabidops	c 787	8.8	46.3	19	10	ADE29644	Ade29644	Mitogen a
c 715	9	47.4	19	14	AEbD80278	AebD80278	Arabidops	c 788	8.8	46.3	19	10	ADb989845	Adb989845	Beta-acti
c 716	9	47.4	19	14	AEbD51669	AebD51669	Human SCD	c 789	8.8	46.3	19	10	ADbF35770	Adbf35770	Human VEG
c 717	9	47.4	19	14	AEbD52159	AebD52159	Human SCD	c 790	8.8	46.3	19	10	ADbF36197	Adbf36197	Human VEG
c 718	9	47.4	19	14	AEbD81157	AebD81157	Human IRX	c 791	8.8	46.3	19	10	ADbF37578	Adbf37578	Human VEG
c 719	9	47.4	19	14	AEbD81156	AebD81156	Human IRX	c 792	8.8	46.3	19	10	ADbF36020	Adbf36020	Human VEG
c 720	9	47.4	19	14	AEbD92233	AebD92233	Target/si	c 793	8.8	46.3	19	10	ADbF37331	Adbf37331	Human VEG
c 721	9	47.4	19	14	AEbD92232	AebD92232	Target/si	c 794	8.8	46.3	19	10	ADbF35447	Adbf35447	Human VEG
c 722	9	47.4	19	14	AEbD93885	AebD93885	s1RNA low	c 795	8.8	46.3	19	10	ADbF49839	Adbf49839	Human BCL
c 723	9	47.4	19	14	AEbD9384	AebD9384	s1RNA low	c 796	8.8	46.3	19	10	ADbF49425	Adbf49425	Human BCL
c 724	9	47.4	19	14	AEbD92231	AebD92231	Target/si	c 797	8.8	46.3	19	10	ADbF53752	Adbf53752	Beta-acti
c 725	9	47.4	19	14	AEbD93983	AebD93983	s1RNA low	c 798	8.8	46.3	19	10	ADbF75673	Adbf75673	Antisense
c 726	9	47.4	19	14	AEbD93429	AebD93429	Human hai	c 799	8.8	46.3	19	10	ADbF75488	Adbf75488	Sense sin
c 727	9	47.4	19	14	AEbD43430	AebD43430	Human hai	c 800	8.8	46.3	19	10	ADbG35350	Adbg35350	HIV s1NA
c 728	9	47.4	19	14	AEbE57282	AebE57282	Human hun	c 801	8.8	46.3	19	10	ADbG35353	Adbg35353	HIV s1NA
c 729	9	47.4	19	15	AEbE57254	AebE57254	Human hun	c 802	8.8	46.3	19	10	ADbG36068	Adbg36068	HIV s1NA
c 730	9	47.4	19	15	AEbE57253	AebE57253	Human hun	c 803	8.8	46.3	19	10	ADbG36071	Adbg36071	HIV s1NA
c 731	9	47.4	19	15	AEbE59006	AebE59006	Human hun	c 804	8.8	46.3	19	10	ADbG36088	Adbg36088	HIV s1NA
c 732	9	47.4	19	15	AEbE59004	AebE59004	Human hun	c 805	8.8	46.3	19	10	ADbG35320	Adbg35320	HIV s1NA
c 733	9	47.4	19	15	AEbE59005	AebE59005	Human hun	c 806	8.8	46.3	19	10	ADbG35330	Adbg35330	HIV s1NA
c 734	9	47.4	19	15	AEbE27114	AebE27114	Arabidops	c 807	8.8	46.3	19	10	ADbG35372	Adbg35372	HIV s1NA
c 735	9	47.4	19	15	AEbE69854	AebE69854	Human TGF	c 808	8.8	46.3	19	10	ADbG36110	Adbg36110	HIV s1NA
c 736	9	47.4	19	15	AEbE6982	AebE6982	Human TGF	c 809	8.8	46.3	19	10	ADbG36008	Adbg36008	HIV s1NA
c 737	9	47.4	19	15	AEbF08599	AebF08599	PFTK1 s1R	c 810	8.8	46.3	19	10	ADbG36059	Adbg36059	HIV s1NA
c 738	9	47.4	19	15	AEbF08355	AebF08355	LOC115209	c 811	8.8	46.3	19	10	ADbG35321	Adbg35321	HIV s1NA
c 739	9	47.4	19	15	AEbF57287	AebF57287	Human gen	c 812	8.8	46.3	19	10	ADbG35270	Adbg35270	HIV s1NA
c 740	9	47.4	19	15	AEbF75559	AebF75559	Human NOG	c 813	8.8	46.3	19	10	ADbG36051	Adbg36051	HIV s1NA
c 741	9	47.4	19	15	AEbF75785	AebF75785	Human NOG	c 814	8.8	46.3	19	10	ADbG35313	Adbg35313	HIV s1NA
c 742	9	47.4	19	15	AEbF73424	AebF73424	Probe tar	c 815	8.8	46.3	19	10	ADbG36058	Adbg36058	HIV s1NA
c 743	9	46.3	19	15	AAO38225	AaQ38225	Sequence	c 816	8.8	46.3	19	10	ADbF6304	Adbf6304	Beta-acti
c 744	9	46.3	19	2	AAO39289	AaQ39289	Glucocere	c 817	8.8	46.3	19	10	ADbG64623	Adbg64623	Human G72
c 745	9	46.3	19	2	AAO73605	AaQ73605	Dactyl1s	c 818	8.8	46.3	19	10	ADbG64567	Adbg64567	Human G72
c 746	9	46.3	19	2	AAO57626	AaQ57626	PCR prime	c 819	8.8	46.3	19	11	ADbL69948	Adbl69948	Human GIP
c 747	9	46.3	19	2	AAI36937	Aat36937	OVCA1 gen	c 820	8.8	46.3	19	11	ADbL70061	Adbl70061	Human GIP
c 748	9	46.3	19	2	AAV05764	Aav05764	Chicken p	c 821	8.8	46.3	19	11	ADbM77346	Adbm77346	Human f1b

822	8.8	46.3	19	11	ADN34785	Adn34785 siNA Lowe	895	8.8	46.3	19	14	ADY87273	Ady87273 VEGFR siR
823	8.8	46.3	19	11	AD014826	Ad014826 Human PDG	896	8.8	46.3	19	14	ADY88584	Ady88584 VEGFR siR
824	8.8	46.3	19	11	AD015137	Ad015137 Human PDG	897	8.8	46.3	19	14	ADZ14976	Adz14976 Hydroxyme
825	8.8	46.3	19	11	ADM52852	Adm52852 siNA uppe	898	8.8	46.3	19	14	ADZ21949	Adz21949 Beta-actl
826	8.8	46.3	19	12	ADP91378	Adp91378 Primer fo	899	8.8	46.3	19	14	ADZ08451	Adz08451 Human pro
827	8.8	46.3	19	12	AD845146	Ad845146 Human bet	900	8.8	46.3	19	14	ADZ08266	Adz08266 Human pro
828	8.8	46.3	19	12	ADH01519	Adh01519 Protein t	901	8.8	46.3	19	14	AEA04617	Aea04617 Human mir
829	8.8	46.3	19	12	ADH01593	Adh01593 Protein t	902	8.8	46.3	19	14	AEA04683	Aea04683 Human mir
830	8.8	46.3	19	12	ADH01594	Adh01594 Protein t	903	8.8	46.3	19	14	AEA04580	Aea04580 Human mir
831	8.8	46.3	19	12	ADP91187	Adp91187 Human bet	904	8.8	46.3	19	14	ADZ82782	Adz82782 MAPK14 ge
832	8.8	46.3	19	12	ADH51312	Adh51312 Human bet	905	8.8	46.3	19	14	ADZ82947	Adz82947 NOTCH3 ge
833	8.8	46.3	19	12	AD128749	Ad128749 Human bet	906	8.8	46.3	19	14	ADZ82705	Adz82705 Method of
834	8.8	46.3	19	12	AD128991	Ad128991 Human bet	907	8.8	46.3	19	14	AEA05372	Aea05372 Human 5-a
835	8.8	46.3	19	12	ADK15292	Adk15292 Human bet	908	8.8	46.3	19	14	AEA05509	Aea05509 Human 5-a
836	8.8	46.3	19	12	ADL27316	Adl27316 PCR prime	909	8.8	46.3	19	14	AEA05509	Aea05509 Human 5-a
837	8.8	46.3	19	12	ADL27540	Adl27540 PCR prime	910	8.8	46.3	19	14	AEA02478	Aea02478 Cholester
838	8.8	46.3	19	12	ADL33228	Adl33228 beta-actl	911	8.8	46.3	19	14	AEA02127	Aea02127 Chollnerg
839	8.8	46.3	19	12	ADL32465	Adl32465 beta-actl	912	8.8	46.3	19	14	AEA02226	Aea02226 Chollnerg
840	8.8	46.3	19	12	ADM94197	Adm94197 Trichoder	913	8.8	46.3	19	14	AEA03169	Aea03169 HairLees
841	8.8	46.3	19	12	ADN75240	Adn75240 DSP13.2 a	914	8.8	46.3	19	14	AEA03476	Aea03476 HairLees
842	8.8	46.3	19	12	ADN75241	Adn75241 DSP13.2 a	915	8.8	46.3	19	14	AEA99293	Aea99293 Human Fas
843	8.8	46.3	19	12	ADN05806	Adn05806 Beta-actl	916	8.8	46.3	19	14	AEA99397	Aea99397 Human Fas
844	8.8	46.3	19	12	ADN98075	Adn98075 Human bet	917	8.8	46.3	19	14	AEA44569	Aea44569 Human TRP
845	8.8	46.3	19	12	AD016066	Ad016066 4 synthes	918	8.8	46.3	19	14	AEA34645	Aea34645 Human TRP
846	8.8	46.3	19	12	AD022062	Ad022062 Beta-actl	919	8.8	46.3	19	14	AEA30961	Aea30961 Human bet
847	8.8	46.3	19	12	ADQ27946	Adq27946 RNA Inter	920	8.8	46.3	19	14	AEA11772	Aea11772 Human ACA
848	8.8	46.3	19	12	AD085736	Ad085736 Human bet	921	8.8	46.3	19	14	AEA11358	Aea11358 Human ACA
849	8.8	46.3	19	12	ADQ61355	Adq61355 Anti-CD7	922	8.8	46.3	19	14	AE806565	Ae806565 Human con
850	8.8	46.3	19	12	ADQ60821	Adq60821 Anti-INSR	923	8.8	46.3	19	14	AE806393	Ae806393 Human con
851	8.8	46.3	19	12	ADQ62246	Adq62246 Anti-PLCG	924	8.8	46.3	19	14	AE817752	Ae817752 G72 siRNA
852	8.8	46.3	19	12	ADQ61190	Adq61190 Anti-TEC	925	8.8	46.3	19	14	AE817696	Ae817696 G72 siRNA
853	8.8	46.3	19	13	ADR44800	Adr44800 Human hC4	926	8.8	46.3	19	14	AE803972	Ae803972 Human ref
854	8.8	46.3	19	13	ADR44802	Adr44802 Human hC4	927	8.8	46.3	19	14	AE872297	Ae872297 Human 5-a
855	8.8	46.3	19	13	ADR47497	Adr47497 Human bet	928	8.8	46.3	19	14	AE872434	Ae872434 Human 5-a
856	8.8	46.3	19	13	ADR43775	Adr43775 MLL seprtl	929	8.8	46.3	19	14	AE829234	Ae829234 Human siR
857	8.8	46.3	19	13	ADR76668	Adr76668 Human apo	930	8.8	46.3	19	14	AE824934	Ae824934 Human MDR
858	8.8	46.3	19	13	ADR79612	Adr79612 Human apo	931	8.8	46.3	19	14	AE824676	Ae824676 Human MDR
859	8.8	46.3	19	13	ADT63932	Adt63932 SARS coro	932	8.8	46.3	19	14	AE854915	Ae854915 siRNA tar
860	8.8	46.3	19	13	ADT64837	Adt64837 SARS coro	933	8.8	46.3	19	14	AE842816	Ae842816 Sna1l tra
861	8.8	46.3	19	13	ADT65583	Adt65583 SARS coro	934	8.8	46.3	19	14	AE850787	Ae850787 Human ADA
862	8.8	46.3	19	13	ADT63186	Adt63186 SARS coro	935	8.8	46.3	19	14	AE850983	Ae850983 Human ADA
863	8.8	46.3	19	13	ADT63170	Adt63170 SARS coro	936	8.8	46.3	19	14	AE846336	Ae846336 Human bet
864	8.8	46.3	19	13	ADT64900	Adt64900 SARS coro	937	8.8	46.3	19	14	AE871654	Ae871654 Human PKC
865	8.8	46.3	19	13	ADT63225	Adt63225 SARS coro	938	8.8	46.3	19	14	AE871779	Ae871779 Human PKC
866	8.8	46.3	19	13	ADT64886	Adt64886 SARS coro	939	8.8	46.3	19	14	AE870744	Ae870744 Beta-actl
867	8.8	46.3	19	13	ADT65588	Adt65588 SARS coro	940	8.8	46.3	19	14	AE890510	Ae890510 STAT-3 si
868	8.8	46.3	19	13	ADT63937	Adt63937 SARS coro	941	8.8	46.3	19	14	AE890787	Ae890787 STAT-3 si
869	8.8	46.3	19	13	ADT64821	Adt64821 SARS coro	942	8.8	46.3	19	14	AE890724	Ae890724 STAT-3 si
870	8.8	46.3	19	13	ADT63249	Adt63249 SARS coro	943	8.8	46.3	19	14	AE890446	Ae890446 STAT-3 si
871	8.8	46.3	19	13	ADT81111	Adt81111 Apolipoptr	944	8.8	46.3	19	14	AE890696	Ae890696 STAT-3 si
872	8.8	46.3	19	13	ADT84055	Adt84055 Apolipoptr	945	8.8	46.3	19	14	AE890418	Ae890418 STAT-3 si
873	8.8	46.3	19	14	ADU64785	Adu64785 Human MAP	946	8.8	46.3	19	14	AE823128	Ae823128 siRNA tar
874	8.8	46.3	19	14	ADU65853	Adu65853 Human MAP	947	8.8	46.3	19	14	AE836935	Ae836935 VEGF or V
875	8.8	46.3	19	14	ADU66034	Adu66034 Human MAP	948	8.8	46.3	19	14	AE836258	Ae836258 VEGF or V
876	8.8	46.3	19	14	ADU64622	Adu64622 Human MAP	949	8.8	46.3	19	14	AE836685	Ae836685 VEGF or V
877	8.8	46.3	19	14	ADM85616	Adm85616 MAP3K9 ma	950	8.8	46.3	19	14	AE837819	Ae837819 VEGF or V
878	8.8	46.3	19	14	ADM85616	Adm85616 MAP3K9 ma	951	8.8	46.3	19	14	AE838066	Ae838066 VEGF or V
879	8.8	46.3	19	14	ADM27813	Adm27813 Chollnerg	952	8.8	46.3	19	14	AE838066	Ae838066 VEGF or V
880	8.8	46.3	19	14	ADM27714	Adm27714 Chollnerg	953	8.8	46.3	19	14	AE836508	Ae836508 VEGF or V
881	8.8	46.3	19	14	ADM79371	Adm79371 Human ace	954	8.8	46.3	19	14	AE834056	Ae834056 Human bet
882	8.8	46.3	19	14	ADY78957	Ady78957 Human ace	955	8.8	46.3	19	14	AE876469	Ae876469 Rat PNP65
883	8.8	46.3	19	14	ADY102581	Ady102581 Extend pr	956	8.8	46.3	19	14	AE876666	Ae876666 Rat PNP65
884	8.8	46.3	19	14	ADY03112	Ady03112 Extend pr	957	8.8	46.3	19	14	AE876567	Ae876567 Human gal
885	8.8	46.3	19	14	ADX86554	Adx86554 XIAP tarq	958	8.8	46.3	19	14	AE851746	Ae851746 Human SCD
886	8.8	46.3	19	14	ADX86661	Adx86661 XIAP tarq	959	8.8	46.3	19	14	AE852036	Ae852036 Human SCD
887	8.8	46.3	19	14	ADX86194	Adx86194 XIAP tarq	960	8.8	46.3	19	14	AE818111	Ae818111 Human bet
888	8.8	46.3	19	14	ADY87021	Ady87021 XIAP tarq	961	8.8	46.3	19	14	AE853622	Ae853622 Human hai
889	8.8	46.3	19	14	ADY57683	Ady57683 Human hai	962	8.8	46.3	19	14	AE853622	Ae853622 Human hai
890	8.8	46.3	19	14	ADY57376	Ady57376 Human hai	963	8.8	46.3	19	14	AE843131	Ae843131 Human hai
891	8.8	46.3	19	14	ADY50909	Ady50909 MAPK14 si	964	8.8	46.3	19	14	AE843135	Ae843135 Human hai
892	8.8	46.3	19	14	ADY87023	Ady87023 VEGFR siR	965	8.8	46.3	19	14	AE846726	Ae846726 Human hai
893	8.8	46.3	19	14	ADY87450	Ady87450 VEGFR siR	966	8.8	46.3	19	14	AE843145	Ae843145 Human hai
894	8.8	46.3	19	14	ADY87700	Ady87700 VEGFR siR	967	8.8	46.3	19	14	AE843132	Ae843132 Human hai

968	8.8	46.3	19	14	AEE43133	Aee43133 Human hai
C 969	8.8	46.3	19	14	AEE43142	Aee43142 Human hai
C 970	8.8	46.3	19	14	AEE46725	Aee46725 Human hai
C 971	8.8	46.3	19	14	AEE43138	Aee43138 Human hai
C 972	8.8	46.3	19	14	AEE46707	Aee46707 Human hai
C 973	8.8	46.3	19	14	AEE46708	Aee46708 Human hai
C 974	8.8	46.3	19	14	AEE53638	Aee53638 Human hai
C 975	8.8	46.3	19	14	AEE53639	Aee53639 Human hai
C 976	8.8	46.3	19	14	AEE43140	Aee43140 Human hai
C 977	8.8	46.3	19	14	AEE43144	Aee43144 Human hai
C 978	8.8	46.3	19	14	AEE53623	Aee53623 Human hai
C 979	8.8	46.3	19	14	AEE43137	Aee43137 Human hai
C 980	8.8	46.3	19	14	AEE43139	Aee43139 Human hai
C 981	8.8	46.3	19	14	AEE43141	Aee43141 Human hai
C 982	8.8	46.3	19	14	AEE43136	Aee43136 Human hai
C 983	8.8	46.3	19	14	AEE43143	Aee43143 Human hai
C 984	8.8	46.3	19	14	AEE43146	Aee43146 Human hai
C 985	8.8	46.3	19	15	AEE61132	Aee61132 Human C-J
C 986	8.8	46.3	19	15	AEE700383	Aee700383 Human MAP
C 987	8.8	46.3	19	15	AEE14461	Aee14461 Human cho
C 988	8.8	46.3	19	15	AEE37645	Aee37645 Human PTP
C 989	8.8	46.3	19	15	AEE37460	Aee37460 Human PTP
C 990	8.8	46.3	19	15	AEE58501	Aee58501 Human bet
C 991	8.8	46.3	19	15	AEE67482	Aee67482 Human PTP
C 992	8.8	46.3	19	15	AEE66884	Aee66884 Human PTP
C 993	8.8	46.3	19	15	AEE80060	Aee80060 Human bet
C 994	8.6	45.3	19	2	AAQ77689	AAQ77689 MTG8-2 pr
C 995	8.6	45.3	19	2	AAQ75022	AAQ75022 PCR prime
C 996	8.6	45.3	19	2	AAQ88258	AAQ88258 Neisseria
C 997	8.6	45.3	19	2	AAQ81240	AAQ81240 Ribozyme
C 998	8.6	45.3	19	2	AAI08591	AAI08591 K-ras pro
C 999	8.6	45.3	19	2	AAI45034	AAI45034 Carboxype
1000	8.6	45.3	19	2	AAV59355	AAV59355 Human MDR

ALIGNMENTS

RESULT 1					
ID	ABK93682	standard; DNA; 19 BP.			
XX	ABK93682;				
AC	26-AUG-2002	(first entry)			
DT					
XX					
DE	Human inhibitor of apoptosis, XIAP, antisense oligonucleotide #29.				
XX					
KW	Human; ss; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;				
KW	cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;				
KW	pancreatic cancer; embryonic development; viral pathogenesis;				
KW	autoimmune disorder; neurodegenerative disease; multiple sclerosis;				
KW	lupus erythematosus; herpes virus infection; pox virus infection;				
KW	adenovirus infection; proliferative disease.				
OS	Homo sapiens.				
XX					
PN	WO200226968-A2.				
XX					
PD	04-APR-2002.				
XX					
PF	27-SEP-2001; 2001WO-CA001379.				
XX					
PR	28-SEP-2000; 2000US-00672717.				
XX					
PA	(UYON-) UNTV OTTAMA.				
XX	(ABGE-) AEGERA THERAPEUTICS INC.				
XX					
PI	Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;				
XX					
DR	WPI; 2002-479562/51.				
XX					
PT	Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing				

PT	apoptosis in a cell, for treating cancer and other proliferative
PT	diseases.
XX	
PS	Claim 8; Page 33; 135pp; English.
XX	
CC	The invention relates to an inhibitor of apoptosis (IAP) antisense
CC	nucleic acid (I) that inhibits IAP biological activity, regardless of
CC	length of the antisense nucleic acid, the IAP proteins may be mouse or
CC	human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC	composition comprising a mammalian IAP antisense molecule and a method of
CC	enhancing apoptosis in a cell, comprising administering a negative
CC	regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC	antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC	mammal diagnosed with a proliferative disease. The method is useful for
CC	treating a patient diagnosed with a proliferative disease like cancer.
CC	The IAP antisense molecule is useful to treat, ameliorate, improve,
CC	sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC	adenocarcinoma, lymphoma, pancreatic cancer.) and also in diseases or
CC	conditions where apoptosis is involved or implicated (e.g. embryonic
CC	development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC	diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC	virus, pox virus and adenovirus). The present sequence is an IAP
CC	antisense molecule of the invention
XX	
SQ	Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAGCGTATCTCTTCTAC 19  
Db 1 CGCAGCGTATCTCTTCTAC 19

XX	RESULT 2
XX	AEA10008
ID	AEA10008 standard; DNA; 19 BP.
XX	
AC	AEA10008;
DT	14-JUL-2005 (first entry)
XX	
DE	Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 29.
XX	
KW	Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.
XX	
OS	Homo sapiens.
XX	Synthetic.
PN	WO2005042030-A1.
XX	
PD	12-MAY-2005.
XX	
PF	29-OCT-2004; 2004WO-CA001900.
XX	
PR	30-OCT-2003; 2003US-0516263P.
XX	
PA	(ABGE-) AEGERA THERAPEUTICS INC.
XX	
PI	Lacasse E, Mcmanus D, Durkin JP;
XX	
DR	WPI; 2005-366517/37.
XX	
PT	Treating proliferative disease such as hepatoma, bile duct carcinoma, choriocarcinoma, seminoma and embryonal carcinoma comprises administering antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic agent.
XX	
PS	Claim 6; SEQ ID NO 29; 285pp; English.
XX	
CC	The invention relates to a method of treating a patient having a proliferative disease, comprising administering to the patient, an

CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a  
CC chemotherapeutic agent, in amounts that together are sufficient to treat  
CC the patient. The method is useful for treating a patient having a  
CC proliferative disease. The proliferative disease is cancer. A composition  
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic  
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or  
CC human cancer cell in vivo or ex vivo, which involves contacting the cell  
CC with the composition. The present sequence represents an antisense  
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the  
CC sequence represents either T or U. There are multiple versions of this  
CC sequence in the patent, the present sequence represents the sequence  
CC shown in the main body of the specification.

XX SQ Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 19; DB 14; Length 19;  
XX Best Local Similarity 100.0%; Pred. No. 5.7;  
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAGGATATCTCTTCAC 19  
Db 1 CGCAGGATATCTCTTCAC 19

RESULT 3  
AEA10086  
ID AEA10086 standard; DNA; 19 BP.  
XX  
AC AEA10086;  
XX  
DT 14-JUL-2005 (first entry)  
XX  
DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 107.  
XX  
KM Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..3  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER = 2'-O-methyl X RNA"  
FT modified\_base 17..19  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER = 2'-O-methyl X RNA"  
XX  
PN WO2005042030-A1.  
XX  
PD 12-MAY-2005.  
XX  
PF 29-OCT-2004; 2004WO-CA001900.  
XX  
PR 30-OCT-2003; 2003US-0516263P.  
XX  
PA (AEGE-) AEGERA THERAPEUTICS INC.  
XX  
PI Lacasease E, Mcmanus D, Durkin JP;  
XX  
DR WPI; 2005-366517/37.  
XX  
PT Treating proliferative disease such as hepatoma, bile duct carcinoma,  
PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering  
PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic  
PT agent.  
XX  
PS Example 1; SEQ ID NO 107; 285bp; English.  
XX  
XX The invention relates to a method of treating a patient having a  
XX proliferative disease, comprising administering to the patient, an  
XX antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a

CC chemotherapeutic agent, in amounts that together are sufficient to treat  
CC the patient. The method is useful for treating a patient having a  
CC proliferative disease. The proliferative disease is cancer. A composition  
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic  
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or  
CC human cancer cell in vivo or ex vivo, which involves contacting the cell  
CC with the composition. The present sequence represents an antisense  
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the  
CC sequence represents either T or U. There are multiple versions of this  
CC sequence in the patent, the present sequence represents the sequence  
CC shown in the main body of the specification.

XX SQ Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 19; DB 14; Length 19;  
XX Best Local Similarity 100.0%; Pred. No. 5.7;  
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAGGATATCTCTTCAC 19  
Db 1 CGCAGGATATCTCTTCAC 19

RESULT 4  
ADX86146/c  
ID ADX86146 standard; RNA; 19 BP.  
XX  
AC ADX86146;  
XX  
DT 05-MAY-2005 (first entry)  
XX  
DE XIAP targeting siRNA SEQ ID NO 17.  
XX  
KM dx; primer; short interfering RNA; siRNA;  
KM X-linked inhibitor of apoptosis protein; XIAP; RNA interference; RNAi;  
KM cytostatic; cancer; gene silencing.  
XX  
OS Synthetic.  
XX  
PN WO2005014811-A2.  
XX  
PD 17-FEB-2005.  
XX  
PF 06-AUG-2004; 2004WO-US025589.  
XX  
PR 08-AUG-2003; 2003US-0493561P.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00727780.  
PR 14-JAN-2004; 2004US-00757803.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826966.  
PR 30-APR-2004; 2004WO-US013456.  
PR 24-MAY-2004; 2004WO-US016390.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswigen J, Chowrira BW;  
XX  
DR WPI; 2005-163247/17.  
XX  
PT New chemically synthesized double stranded short interfering nucleic acid  
PT that directs cleavage of an X-linked inhibitor of apoptosis protein  
PT (XIAP) RNA via RNA interference, useful in preparing a composition for  
PT treating cancer.  
XX  
PS Claim 33; SEQ ID NO 17; 202bp; English.  
XX  
XX This invention describes novel chemically synthesized double stranded  
XX short interfering nucleic acid (siRNA) molecules which direct cleavage of  
XX a X-linked inhibitor of apoptosis protein (XIAP) RNA via RNA interference  
XX (RNAi), where each strand of the siRNA molecule is about 18-23



OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1..19  
 FT /\*tag= a  
 FT /note= "N = T or U where each nucleobase may be part of a  
 FT ribonucleotide, deoxyribonucleotide, or nucleotide  
 FT analogue"  
 XX  
 XX WO2003080638-A2.  
 XX  
 XX 02-OCT-2003.  
 XX  
 XX 27-MAR-2003; 2003WO-IB001670.  
 XX  
 XX 27-MAR-2002; 2002US-0367853P.  
 XX  
 XX (AEGE-) AEGERA THERAPEUTICS INC.  
 XX  
 XX Lacasease E, Mcmanus D, Durkin JP;  
 XX WPI; 2003-779241/73.  
 XX  
 XX New nucleobase oligomers that inhibit expression of inhibitor of  
 PT apoptosis gene, useful for treating cancer and other lymphoproliferative  
 PT disorders by inducing apoptosis.  
 XX  
 XX Claim 54; SEQ ID NO 29; 259pp; English.  
 XX  
 XX The present invention describes a substantially pure nucleobase oligomer  
 CC (1) of up to 30 nucleobases in length or comprising eleven DNA residues  
 CC flanked on each side by four 2'-O-methyl RNA residues that inhibits the  
 CC expression of an inhibitor-of apoptosis (IAP) in the cell. Also  
 CC described: (1) a pharmaceutical composition (II) comprising (I) and a  
 CC carrier; (2) a catalytic RNA molecule (III) capable of cleaving XIAP,  
 CC XIAP1, or XIAP2 mRNA; (3) an expression vector (IV) comprising a nucleic  
 CC acid encoding one or more (II) positioned for expression in a mammalian  
 CC cell; (4) a double-stranded RNA molecule (IV) consisting of 21-29  
 CC nucleobases, comprising at least eight consecutive nucleobases  
 CC corresponding to a sequence comprising 19 nucleotides, as given in  
 CC specification; (5) a double-stranded hairpin RNA molecule (V) consisting  
 CC of 50-70 nucleobases, comprising a first domain of 21-29 nucleobases that  
 CC comprise at least eight consecutive nucleobases corresponding to a  
 CC sequence fully defined in the specification, comprising e.g. 19  
 CC nucleotides, and a second domain complementary to the first domain, and a  
 CC loop domain situated between the first and the second domains such that  
 CC the first domain and the second domain are capable of duplexing to form  
 CC the double-stranded hairpin RNA molecule; and (6) an expression vector  
 CC (VI) comprising a nucleic acid molecule encoding the double stranded RNA  
 CC molecule positioned for expression in a mammalian cell. (I) has  
 CC cytoskeletal activity, and can be used in antisense therapy. (I) is useful  
 CC for enhancing the apoptosis of a cell in an animal, preferably human  
 CC where (I) inhibits the expression of an IAP in the cell. (I) is also  
 CC useful for treating an animal having a cancer or lymphoproliferative  
 CC disorder. The cancer includes acute leukemia, acute lymphocytic  
 CC leukemia, acute myelocytic leukemia, acute myeloblastic leukemia,  
 CC acute promyelocytic leukemia, acute myelomonocytic leukemia, acute  
 CC monocytic leukemia, acute erythroleukemia, chronic leukemia, chronic  
 CC myelocytic leukemia, acute myelodysplastic syndrome, chronic lymphocytic  
 CC leukemia, polycythemia vera, lymphoma, Hodgkin's disease, Waldenstrom's  
 CC macroglobulinemia, breast cancer, basal cell carcinoma, lung carcinoma,  
 CC melanoma and retinoblastoma. The present sequence is used in the  
 CC exemplification of the present invention.  
 XX  
 XX Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;  
 XX  
 XX Query Match 73.7%; Score 14; DB 10; Length 19;  
 XX Best Local Similarity 73.7%; Pred. No. 2.4e+03;  
 XX Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 7  
 ID ADF68262 standard; DNA; 19 BP.  
 XX  
 AC ADF68262;  
 XX  
 XX 12-FEB-2004 (first entry)  
 XX  
 XX Human antisense IAP nucleobase oligomer SEQ ID NO:107.  
 XX  
 XX nucleobase oligomer; inhibitor-of apoptosis inhibitor; IAP inhibitor;  
 KM cytoskeletal; antisense therapy; apoptosis enhancer; cancer;  
 KM lymphoproliferative disorder; leukemia; myelodysplastic syndrome;  
 KM polycythemia vera; lymphoma; Hodgkin's disease;  
 KM Waldenstrom's macroglobulinemia; breast cancer; basal cell carcinoma;  
 KM lung carcinoma; melanoma; retinoblastoma; human; ss.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH misc\_feature 1..19  
 FT /\*tag= a  
 FT /note= "N = T or U where each nucleobase may be part of a  
 FT ribonucleotide, deoxyribonucleotide, or nucleotide  
 FT analogue"  
 XX  
 XX WO2003080638-A2.  
 XX  
 XX 02-OCT-2003.  
 XX  
 XX 27-MAR-2003; 2003WO-IB001670.  
 XX  
 XX 27-MAR-2002; 2002US-0367853P.  
 XX  
 XX (AEGE-) AEGERA THERAPEUTICS INC.  
 XX  
 XX Lacasease E, Mcmanus D, Durkin JP;  
 XX WPI; 2003-779241/73.  
 XX  
 XX New nucleobase oligomers that inhibit expression of inhibitor of  
 PT apoptosis gene, useful for treating cancer and other lymphoproliferative  
 PT disorders by inducing apoptosis.  
 XX  
 XX Claim 54; SEQ ID NO 107; 259pp; English.  
 XX  
 XX The present invention describes a substantially pure nucleobase oligomer  
 CC (1) of up to 30 nucleobases in length or comprising eleven DNA residues  
 CC flanked on each side by four 2'-O-methyl RNA residues that inhibits the  
 CC expression of an inhibitor-of apoptosis (IAP) in the cell. Also  
 CC described: (1) a pharmaceutical composition (II) comprising (I) and a  
 CC carrier; (2) a catalytic RNA molecule (III) capable of cleaving XIAP,  
 CC XIAP1, or XIAP2 mRNA; (3) an expression vector (IV) comprising a nucleic  
 CC acid encoding one or more (II) positioned for expression in a mammalian  
 CC cell; (4) a double-stranded RNA molecule (IV) consisting of 21-29  
 CC nucleobases, comprising at least eight consecutive nucleobases  
 CC corresponding to a sequence comprising 19 nucleotides, as given in  
 CC specification; (5) a double-stranded hairpin RNA molecule (V) consisting  
 CC of 50-70 nucleobases, comprising a first domain of 21-29 nucleobases that  
 CC comprise at least eight consecutive nucleobases corresponding to a  
 CC sequence fully defined in the specification, comprising e.g. 19  
 CC nucleotides, and a second domain complementary to the first domain, and a  
 CC loop domain situated between the first and the second domains such that  
 CC the first domain and the second domain are capable of duplexing to form  
 CC the double-stranded hairpin RNA molecule; and (6) an expression vector  
 CC (VI) comprising a nucleic acid molecule encoding the double stranded RNA  
 CC molecule positioned for expression in a mammalian cell. (I) has  
 CC cytoskeletal activity, and can be used in antisense therapy. (I) is useful  
 CC for enhancing the apoptosis of a cell in an animal, preferably human  
 CC where (I) inhibits the expression of an IAP in the cell. (I) is also

CC useful for treating an animal having a cancer or lymphoproliferative  
CC disorder. The cancer includes acute leukaemia, acute lymphocytic  
CC leukemia, acute myelocytic leukemia, acute myeloblastic leukemia,  
CC acute promyelocytic leukemia, acute myelomonocytic leukemia, acute  
CC monocytic leukemia, acute erythroleukemia, chronic leukemia, chronic  
CC myelocytic leukemia, myelodysplastic syndrome, chronic lymphocytic  
CC leukemia, polycythemia vera, lymphoma, Hodgkin's disease, Waldenstrom's  
CC macroglobulinemia, breast cancer, basal cell carcinoma, lung carcinoma,  
CC melanoma and retinoblastoma. The present sequence is used in the  
CC exemplification of the present invention.

XX Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;

XX Query Match 73.7%; Score 14; DB 10; Length 19;

XX Best Local Similarity 73.7%; Pred. No. 2.4e+03;

XX Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTCAC 19  
|||  
1 CGCAGCGANANNCNNCAC 19

DB 1 CGCAGCGANANNCNNCAC 19

RESULT 8  
AEA10122

XX ID AEA10122 standard; DNA; 19 BP.

XX AEA10122;

XX 14-JUL-2005 (first entry)

XX Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 143.

XX Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX modified\_base 1..4

XX /tag= a

XX /mod\_base= OTHER

XX /note= "OTHER = 2'-O-methyl X RNA"

XX modified\_base 16..19

XX /tag= b

XX /mod\_base= OTHER

XX /note= "OTHER = 2'-O-methyl X RNA"

XX WO2005042030-A1.

XX 12-MAY-2005.

XX 29-OCT-2004; 2004WO-CA001900.

XX 30-OCT-2003; 2003US-0516263P.

XX (AEGE-) AEGERA THERAPEUTICS INC.

XX Lacasease E, Mcmanus D, Durkin JP;

XX WPI; 2005-366517/37.

XX Treating proliferative disease such as hepatoma, bile duct carcinoma,  
XX choriocarcinoma, seminoma and embryonal carcinoma comprises administering

XX antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic  
XX agent.

XX Claim 6; SEQ ID NO 143; 285pp; English.

XX The invention relates to a method of treating a patient having a  
XX proliferative disease, comprising administering to the patient, an  
XX antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a  
XX chemotherapeutic agent, in amounts that together are sufficient to treat  
XX the patient. The method is useful for treating a patient having a

CC proliferative disease. The proliferative disease is cancer. A composition  
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic  
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or  
CC human cancer cell in vivo or ex vivo, which involves contacting the cell  
CC with the composition. The present sequence represents an antisense  
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the  
CC sequence represents either T or U. There are multiple versions of this  
CC sequence in the patent, the present sequence represents the sequence  
CC shown in the main body of the specification.

XX Sequence 19 BP; 4 A; 6 C; 3 G; 4 T; 2 U; 0 Other;

XX Query Match 73.9%; Score 14; DB 14; Length 19;

XX Best Local Similarity 92.9%; Pred. No. 2.4e+03;

XX Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGTATCTCTCTTCAC 19  
|||  
1 GGTATCTCTCTTCAC 14

DB 1 GGTATCTCTCTTCAC 14

RESULT 9  
AEA10076

XX ID AEA10076 standard; DNA; 19 BP.

XX AEA10076;

XX 14-JUL-2005 (first entry)

XX Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 97.

XX Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX modified\_base 1..2

XX /tag= a

XX /mod\_base= OTHER

XX /note= "OTHER = 2'-O-methyl X RNA"

XX modified\_base 18..19

XX /tag= b

XX /mod\_base= OTHER

XX /note= "OTHER = 2'-O-methyl X RNA"

XX WO2005042030-A1.

XX 12-MAY-2005.

XX 29-OCT-2004; 2004WO-CA001900.

XX 30-OCT-2003; 2003US-0516263P.

XX (AEGS-) AEGERA THERAPEUTICS INC.

XX Lacasease E, Mcmanus D, Durkin JP;

XX WPI; 2005-366517/37.

XX Treating proliferative disease such as hepatoma, bile duct carcinoma,  
XX choriocarcinoma, seminoma and embryonal carcinoma comprises administering

XX antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic  
XX agent.

XX Claim 6; SEQ ID NO 97; 285pp; English.

XX The invention relates to a method of treating a patient having a  
XX proliferative disease, comprising administering to the patient, an  
XX antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a  
XX chemotherapeutic agent, in amounts that together are sufficient to treat  
XX the patient. The method is useful for treating a patient having a  
XX proliferative disease. The proliferative disease is cancer. A composition



CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic  
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or  
CC human cancer cell in vivo or ex vivo, which involves contacting the cell  
CC with the composition. The present sequence represents an antisense  
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the  
CC sequence represents either T or U. There are multiple versions of this  
CC sequence in the patent, the present sequence represents the sequence  
CC shown in the main body of the specification.  
XX  
SQ Sequence 19 BP; 4 A; 6 C; 3 G; 5 T; 1 U; 0 Other;  
XX  
Query Match 73.7%; Score 14; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 GGATCTCTCTTAC 19  
Db 1 GGATCTCTCTTAC 14  
XX  
RESULT 10  
AEA10108  
ID AEA10108 standard; DNA; 19 BP.  
XX  
AC AEA10108;  
XX  
DT 14-JUL-2005 (first entry)  
XX  
DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 129.  
XX  
KW Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
PN WO2005042030-A1.  
XX  
PD 12-MAY-2005.  
XX  
PF 29-OCT-2004; 2004WO-CA001900.  
XX  
PR 30-OCT-2003; 2003US-0516263P.  
XX  
PA (AEGE-) AEGERA THERAPEUTICS INC.  
XX  
PI Lacasease E, Mcmanus D, Durkin JP;  
XX  
PI Lacasease E, Mcmanus D, Durkin JP;  
XX  
DR WPI; 2005-366517/37.  
XX  
PT Treating proliferative disease such as hepatoma, bile duct carcinoma,  
PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering  
PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic  
PT agent.  
XX  
PS Example 1; SEQ ID NO 129; 285pp; English.  
XX  
CC The invention relates to a method of treating a patient having a  
CC proliferative disease, comprising administering to the patient, an  
CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a  
CC chemotherapeutic agent, in amounts that together are sufficient to treat  
CC the patient. The method is useful for treating a patient having a  
CC proliferative disease. The proliferative disease is cancer. A composition  
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic  
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or  
CC human cancer cell in vivo or ex vivo, which involves contacting the cell  
CC with the composition. The present sequence represents an antisense  
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the  
CC sequence represents either T or U. There are multiple versions of this  
CC sequence in the patent, the present sequence represents the sequence  
CC shown in the main body of the specification.  
XX  
SQ Sequence 19 BP; 4 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 73.7%; Score 14; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 GGATCTCTCTTAC 19  
Db 1 GGATCTCTCTTAC 14  
XX  
RESULT 11  
AEA09518  
ID AEA09518 standard; DNA; 19 BP.  
XX  
AC AEA09518;  
XX  
DT 14-JUL-2005 (first entry)  
XX  
DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 29.  
XX  
KW Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_difference 1..19  
FT /tag= a  
FT /note= "The residues represented by N are either T or U"  
XX  
PN WO2005042030-A1.  
XX  
PD 12-MAY-2005.  
XX  
PF 29-OCT-2004; 2004WO-CA001900.  
XX  
PR 30-OCT-2003; 2003US-0516263P.  
XX  
PA (AEGE-) AEGERA THERAPEUTICS INC.  
XX  
PI Lacasease E, Mcmanus D, Durkin JP;  
XX  
PI Lacasease E, Mcmanus D, Durkin JP;  
XX  
DR WPI; 2005-366517/37.  
XX  
PT Treating proliferative disease such as hepatoma, bile duct carcinoma,  
PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering  
PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic  
PT agent.  
XX  
PS Claim 6; SEQ ID NO 29; 285pp; English.  
XX  
CC The invention relates to a method of treating a patient having a  
CC proliferative disease, comprising administering to the patient, an  
CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a  
CC chemotherapeutic agent, in amounts that together are sufficient to treat  
CC the patient. The method is useful for treating a patient having a  
CC proliferative disease. The proliferative disease is cancer. A composition  
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic  
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or  
CC human cancer cell in vivo or ex vivo, which involves contacting the cell  
CC with the composition. The present sequence represents an antisense  
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the  
CC sequence represents either T or U. There are multiple versions of this  
CC sequence in the patent, the present sequence represents the sequence  
CC shown in the sequence listing.  
XX  
SQ Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;  
XX  
Query Match 73.7%; Score 14; DB 14; Length 19;  
Best Local Similarity 73.7%; Pred. No. 2.4e+03;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 CGCAGGTATCTCTTAC 19  
XX

Db 1 CGCAGCGNANCCNNCAC 19

RESULT 12  
AEA10267  
ID AEA10267 standard; DNA; 19 BP.

XX  
XX AEA10267;  
XX  
XX  
XX 14-JUL-2005 (first entry)  
XX  
XX Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 289.

DE Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.  
XX  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO2005042030-A1.  
XX  
XX 12-MAY-2005.  
XX  
XX 29-OCT-2004; 2004WO-CA001900.  
XX  
XX 30-OCT-2003; 2003US-0516263P.  
XX  
XX (AEGE-) AEGERA THERAPEUTICS INC.  
XX  
XX Lacasease E, Mcmanus D, Durkin JP;  
PI  
XX WPI; 2005-366517/37.  
XX  
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,  
PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering  
PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic  
PT agent.

XX  
XX Claim 6; SEQ ID NO 289; 285pp; English.

XX  
XX The invention relates to a method of treating a patient having a  
CC proliferative disease, comprising administering to the patient, an  
CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a  
CC chemotherapeutic agent, in amounts that together are sufficient to treat  
CC the patient. The method is useful for treating a patient having a  
CC proliferative disease. The proliferative disease is cancer. A composition  
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic  
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or  
CC human cancer cell in vivo or ex vivo, which involves contacting the cell  
CC with the composition. The present sequence represents an antisense  
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the  
CC sequence represents either T or U. There are multiple versions of this  
CC sequence in the patent, the present sequence represents the sequence  
CC shown in the main body of the specification.

XX  
XX Sequence 19 BP; 4 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

XX  
XX Query Match 73.7%; Score 14; DB 14; Length 19;  
XX Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGATATCTCCTTCAC 19  
DB 1 GGATATCTCCTTCAC 14

RESULT 13  
AEA09596  
ID AEA09596 standard; DNA; 19 BP.

XX  
XX AEA09596;  
XX  
XX 14-JUL-2005 (first entry)  
XX

DE Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 107.

XX  
XX Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
XX misc\_difference 1..19  
XX /tag= a  
XX /note= "The residues represented by N are either T or U"

XX  
XX WO2005042030-A1.  
XX  
XX 12-MAY-2005.  
XX  
XX 29-OCT-2004; 2004WO-CA001900.  
XX  
XX 30-OCT-2003; 2003US-0516263P.  
XX  
XX (AEGE-) AEGERA THERAPEUTICS INC.  
XX  
XX Lacasease E, Mcmanus D, Durkin JP;  
PI  
XX WPI; 2005-366517/37.  
XX  
XX Treating proliferative disease such as hepatoma, bile duct carcinoma,  
PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering  
PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic  
PT agent.

XX  
XX Example 1; SEQ ID NO 107; 285pp; English.

XX  
XX The invention relates to a method of treating a patient having a  
CC proliferative disease, comprising administering to the patient, an  
CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a  
CC chemotherapeutic agent, in amounts that together are sufficient to treat  
CC the patient. The method is useful for treating a patient having a  
CC proliferative disease. The proliferative disease is cancer. A composition  
CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic  
CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or  
CC human cancer cell in vivo or ex vivo, which involves contacting the cell  
CC with the composition. The present sequence represents an antisense  
CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the  
CC sequence represents either T or U. There are multiple versions of this  
CC sequence in the patent, the present sequence represents the sequence  
CC shown in the sequence listing.

XX  
XX Sequence 19 BP; 3 A; 8 C; 3 G; 0 T; 0 U; 5 Other;

XX  
XX Query Match 73.7%; Score 14; DB 14; Length 19;  
XX Best Local Similarity 73.7%; Pred. No. 2.4e+03;  
XX Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCCTTCAC 19  
DB 1 CGCAGCGNANCCNNCAC 19

RESULT 14  
AEC23674/C  
ID AEC23674 standard; DNA; 19 BP.

XX  
XX AEC23674;  
XX  
XX 20-OCT-2005 (first entry)  
XX  
XX Forward primer for amplification of genomic CAPN1, seq id 10.  
XX  
XX Meat; animal breeding; SNP detection;  
XX micromolar calcium activated neutral protease; mu-calpain; CAPN1; PCR;  
XX primer; ss.  
XX

OS Bos taurus.  
 XX US2005181373-A1.  
 XX  
 XX 18-AUG-2005.  
 PD  
 XX 18-DEC-2003; 2003US-00739904.  
 PF  
 XX 18-DEC-2003; 2003US-00739904.  
 PR  
 XX 18-DEC-2003; 2003US-00739904.  
 XX  
 PA (SMIT/) SMITH T P.  
 PA (CASA/) CASAS E.  
 XX  
 PI Smith TP, Casas E;  
 XX  
 DR WPI; 2005-554241/56.  
 XX  
 XX  
 PT Determining one or more alleles of the gene encoding micromolar calcium  
 PT activated neutral protease effecting meat tenderness by assaying a sample  
 PT of nucleic acids from a bovine for the presence of single nucleotide  
 PT polymorphisms.  
 XX

Example 2; SEQ ID NO 10; 39pp; English.

XX The invention relates to a method for determining one or more alleles of  
 CC the gene encoding micromolar calcium activated neutral protease effecting  
 CC meat tenderness in a bovine animal. The method comprises assaying a  
 CC sample of nucleic acids (genomic DNA, cDNA, or RNA) from a bovine for the  
 CC presence of one or more single nucleotide polymorphisms in the bovine  
 CC CAPN1 gene encoding micromolar calcium activated neutral protease (mu-  
 CC calpain). In determining one or more alleles of the gene encoding  
 CC micromolar calcium activated neutral protease effecting meat tenderness  
 CC in a bovine animal, the single nucleotide polymorphisms correspond to  
 CC position 18 of exon 9 of AEC23667, position 17 of exon 14 of AEC23668,  
 CC and position 185 on intron 19 of AEC23668. The method further comprises  
 CC selecting those bovine for breeding where the polymorphism at position 18  
 CC on exon 9 encodes alanine at amino acid 316 of the bovine micromolar  
 CC calcium activated neutral protease. The method further comprises  
 CC selecting those bovine for breeding where the polymorphism at position 17  
 CC on exon 14 encodes valine at amino acid 530 of the bovine micromolar  
 CC calcium activated neutral protease. The method further comprises  
 CC selecting those bovine for breeding where the polymorphism at position  
 CC 185 on intron 19 comprises the presence of cytosine. In identifying one  
 CC or more mutations in micromolar calcium activated neutral protease of  
 CC bovine, the presence of alanine at amino acid 316, or valine at amino  
 CC acid 539 of the bovine micromolar calcium activated neutral protease is  
 CC indicative of increased meat tenderness. The method is useful for  
 CC determining one or more alleles of the gene encoding micromolar calcium  
 CC activated neutral protease effecting meat tenderness in a bovine animal.  
 CC Sequences given in records for AEC23672-AEC23741 represent primers used  
 CC in an example from the invention in the amplification of genomic CAPN1.  
 XX

XX Sequence 19 BP; 6 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 68.4%; Score 13; DB 14; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CACGGATCTCTCT 15  
 |||||  
 DB 17 CACGGATCTCTCT 5

RESULT 15  
 AEA10089  
 ID AEA10089 standard; DNA; 19 BP.  
 XX  
 AC AEA10089;

XX 14-JUL-2005 (first entry)  
 XX Antisense inhibitor of apoptosis (IAP) nucleobase oligomer SEQ ID NO 110.  
 DE  
 XX

KW Cytostatic; neoplasm; cancer; Antisense; apoptosis inhibitor; ss.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 XX modified\_base 1..3  
 FT /+tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER = 2'-O-methyl X RNA"  
 FT modified\_base 17..19  
 FT /+tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER = 2'-O-methyl X RNA"  
 XX  
 XX W0205042030-A1.  
 XX  
 XX 12-MAY-2005.  
 PD  
 XX 29-OCT-2004; 2004WO-CA001900.  
 PF  
 XX 30-OCT-2003; 2003US-0516263P.  
 XX  
 XX (AEGE-) AEGERA THERAPEUTICS INC.  
 PA  
 PI Lacasease E, Mcmanus D, Durkin JP;  
 XX  
 XX WPI; 2005-366517/37.  
 DR

XX Treating proliferative disease such as hepatoma, bile duct carcinoma,  
 PT choriocarcinoma, seminoma and embryonal carcinoma comprises administering  
 PT antisense inhibitor of apoptosis nucleobase oligomer and chemotherapeutic  
 PT agent.  
 XX

Example 1; SEQ ID NO 110; 285pp; English.

XX The invention relates to a method of treating a patient having a  
 CC proliferative disease, comprising administering to the patient, an  
 CC antisense inhibitor of apoptosis (IAP) nucleobase oligomer and a  
 CC chemotherapeutic agent, in amounts that together are sufficient to treat  
 CC the patient. The method is useful for treating a patient having a  
 CC proliferative disease. The proliferative disease is cancer. A composition  
 CC comprising an antisense IAP nucleobase oligomer and a chemotherapeutic  
 CC agent is useful for enhancing apoptosis of a cell, e.g. cancer cell or  
 CC human cancer cell in vivo or ex vivo, which involves contacting the cell  
 CC with the composition. The present sequence represents an antisense  
 CC inhibitor of apoptosis (IAP) nucleobase oligomer. Note: The N's in the  
 CC sequence represents either T or U. There are multiple versions of this  
 CC sequence in the patent, the present sequence represents the sequence  
 CC shown in the main body of the specification.  
 XX

XX Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 66.3%; Score 12.6; DB 14; Length 19;  
 Best Local Similarity 78.9%; Pred. No. 1.3e+04;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCACGGATCTCTCTCAC 19  
 |||||  
 DB 1 CGCACCGTATCTGTCTCAC 19

RESULT 16  
 ADQ61052/c  
 ID ADQ61052 standard; RNA; 19 BP.  
 XX  
 AC ADQ61052;

XX 09-SEP-2004 (first entry)  
 XX Anti-HCK siRNA related DNA sequence SEQ ID NO:754.  
 DE  
 XX siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;  
 KM



XX WPI; 1999-142853/12.  
 XX Novel murine oestrogen receptor-beta genes and splice variants - useful  
 PT for treating oestrogen receptor-beta mediated disorders.  
 XX  
 XX Example 1; Page 43; 89pp; English.  
 CC The present invention describes the murine complete oestrogen receptor  
 CC beta (MER beta c), also designated MER beta-3). The present sequence  
 CC represents a PCR primer used in the cloning of MER beta c. The protein  
 CC can be used to screen for agents that modulate or block the interaction  
 CC between the ER beta c protein and physiological, stilbene or  
 CC triphenylethylene (anti)oestrogens. The antibody which binds the protein  
 CC can be used in assays to detect activation of the ER beta protein and can  
 CC be used for subcellular localisation of the protein. The complementary  
 CC nucleic acid can be used to inhibit expression of the ER beta c nucleic  
 CC acid  
 XX  
 SQ Sequence 19 BP; 3 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 62.1%; Score 11.8; DB 2; Length 19;  
 Best Local Similarity 86.7%; Pred. No. 3.4e+04;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 5 CGGTATCTCCTTCAC 19  
 Db 2 CAGTACCTCCTTCAC 16  
 RESULT 19  
 AEF14562/c  
 ID AEF14562 standard; DNA; 19 BP.  
 AC AEF14562;  
 XX 09-MAR-2006 (first entry)  
 DT  
 XX Human chondrocyte anabolic stimulation associated KD SEQ ID NO 279.  
 DE  
 XX Osteopathic; Nootropic; Neuroprotective; Dermatological;  
 KM Antiinflammatory; Antiarthritic; Antiarthritic; musculoskeletal disease;  
 KM chondrocyte anabolic stimulator; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005124342-A2.  
 XX  
 PD 29-DEC-2005.  
 XX  
 PF 21-JUN-2005; 2005WO-EP052875.  
 XX  
 PR 21-JUN-2004; 2004US-0581568P.  
 XX  
 PA (GALA-) GALAPAGOS NV.  
 XX  
 PI Vandeghinste N, Tomme PHM, Michiels F, Ma L, Mille-Baker B;  
 PI Van Es HMG;  
 XX  
 DR WPI; 2006-067565/07.  
 XX  
 PT Identifying a compound that induces chondrocyte anabolic stimulation,  
 PT useful for treating osteoarthritis, comprises measuring a compound-  
 PT polypeptide property related to the anabolic stimulation of chondrocytes.  
 CC  
 PS Claim 19; SEQ ID NO 279; 179pp; English.  
 XX  
 CC The invention relates to a method of identifying a compound that induces  
 CC chondrocyte anabolic stimulation. The methods and agent are useful for  
 CC treating and/or preventing a disease involving a systemic or local  
 CC decrease in cartilage, e.g. osteoarthritis, rheumatoid arthritis,  
 CC psoriatic arthritis, juvenile rheumatoid arthritis, gouty arthritis,  
 CC septic or infectious arthritis, reactive arthritis, reflex sympathetic

CC dystrophy, algodystrophy, Tietze syndrome or costal chondritis.  
 CC fibromyalgia, osteoarthritis, neurogenic or neuropathic arthritis,  
 CC arthropathy, osteoarthritis deformans endemica, Meulens disease,  
 CC Handipodu disease, degeneration resulting from fibromyalgia, systemic  
 CC lupus erythematosus, scleroderma, ankylosing spondylitis, hereditary  
 CC chondrolysis, chondrodysplasias, pseudochondrodysplasias, microtia,  
 CC anelia, and metaphyseal chondrodysplasia. The agent is useful in the  
 CC manufacture of a medicament for the treating and/or preventing a disease  
 CC involving a decrease in mean cartilage thickness, e.g. osteoarthritis,  
 CC hyperaldemia of malignancy, multiple myelomatosis, hyperparathyroidism,  
 CC and hyperthyroidism. The present sequence represents a human chondrocyte  
 CC anabolic stimulation associated KD target sequence.  
 XX  
 SQ Sequence 19 BP; 6 A; 3 C; 6 G; 4 T; 0 U; 0 Other;  
 Query Match 62.1%; Score 11.8; DB 15; Length 19;  
 Best Local Similarity 86.7%; Pred. No. 3.4e+04;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 5 CGGTATCTCCTTCAC 19  
 Db 17 CAGTATCTCCTTCAC 3  
 RESULT 20  
 ADF73037  
 ID ADF73037 standard; cDNA; 19 BP.  
 AC ADF73037;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE DNA sequence of the invention #7.  
 XX  
 KM human repair gene DNA polymerase beta; gene therapy; esophagus cancer;  
 KM es.  
 XX  
 OS Synthetic.  
 XX  
 PN CN1366047-A.  
 XX  
 PD 28-AUG-2002.  
 XX  
 PF 24-AUG-2001; 2001CN-00128374.  
 XX  
 PR 24-AUG-2001; 2001CN-00128374.  
 XX  
 PA (UYZH-) UNIV ZHENGZHOU.  
 XX  
 PI Dong Z, Zhao G, Zhao Q;  
 XX  
 DR WPI; 2003-240398/24.  
 XX  
 PT Human DNA polymerase beta mutant gene and its corresponding protein.  
 PT  
 XX  
 PS Disclosure; SEQ ID NO 14; 18pp; Chinese.  
 XX  
 CC The present invention relates to a cDNA sequence of human repair gene DNA  
 CC polymerase beta, which is a specific representation of DNA polymerase  
 CC beta in esophagus cancer. The protein coded by it has fully lost the DNA  
 CC repair activity of DNA polymerase beta. It can be used for early  
 CC diagnosis and gene therapy of esophagus cancer. The present sequence is a  
 CC DNA sequence of the invention.  
 XX  
 SQ Sequence 19 BP; 3 A; 7 C; 3 G; 6 T; 0 U; 0 Other;  
 Query Match 60.0%; Score 11.4; DB 10; Length 19;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+04;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 6 GGATATCTCCTTCAC 18  
 Db 6 GGATATCTCCTTCAC 18

```
RESULT 21
ACD28194
ID ACD28194 standard; DNA; 19 BP.
XX
XX ACD28194;
AC
XX
XX 08-OCT-2003 (first entry)
DT
XX
XX Human repair gene DNA polymerase beta related oligonucleotide #5.
DE
XX
XX Human; repair gene; DNA polymerase beta; oesophagus cancer;
KW
XX DNA repair activity; gene therapy; ss.
XX
XX Unidentified.
OS
XX
XX CN1366047-A.
PN
XX
XX 28-AUG-2002.
PD
XX
XX 24-AUG-2001; 2001CN-00128374.
PF
XX
XX 24-AUG-2001; 2001CN-00128374.
PR
XX
XX (UYZH-) UNIV ZHENGZHOU.
XX
XX Dong Z, Zhao G, Zhao Q;
PI
XX
XX WPI; 2003-240398/24.
PT
XX
XX Human DNA polymerase beta mutant gene and its corresponding protein.
PS
XX
XX Example 2; Page 9 (Disclosure); 11pp; Chinese.
XX
XX The present invention discloses a cDNA sequence of human repair gene DNA
CC
XX polymerase beta, which is a specific representation of DNA polymerase
CC
XX beta in oesophagus cancer. The protein coded by it has fully lost the DNA
CC
XX repair activity of DNA polymerase beta. It can be used for early
CC
XX diagnosis and gene therapy of esophagus cancer. This sequence represents
CC
XX a human DNA polymerase beta associated oligonucleotide
XX
XX
SQ Sequence 19 BP; 3 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 60.0%; Score 11.4; DB 10; Length 19;
Best Local Similarity 92.3%; Pred. No. 5.5e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 GGATCTCCTTCA 18
    |||||
Db 6 GGTACTCCTTCA 18

RESULT 22
AAZ73203
ID AAZ73203 standard; DNA; 19 BP.
XX
XX AAZ73203;
AC
XX
XX 10-SEP-2001 (first entry)
DT
XX
XX Human biallelic marker upstream amplification primer SEQ ID NO:7559.
DE
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW
XX haplotyping; hybridisation; identification; characterisation;
KW
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
KW
XX diagnosis; ss.
XX
XX Homo sapiens.
OS
XX
XX W0954500-A2.
PN
XX
XX
```

```
PD 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-1B000822.
PF
XX
XX 21-APR-1998; 98US-0082614P.
PR
XX
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GSEST ) GENSEST.
PA
XX
XX Cohen D, Blumenfeld M, Chumakov I;
PI
XX
XX WPI; 2000-013267/01.
PT
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT
XX map of the human genome.
PS
XX
XX Claim 9; Page 1842; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC
XX invention, which contain a polymorphic base at position 24 of their
CC
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC
XX primers for the biallelic markers. The biallelic markers of the invention
CC
XX have a variety of uses: they can be used for high density mapping of the
CC
XX human genome, and in complex association studies and haplotyping studies
CC
XX which are useful in determining the genetic basis for disease states.
CC
XX Compositions and methods of the invention can also be useful for the
CC
XX identification of the targets for the development of pharmaceutical
CC
XX agents and diagnostic methods, as well as the characterisation of the
CC
XX differential efficacious responses to and side effects from
CC
XX pharmaceutical agents acting on a disease as well as other treatment.
CC
XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC
XX 3367, are not actually given a sequence in the Sequence Listing from the
CC
XX present invention
XX
XX
SQ Sequence 19 BP; 1 A; 6 C; 2 G; 10 T; 0 U; 0 Other;
Query Match 57.9%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GTATCTCCTTC 17
    |||||
Db 1 GTATCTCCTTC 11

RESULT 23
AD061051/C
ID AD061051 standard; RNA; 19 BP.
XX
XX AD061051;
AC
XX
XX 09-SEP-2004 (first entry)
DT
XX
XX Anti-HCK siRNA related DNA sequence SEQ ID NO:753.
DE
XX
XX ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW
XX RNA interference.
XX
XX Synthetic.
OS
XX
XX W02004045543-A2.
PN
XX
XX 03-JUN-2004.
PD
XX
XX 14-NOV-2003; 2003WO-US036787.
PF
XX
XX 14-NOV-2002; 2002US-0426137P.
PR
XX
XX 10-SEP-2003; 2003US-0502050P.
XX
XX (DHAR-) DHARMACON INC.
PA
XX
XX Anastasia K, Angela R, Devin L, William M, Stephen S;
XX
XX
```

DR WPI; 2004-420527/39.  
XX Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases  
PT by selecting a target gene and measuring the functionality of the  
PT nucleotide sequences that are complementary to a stretch of nucleotides  
PT of the target sequence.  
PS Example 12; SEQ ID NO 753; 199pp; English.  
XX  
XX The invention relates to a novel method for selecting siRNA (short  
CC interfering RNA) comprising selecting an siRNA molecule of 19-25  
CC nucleoside bases by selecting a target gene and measuring the  
CC functionality of sequences of 19-25 nucleotides in length that are  
CC substantially complementary to a stretch of nucleotides of the target  
CC sequence, where the functionality is dependent upon non-target specific  
CC criteria. Also claimed are methods for gene-silencing, developing an  
CC siRNA algorithm for selecting siRNA, selecting an siRNA with improved  
CC functionality, selecting hyperfunctional siRNA, an siRNA molecule  
CC effective at silencing Bcl-2, and a kit for gene silencing comprising the  
CC siRNA. The siRNA molecule comprises a sequence substantially similar to a  
CC sequence consisting of GGGGAGUAGUGAUGAUA; GAAGUACUCCUCCAGUU;  
CC GUACGACACCGGAGUA; AGAUAUGUAGAUAUAU; UGAAGUCCUCCUCCAGUU;  
CC CAGCGGCUCCUCCUCCAGUU; UGCAGCUCCUCCUCCAGUU; GAGAUAGUAGUAGUAGUA;  
CC GGAUAGUAGUAGUAGUA; and GAAAGUCCUCCUCCAGUU. The siRNA molecule  
CC comprises a sense strand and an anti-sense strand. The siRNA molecule  
CC comprises a hairpin. The siRNA molecule comprises between 18 and 30 base  
CC pairs. The kit comprises at least two siRNA, comprising a first optimised  
CC siRNA and a second optimised siRNA. The method is useful in selecting  
CC siRNA for generating a gene silencing reagent. The present sequence is  
CC used in the exemplification of the invention. The sequence is shown in  
CC the specification as DNA, but described as siRNA.  
XX  
SQ Sequence 19 BP; 8 A; 3 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 57.9%; Score 11; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.8e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 CAGCGTATCTC 13  
DB 11 CAGCGTATCTC 1  
RESULT 24  
ADY83894  
XX ADY83894 standard; DNA, 19 BP.  
XX  
XX ADY83894;  
XX  
XX 16-JUN-2005 (first entry)  
XX  
XX Becherichia coli gyrA gene microarray capture probe, E.coli\_GYA87G5.  
XX quinolone; DNA microarray; probe; ss.  
XX  
XX Becherichia coli.  
XX Synthetic.  
XX US2005069897-A1.  
XX PN  
XX 31-MAR-2005.  
XX PD  
XX 29-SEP-2003; 2003US-00671883.  
XX PF  
XX 29-SEP-2003; 2003US-00671883.  
XX PR  
XX (EPPE-) EPPENDORF AG.  
XX PA  
XX  
XX Yu X, Susa M, Knabbe C, Schmidt R, Bachmann TT;  
XX WPI; 2005-261625/27.  
XX  
XX Detecting quinolone resistant Escherichia coli strains in biological

PT sample by contacting DNA of sample with microarray having capture probes  
PT derived from gyrA gene of E.coli, determining change in nucleic acid at  
PT specific positions.  
XX  
XX Claim 8; SEQ ID NO 35; 20pp; English.  
XX  
XX The invention relates to a novel method for detecting quinolone resistant  
CC Escherichia coli strains in a biological sample. The method involves  
CC contacting sample DNA with a microarray having two sets of capture probes  
CC and determining at which location on the array binding occurs, where a  
CC change in a nucleic acid at one or more positions results in a change of  
CC an amino acid and is indicative of a resistance against quinolones. The  
CC invention further comprises: a microarray containing, at specific  
CC predetermined locations of the array, two sets of capture probes derived  
CC from the sequence of a gyrA gene of E. coli; and a kit for performing the  
CC method, containing the microarray, and optionally buffers and reagents.  
CC The method is useful for detecting the presence of quinolone resistant  
CC Escherichia coli strains in a biological sample. This polynucleotide  
CC sequence represents a possible capture probe of the E. coli gyrA gene for  
CC use in the microarray of the invention.  
XX  
SQ Sequence 19 BP; 3 A; 4 C; 7 G; 5 T; 0 U; 0 Other;  
Query Match 57.9%; Score 11; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.8e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GCACGGTATCT 12  
DB 5 GCACGGTATCT 15  
RESULT 25  
ADY83902  
XX ADY83902 standard; DNA, 19 BP.  
XX  
XX ADY83902;  
XX  
XX 16-JUN-2005 (first entry)  
XX  
XX Becherichia coli gyrA gene microarray capture probe, E.coli\_GYA87G7.  
XX quinolone; DNA microarray; probe; ss.  
XX  
XX Becherichia coli.  
XX Synthetic.  
XX US2005069897-A1.  
XX PN  
XX 31-MAR-2005.  
XX PD  
XX 29-SEP-2003; 2003US-00671883.  
XX PF  
XX 29-SEP-2003; 2003US-00671883.  
XX PR  
XX (EPPE-) EPPENDORF AG.  
XX PA  
XX  
XX Yu X, Susa M, Knabbe C, Schmidt R, Bachmann TT;  
XX WPI; 2005-261625/27.  
XX DR  
XX  
XX Detecting quinolone resistant Escherichia coli strains in biological  
PT sample by contacting DNA of sample with microarray having capture probes  
PT derived from gyrA gene of E.coli, determining change in nucleic acid at  
PT specific positions.  
XX  
XX Claim 8; SEQ ID NO 43; 20pp; English.  
XX  
XX The invention relates to a novel method for detecting quinolone resistant  
CC Escherichia coli strains in a biological sample. The method involves  
CC contacting sample DNA with a microarray having two sets of capture probes  
CC and determining at which location on the array binding occurs, where a  
CC change in a nucleic acid at one or more positions results in a change of

CC an amino acid and is indicative of a resistance against quinolones. The  
CC invention further comprises: a microarray containing, at specific  
CC predetermined locations of the array, two sets of capture probes derived  
CC from the sequence of a gyrA gene of E. coli; and a kit for performing the  
CC method, containing the microarray, and optionally buffers and reagents.  
CC The method is useful for detecting the presence of quinolone resistant  
CC Escherichia coli strains in a biological sample. This polynucleotide  
CC sequence represents a possible capture probe of the E. coli gyrA gene for  
CC use in the microarray of the invention.

XX Sequence 19 BP; 3 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 57.9%; Score 11; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.8e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 2 GCACGGTATCT 12  
Db 5 GCACGGTATCT 15

RESULT 26  
AEA02570/c  
ID AEA02570 standard; RNA; 19 BP.

AC AEA02570;

DT 28-JUL-2005 (first entry)

XX Cholesteryl ester transfer protein siRNA SEQ ID NO 139.

XX short interfering RNA; siRNA; gene silencing; RNA interference;

XX Respiratory-Gen.; Antiasthmatic; Antiallergic; Antiinflammatory;

XX Neuroprotective; Nootropic; Uropathic;

XX chronic obstructive pulmonary disease; asthma; allergic rhinitis;

XX sinusitis; inflammation; allergy; cystic fibrosis; alzheimer's disease;

XX mucritution disorder; cholinergic receptor muscarinic 3; CHRM3; ss.

XX Synthetic.

XX WO2005045041-A2.

XX 19-MAY-2005.

PF 19-AUG-2004; 2004WO-US027404.

XX 23-OCT-2003; 2003US-00693059.

PR 24-NOV-2003; 2003US-00720448.

PR 03-DEC-2003; 2003US-00727780.

PR 14-JAN-2004; 2004US-00757803.

PR 10-FEB-2004; 2004US-0543480P.

PR 13-FEB-2004; 2004US-00780447.

PR 16-APR-2004; 2004US-00826966.

PR 30-APR-2004; 2004WO-US013456.

PR 24-MAY-2004; 2004WO-US016390.

PR 09-JUN-2004; 2004US-00864044.

XX (SIRN-) SIRNA THERAPEUTICS INC.

PI Mcswiggen J, Polisky B;

XX WPI; 2005-347065/35.

DR New short interfering nucleic acid molecule that directs cleavage of a

XX cholesteryl ester transfer protein RNA, useful for treating or preventing

PT hypercholesterolemia, hyperlipidemia, and/or cardiovascular disease.

XX Claim 33; SEQ ID NO 139; 185bp; English.

XX The invention relates to a chemically synthesized double stranded short  
CC interfering nucleic acid (siRNA) molecule that directs cleavage of a  
CC cholesteryl ester transfer protein (CETP) RNA via RNA interference  
CC (RNAi). The siRNA molecule, compounds, compositions, and methods are

CC useful for treating or preventing hypercholesterolemia, hyperlipidemia,  
CC and/or cardiovascular disease, e.g. coronary heart disease,  
CC cerebrovascular disease, aortic stenosis, peripheral vascular disease  
CC and/or atherosclerosis. The present sequence represents a cholesteryl  
CC ester transfer protein siRNA.

XX Sequence 19 BP; 8 A; 0 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 57.9%; Score 11; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.8e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 9 ATCTCCTTAC 19  
Db 14 ATCTCCTTAC 4

RESULT 27  
AEA02470  
ID AEA02470 standard; RNA; 19 BP.

AC AEA02470;

DT 28-JUL-2005 (first entry)

XX Cholesteryl ester transfer protein siRNA SEQ ID NO 39.

XX short interfering RNA; siRNA; gene silencing; RNA interference;

XX Respiratory-Gen.; Antiasthmatic; Antiallergic; Antiinflammatory;

XX Neuroprotective; Nootropic; Uropathic;

XX chronic obstructive pulmonary disease; asthma; allergic rhinitis;

XX sinusitis; inflammation; allergy; cystic fibrosis; alzheimer's disease;

XX mucritution disorder; cholinergic receptor muscarinic 3; CHRM3; ss.

XX Synthetic.

XX WO2005045041-A2.

XX 19-MAY-2005.

PF 19-AUG-2004; 2004WO-US027404.

XX 23-OCT-2003; 2003US-00693059.

PR 24-NOV-2003; 2003US-00720448.

PR 03-DEC-2003; 2003US-00727780.

PR 14-JAN-2004; 2004US-00757803.

PR 10-FEB-2004; 2004US-0543480P.

PR 13-FEB-2004; 2004US-00780447.

PR 16-APR-2004; 2004US-00826966.

PR 30-APR-2004; 2004WO-US013456.

PR 24-MAY-2004; 2004WO-US016390.

PR 09-JUN-2004; 2004US-00864044.

XX (SIRN-) SIRNA THERAPEUTICS INC.

PI Mcswiggen J, Polisky B;

XX WPI; 2005-347065/35.

DR New short interfering nucleic acid molecule that directs cleavage of a

XX cholesteryl ester transfer protein RNA, useful for treating or preventing

PT hypercholesterolemia, hyperlipidemia, and/or cardiovascular disease.

XX Claim 33; SEQ ID NO 39; 185bp; English.

XX The invention relates to a chemically synthesized double stranded short  
CC interfering nucleic acid (siRNA) molecule that directs cleavage of a  
CC cholesteryl ester transfer protein (CETP) RNA via RNA interference  
CC (RNAi). The siRNA molecule, compounds, compositions, and methods are  
CC useful for treating or preventing hypercholesterolemia, hyperlipidemia,  
CC and/or cardiovascular disease, e.g. coronary heart disease,  
CC cerebrovascular disease, aortic stenosis, peripheral vascular disease  
CC and/or atherosclerosis. The present sequence represents a cholesteryl



CC ester transfer protein siRNA.

XX Sequence 19 BP; 3 A; 8 C; 0 G; 0 T; 8 U; 0 Other;

Query Match 57.9%; Score 11; DB 14; Length 19;

Best Local Similarity 63.6%; Pred. No. 8.8e+04; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

9 ATCTGCTTAC 19

6 AUCUCCUCCAC 16

RESULT 28

ABE43434 ID ABE43434 standard; cDNA, 19 BP.

AC ABE43434;

DT 09-FEB-2006 (first entry)

DE Human hairless homolog cDNA 19-mer fragment SEQ ID NO 2570.

KM ss; hirsutism; depilatory; hairless homolog.

OS Homo sapiens.

PN WO2005105157-A2.

PD 10-NOV-2005.

PF 22-APR-2005; 2005WO-US013770.

PR 23-APR-2004; 2004US-0565127P.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Cristiano AM;

PI WPI; 2005-769492/78.

PT Removing human hair comprises applying to a human in an area comprising hair follicles a double stranded nucleic acid molecule comprising a sequence of at least a portion of human hairless protein mRNA.

PS Disclosure; SEQ ID NO 2570; 216pp; English.

CC The invention relates to a method of human hair removal which comprises applying to a human in an area comprising hair follicles a double stranded nucleic acid molecule comprising a sequence of at least a portion of human hairless protein mRNA or its complement. In the method of human hair removal, inhibition of hair growth in the area persists at least one month. The method comprises synchronizing hair growth cycles for hair follicles in the area. The method alternatively comprises contacting hair follicles in the region with a composition comprising at least one double stranded nucleic acid molecule able to inhibit hairless mRNA translation. The mammal is a human, mouse, rat, or bovine. The method, nucleic acid molecules and compositions useful for removing undesirable hair e.g. hirsutism. The present sequence represents a human hairless homolog cDNA 19-mer fragment.

CC Sequence 19 BP; 0 A; 11 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 57.9%; Score 11; DB 14; Length 19;

Best Local Similarity 73.7%; Pred. No. 8.8e+04; Mismatches 5; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 CGCAGGATCTCTTCC 19

1 CGCTCGGCTCTCTTCC 19

RESULT 29

ABE43433/C ID ABE43433 standard; cDNA; 19 BP.

AC ABE43433;

DT 09-FEB-2006 (first entry)

DE Human hairless homolog cDNA 19-mer fragment SEQ ID NO 2569.

KM ss; hirsutism; depilatory; hairless homolog.

OS Homo sapiens.

PN WO2005105157-A2.

PD 10-NOV-2005.

PF 22-APR-2005; 2005WO-US013770.

PR 23-APR-2004; 2004US-0565127P.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Cristiano AM;

PI WPI; 2005-769492/78.

PT Removing human hair comprises applying to a human in an area comprising hair follicles a double stranded nucleic acid molecule comprising a sequence of at least a portion of human hairless protein mRNA.

PS Disclosure; SEQ ID NO 2569; 216pp; English.

CC The invention relates to a method of human hair removal which comprises applying to a human in an area comprising hair follicles a double stranded nucleic acid molecule comprising a sequence of at least a portion of human hairless protein mRNA or its complement. In the method of human hair removal, inhibition of hair growth in the area persists at least one month. The method comprises synchronizing hair growth cycles for hair follicles in the area. The method alternatively comprises contacting hair follicles in the region with a composition comprising at least one double stranded nucleic acid molecule able to inhibit hairless mRNA translation. The mammal is a human, mouse, rat, or bovine. The method, nucleic acid molecules and compositions useful for removing undesirable hair e.g. hirsutism. The present sequence represents a human hairless homolog cDNA 19-mer fragment.

CC Sequence 19 BP; 5 A; 3 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 57.9%; Score 11; DB 14; Length 19;

Best Local Similarity 73.7%; Pred. No. 8.8e+04; Mismatches 5; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 CGCAGGATCTCTTCC 19

19 CGCTCGGCTCTCTTCC 1

RESULT 30

AAA85544 ID AAA85544 standard; DNA; 19 BP.

AC AAA85544;

DT 04-DEC-2000 (first entry)

DE Cyclin A1 ribozyme binding site #166.

KM Ribozyme; hairpin; hammerhead; gene therapy; vasotrophic; restenosis; ss.

OS Mammalia.

PN WO200032765-A2.

```
XX 08-JUN-2000.
XX
XX 06-DEC-1999; 99WO-US028772.
XX
XX 04-DEC-1998; 98US-0110954P.
XX
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 94; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AA82415 to AA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells. The
XX ribozyme is resistant to endonuclease activity and hence is efficient in
XX restenosis treatment
XX
XX Sequence 19 BP; 4 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
SQ
Query Match 56.8%; Score 10.8; DB 3; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 CGGTATCTCCTTCA 18
DB 4 CAGTTTCTCCTTCA 17
RESULT 31
AA85545
ID AA85545 standard; DNA; 19 BP.
XX
XX AA85545;
XX
XX 04-DEC-2000 (first entry)
XX
XX Cyclin A1 ribozyme binding site #167.
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
XX Mammalia.
XX
XX WO200032765-A2.
XX
XX 08-JUN-2000.
XX
XX 06-DEC-1999; 99WO-US028772.
XX
XX 04-DEC-1998; 98US-0110954P.
XX
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 94; 109pp; English.
XX
```

```
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
CC
CC Sequence 19 BP; 3 A; 8 C; 1 G; 6 T; 0 U; 0 Other;
SQ
Query Match 56.8%; Score 10.8; DB 3; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 CGGTATCTCCTTCA 18
DB 2 CAGTTTCTCCTTCA 15
RESULT 32
AA85542
ID AA85542 standard; DNA; 19 BP.
XX
XX AA85542;
XX
XX 04-DEC-2000 (first entry)
XX
XX Cyclin A1 ribozyme binding site #164.
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
XX Mammalia.
XX
XX WO200032765-A2.
XX
XX 08-JUN-2000.
XX
XX 06-DEC-1999; 99WO-US028772.
XX
XX 04-DEC-1998; 98US-0110954P.
XX
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 94; 109pp; English.
XX
```

```
QY 5 CGGTATCTCCTTCA 18
DB 6 CAGTTTCTCCTTCA 19
Query Match 56.8%; Score 10.8; DB 3; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
RESULT 33
AA85543
ID AA85543 standard; DNA; 19 BP.
XX
AC AA85543;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cyclin A1 ribozyme binding site #165.
XX
KM Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tiltz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 94; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
XX
Query Match 56.8%; Score 10.8; DB 3; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 CGGTATCTCCTTCA 18
DB 5 CAGTTCTCCTTCA 18
XX
RESULT 34
AA85448/C
ID AA85448 standard; DNA; 19 BP.
XX
AC AA85448;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cyclin A1 ribozyme binding site #70.
XX
KM Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
```

```
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tiltz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 92; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match 56.8%; Score 10.8; DB 3; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 CGGTATCTCCTTCA 18
DB 17 CGGTGCTACTTCA 4
XX
RESULT 35
AAC59851
ID AAC59851 standard; DNA; 19 BP.
XX
AC AAC59851;
XX
DT 26-JAN-2001 (first entry)
XX
DE Oligonucleotide probe for human DNA clone vpl6 1.
XX
XX
KM Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
KM systemic lupus erythematosus; rheumatoid arthritis; anemia; stroke;
KM haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;
KM Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;
KM contraceptive; infection; growth inhibition; hyperproliferative disorder;
KM psoriasis; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200055375-A1.
XX
PD 21-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-US007285.
XX
PR 17-MAR-1999; 99US-0124808P.
PR 17-MAR-1999; 99US-0124916P.
PR 17-AUG-1999; 99US-0149639P.
PR 01-OCT-1999; 99US-0157247P.
PR 29-NOV-1999; 99US-0167824P.
PR 15-FEB-2000; 2000US-0182711P.
XX
PA (ALPH-) ALPHAGEN INC.
XX
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-638211/61.
```



KM sickle cell retinopathy; ss.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200130362-A2.  
XX  
XX 03-MAY-2001.  
XX  
XX 26-OCT-2000; 2000WO-US029500.  
XX  
XX 26-OCT-1999; 99US-0161532P.  
XX  
XX (IMMU-) IMMUSOL INC.  
XX  
XX Robbins JM, Tritz R;  
XX WPI; 2001-300427/31.  
XX  
XX Treating proliferative skin or eye diseases and scarring, using ribozymes  
PT that cleave RNA encoding cytokines involved in inflammation, matrix  
PT metalloproteinases, growth factors and cell-cycle dependent kinases.  
XX  
XX Example 1; Page 299; 408pp; English.  
XX  
XX The present invention describes a method for treating a proliferative  
CC skin or eye disease and scarring. The method involves administering a  
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in  
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
CC dependent kinase, growth factor or a reductase, or administering a  
CC nucleic acid molecule (II) comprising a promoter operably linked to a  
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,  
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,  
CC ophthalmological, vulnary, keratolytic and vitruide activities, and  
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used  
CC in gene therapy. (I) and (II) are useful for treating proliferative skin  
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,  
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can  
CC also be used for treating proliferative eye diseases such as diabetic  
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
CC prematurity and retinal detachment, and for treating and preventing  
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
CC scar. AAH57577 to AAH62099 represent sequences used in the  
CC exemplification of the present invention  
XX  
XX Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 56.8%; Score 10.8; DB 5; Length 19;  
Best Local Similarity 85.7%; Pred. No. 1.1e+05;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 CGGTATCTCCTTCA 18  
Db 5 CAGTTCTCCTTCA 18  
RESULT 38  
AAH60706  
ID AAH60706 standard; DNA; 19 BP.  
XX  
XX AAH60706;  
XX  
XX 10-SEP-2001 (first entry)  
XX  
XX Cyclin A1 ribozyme binding site SEQ ID NO:3130.  
XX  
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
KM recognition site; target; ribozyme binding site; eye disease; vulnary;  
KM proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
KM cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
KM matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;  
KM antipsoriatic; dermatological; antiseborrheic; antidiabetic; vitruide;  
KM antisickling; ophthalmological; keratolytic; gene therapy; viral wart;

KM atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
KM basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;  
KM sickle cell retinopathy; ss.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200130362-A2.  
XX  
XX 03-MAY-2001.  
XX  
XX 26-OCT-2000; 2000WO-US029500.  
XX  
XX 26-OCT-1999; 99US-0161532P.  
XX  
XX (IMMU-) IMMUSOL INC.  
XX  
XX Robbins JM, Tritz R;  
XX WPI; 2001-300427/31.  
XX  
XX Treating proliferative skin or eye diseases and scarring, using ribozymes  
PT that cleave RNA encoding cytokines involved in inflammation, matrix  
PT metalloproteinases, growth factors and cell-cycle dependent kinases.  
XX  
XX Example 1; Page 299; 408pp; English.  
XX  
XX The present invention describes a method for treating a proliferative  
CC skin or eye disease and scarring. The method involves administering a  
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in  
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
CC dependent kinase, growth factor or a reductase, or administering a  
CC nucleic acid molecule (II) comprising a promoter operably linked to a  
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,  
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,  
CC ophthalmological, vulnary, keratolytic and vitruide activities, and  
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used  
CC in gene therapy. (I) and (II) are useful for treating proliferative skin  
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,  
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can  
CC also be used for treating proliferative eye diseases such as diabetic  
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
CC prematurity and retinal detachment, and for treating and preventing  
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
CC scar. AAH57577 to AAH62099 represent sequences used in the  
CC exemplification of the present invention  
XX  
XX Sequence 19 BP; 4 A; 6 C; 2 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 56.8%; Score 10.8; DB 5; Length 19;  
Best Local Similarity 85.7%; Pred. No. 1.1e+05;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 CGGTATCTCCTTCA 18  
Db 4 CAGTTCTCCTTCA 17  
RESULT 39  
AAH60610/c  
ID AAH60610 standard; DNA; 19 BP.  
XX  
XX AAH60610;  
XX  
XX 10-SEP-2001 (first entry)  
XX  
XX Cyclin A1 ribozyme binding site SEQ ID NO:3034.  
XX  
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
KM recognition site; target; ribozyme binding site; eye disease; vulnary;  
KM proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
KM cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
KM matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;

KM antipsoaratic; dermatological; antiseborrheic; antidiabetic; virucide;  
 KM antisticking; ophthalmological; keratolytic; gene therapy; viral wart;  
 KM atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
 KM basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;  
 KM sickle cell retinopathy; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 WO200130362-A2.  
 PN  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 26-OCT-2000; 2000WO-US029500.  
 XX  
 PR 26-OCT-1999; 99US-0161532P.  
 XX  
 PA (TMU-) IMMUSOL INC.  
 PI Robbins JM, Tritz R;  
 XX  
 DR WPI; 2001-300427/31.  
 XX  
 PT Treating proliferative skin or eye diseases and scarring, using ribozymes  
 PT that cleave RNA encoding cytokines involved in inflammation, matrix  
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.  
 XX  
 SS Example 1; Page 292; 408bp; English.

CC The present invention describes a method for treating a proliferative  
CC skin or eye disease and scarring. The method involves administering a  
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in  
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
CC dependent kinase, growth factor or a reductase, or administering a  
CC nucleic acid molecule (II) comprising a promoter operably linked to a  
CC nucleic acid segment encoding (I). (I) can have anti-proliferative,  
CC dermatological, cytostatic, anti-seborrheic, anti-diabetic, anti-sclerotic,  
CC ophthalmological, vulvar, keratolytic and antiviral activities, and  
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used  
CC in gene therapy. (I) and (II) are useful for treating proliferative skin  
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,  
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can  
CC also be used for treating proliferative eye diseases such as diabetic  
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
CC prematurity and retinal detachment, and for treating and preventing  
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
CC scar. AA57577 to AA82099 represent sequences used in the  
CC exemplification of the present invention  
CC  
CC Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;  
CC XX

Query Match	56.8%	Score 10.8	DB 5	Length 19
Best Local Similarity	85.7%	Pred. No. 1.1e+05		
Matches 12; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	5	CGGATCTCCTTCA	18	
db	17	CGGTGCTACTTCA	4	

RESULT	40
AAH60707	
ID	AAH60707 standard; DNA; 19 BP.
XX	
AC	AAH60707;
XA	
DT	10-SEP-2001 (first entry)
DE	Cyclin A1 ribozyme binding site SEQ ID NO:3131

KM Human; ribozyme therapy; hairpin ribozyme;  
 KM recognition site; target; ribozyme binding site; eye disease; vulnery;  
 KM proliferative disease; skin disease; psoriasis; diabetic retinopathy;

KW	cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW	matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW	matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW	antiproliferative; dermatological; antiherpetic; antiviral; antiviral;
KW	antiproliferative; dermatological; antiherpetic; antiviral; antiviral;
KW	antiproliferative; dermatological; antiherpetic; antiviral; antiviral;
KW	basal cell carcinoma; sebaceous wart; vitreoretinopathy; scar;
KW	basal cell carcinoma; sebaceous wart; vitreoretinopathy; scar;
XX	stickle cell retinopathy; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	WO200130362-A2.
XX	
PD	03-MAY-2001.
XX	
PP	26-OCT-2000; 2000WO-US029500.
XX	
PR	26-OCT-1999; 99US-0161532P.
XX	
PA	(IMMU-) IMMUSOL INC.
XX	
P1	Robbins JM, Tritz R;
XX	
DR	WPI; 2001-300427/31.
XX	
PT	Treating proliferative skin or eye diseases and scarring, using ribozymes
PT	that cleave RNA encoding cytokines involved in inflammation, matrix
PT	metalloproteinases, growth factors and cell-cycle dependent kinases.

PS Example 1, Page 239, 408bp; English.

XX The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (I) which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (II). (I) can have antiproliferatic, dermatological, cytostatic, antiseborrheic, antidiabetic, antiscarring, ophthalmological, vulnery, keratolytic and vitruide activities, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, squamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, asticle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn scar. AAH57577 to AAH62099 represent sequences used in the exemplification of the present invention

SQ Sequence 19 BP, 3 A, 7 C, 2 G, 7 T, 0 U, 0 Other;  
 Query Match 56.8%, Score 10.8, DB 5, Length 19;  
 Best Local Similarity 85.7%, Pred. No. 1,1e+05;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	5	CGGATCTCCTTCA	18
Db	2	CAGTTCTCCTTCA	15

Search completed: August 10, 2006, 08:56:12  
Job time : 309.667 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 08:37:42 ; Search time 981.667 Seconds  
(without alignments)  
1237.692 Million cell updates/sec

Title: US-10-636-065-29  
Perfect score: 19  
Sequence: 1 cgcacgcatccttcac 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 141404

Minimum DB seq length: 19  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl: \*  
1: gb\_pat: \*  
2: gb\_pat: \*  
3: gb\_ph: \*  
4: gb\_ph: \*  
5: gb\_ph: \*  
6: gb\_ph: \*  
7: gb\_ph: \*  
8: gb\_ph: \*  
9: gb\_ph: \*  
10: gb\_ph: \*  
11: gb\_ph: \*  
12: gb\_ph: \*  
13: gb\_ph: \*  
14: gb\_ph: \*  
15: gb\_ph: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	AR451384	Sequence
2	19	100.0	19	AX411929	Sequence
3	15	78.9	19	CS027764	Sequence
4	15	78.9	19	CS028231	Sequence
5	14	73.7	19	AX923594	Sequence
6	14	73.7	19	AX923672	Sequence
7	11.8	62.1	19	BD080793	Sequence
8	11.8	62.1	19	BD080808	Sequence
9	11.8	62.1	19	CS251594	Sequence
10	11	57.9	19	CS094047	Sequence
11	11	57.9	19	CS094147	Sequence
12	11	57.9	19	AR295824	Sequence
13	10.8	56.8	19	AR573706	Sequence
14	10.8	56.8	19	AR573801	Sequence
15	10.8	56.8	19	AR573802	Sequence
16	10.8	56.8	19	AR573803	Sequence
17	10.8	56.8	19	AX131816	Sequence
18	10.8	56.8	19	AX131816	Sequence

19	10.8	56.8	19	2	AX131910	Sequence
20	10.8	56.8	19	2	AX131911	Sequence
21	10.8	56.8	19	2	AX131912	Sequence
22	10.8	56.8	19	2	AX131913	Sequence
23	10.6	55.8	19	2	CQ824220	Sequence
24	10.6	55.8	19	2	CS171759	Sequence
25	10.6	55.8	19	2	ES4494	Heat-resist
26	10.6	55.8	19	2	AR297589	Sequence
27	10.6	55.8	19	2	AX117403	Sequence
28	10.6	55.8	19	2	AX751584	Sequence
29	10.6	55.8	19	2	AX837880	Sequence
30	10.4	54.7	19	2	CS246174	Sequence
31	10.4	54.7	19	2	AR293205	Sequence
32	10.4	54.7	19	2	AR294484	Sequence
33	10.4	54.7	19	2	AR533333	Sequence
34	10.4	54.7	19	2	AR573804	Sequence
35	10.4	54.7	19	2	AX131914	Sequence
36	10.2	53.7	19	2	BD244859	Sequence
37	10.2	53.7	19	2	CS128821	Sequence
38	10.2	53.7	19	2	CS132095	Sequence
39	10.2	53.7	19	2	CS197806	Sequence
40	10.2	53.7	19	2	CS197807	Sequence
41	10.2	53.7	19	2	CS197808	Sequence
42	10.2	53.7	19	2	CS197809	Sequence
43	10.2	53.7	19	2	CS197810	Sequence
44	10.2	53.7	19	2	CS199558	Sequence
45	10.2	53.7	19	2	CS199559	Sequence
46	10.2	53.7	19	2	CS199560	Sequence
47	10.2	53.7	19	2	CS199561	Sequence
48	10.2	53.7	19	2	CS199562	Sequence
49	10.2	53.7	19	2	AX378611	Sequence
50	10.2	52.6	19	2	AR070723	Sequence
51	10	52.6	19	2	BD000812	Methods a
52	10	52.6	19	2	BD105849	Novel ant
53	10	52.6	19	2	CS189923	Sequence
54	10	52.6	19	2	CS193344	Sequence
55	10	52.6	19	2	CS231374	Sequence
56	10	52.6	19	2	CS248893	Sequence
57	10	52.6	19	2	DD201537	RNA Inter
58	10	52.6	19	2	DD201964	RNA Inter
59	10	52.6	19	2	117109	Sequence 2
60	10	52.6	19	2	162398	Sequence 2
61	10	52.6	19	2	AR481863	Sequence
62	10	52.6	19	2	AX769415	Sequence
63	9.8	51.6	19	2	A98471	Sequence 10
64	9.8	51.6	19	2	AR067391	Sequence
65	9.8	51.6	19	2	AR080800	Sequence
66	9.8	51.6	19	2	AR160473	Sequence
67	9.8	51.6	19	2	AR164071	Sequence
68	9.8	51.6	19	2	BD015691	Novel pro
69	9.8	51.6	19	2	BD015692	Novel pro
70	9.8	51.6	19	2	BD094844	Novel pro
71	9.8	51.6	19	2	BD094845	Novel pro
72	9.8	51.6	19	2	BD124109	Novel GAB
73	9.8	51.6	19	2	BD266184	Universal
74	9.8	51.6	19	2	CQ988169	Sequence
75	9.8	51.6	19	2	CQ988252	Sequence
76	9.8	51.6	19	2	CS094102	Sequence
77	9.8	51.6	19	2	CS094202	Sequence
78	9.8	51.6	19	2	DD202532	Sequence
79	9.8	51.6	19	2	DD202856	RNA Inter
80	9.8	51.6	19	2	AR294258	Sequence
81	9.8	51.6	19	2	AR631270	Sequence
82	9.8	51.6	19	2	AR631271	Sequence
83	9.8	51.6	19	2	AX054675	Sequence
84	9.8	51.6	19	8	AB213933	Synthetic
85	9.6	50.5	19	2	AX965573	Sequence
86	9.6	50.5	19	2	BD195704	In vivo u
87	9.6	50.5	19	2	BD243891	STE20-rel
88	9.6	50.5	19	2	CQ776074	Sequence
89	9.6	50.5	19	2	CQ779515	Sequence
90	9.6	50.5	19	2	CQ965695	Sequence
91	9.6	50.5	19	2	CQ965800	Sequence

C 92	9.6	50.5	19	2	CS200808	Sequence	C 165	9.2	48.4	19	2	CS246098	Sequence
C 93	9.6	50.5	19	2	CS251845	Sequence	C 166	9.2	48.4	19	2	CS256216	Sequence
C 94	9.6	50.5	19	2	DD162073	Transgent	C 167	9.2	48.4	19	2	DD193039	Sequence
C 95	9.6	50.5	19	2	E33605	Novel proka	C 168	9.2	48.4	19	2	DD199036	RNA Inter
C 96	9.6	50.5	19	2	AR282797	Sequence	C 169	9.2	48.4	19	2	DD199361	RNA Inter
C 97	9.6	50.5	19	2	AR295377	Sequence	C 170	9.2	48.4	19	2	DD201552	RNA Inter
C 98	9.6	50.5	19	2	AR435644	Sequence	C 171	9.2	48.4	19	2	DD201552	RNA Inter
C 99	9.6	50.5	19	2	AR453245	Sequence	C 172	9.2	48.4	19	2	DD201979	RNA Inter
C 100	9.6	50.5	19	2	AR569954	Sequence	C 173	9.2	48.4	19	2	AR203016	Sequence
C 101	9.6	50.5	19	2	AX378467	Sequence	C 174	9.2	48.4	19	2	AR293419	Sequence
C 102	9.6	50.5	19	2	AX676163	Sequence	C 175	9.2	48.4	19	2	AR353644	Sequence
C 103	9.4	49.5	19	2	BD061246	A method	C 176	9.2	48.4	19	2	AR363491	Sequence
C 104	9.4	49.5	19	2	CQ902499	Sequence	C 177	9.2	48.4	19	2	AR365227	Sequence
C 105	9.4	49.5	19	2	CQ902510	Sequence	C 178	9.2	48.4	19	2	AR571809	Sequence
C 106	9.4	49.5	19	2	CQ902523	Sequence	C 179	9.2	48.4	19	2	AR571810	Sequence
C 107	9.4	49.5	19	2	CQ902524	Sequence	C 180	9.2	48.4	19	2	AR572102	Sequence
C 108	9.4	49.5	19	2	CQ902531	Sequence	C 181	9.2	48.4	19	2	AR572102	Sequence
C 109	9.4	49.5	19	2	CQ902542	Sequence	C 182	9.2	48.4	19	2	AX129919	Sequence
C 110	9.4	49.5	19	2	CQ902553	Sequence	C 183	9.2	48.4	19	2	AX129920	Sequence
C 111	9.4	49.5	19	2	CQ902564	Sequence	C 184	9.2	48.4	19	2	AX130211	Sequence
C 112	9.4	49.5	19	2	CQ902575	Sequence	C 185	9.2	48.4	19	2	AX130212	Sequence
C 113	9.4	49.5	19	2	CQ902586	Sequence	C 186	9.2	48.4	19	2	AX298518	Sequence
C 114	9.4	49.5	19	2	CQ902597	Sequence	C 187	9.2	48.4	19	2	AX302081	Sequence
C 115	9.4	49.5	19	2	CQ988227	Sequence	C 188	9.2	47.4	19	2	A49480	Sequence
C 116	9.4	49.5	19	2	CQ988310	Sequence	C 189	9.2	47.4	19	2	A50818	Sequence
C 117	9.4	49.5	19	2	CS052710	Sequence	C 190	9.2	47.4	19	2	AR079665	Sequence
C 118	9.4	49.5	19	2	CS092098	Sequence	C 191	9.2	47.4	19	2	AR125649	Sequence
C 119	9.4	49.5	19	2	CS092272	Sequence	C 192	9.2	47.4	19	2	AR923662	Sequence
C 120	9.4	49.5	19	2	CS096531	Sequence	C 193	9.2	47.4	19	2	AX923594	Sequence
C 121	9.4	49.5	19	2	CS096618	Sequence	C 194	9.2	47.4	19	2	AX923594	Sequence
C 122	9.4	49.5	19	2	CS223422	Sequence	C 195	9.2	47.4	19	2	AX923854	Sequence
C 123	9.4	49.5	19	2	CS231378	Sequence	C 196	9.2	47.4	19	2	BD087967	A method
C 124	9.4	49.5	19	2	CS231396	Sequence	C 197	9.2	47.4	19	2	BD174508	Method fo
C 125	9.4	49.5	19	2	DD202505	RNA Inter	C 198	9.2	47.4	19	2	BD186492	Method of
C 126	9.4	49.5	19	2	DD202829	RNA Inter	C 199	9.2	47.4	19	2	BD196939	Prostatic
C 127	9.4	49.5	19	2	AR573805	Sequence	C 200	9.2	47.4	19	2	CQ759039	Sequence
C 128	9.4	49.5	19	2	AR765023	Sequence	C 201	9.2	47.4	19	2	CQ801708	Sequence
C 129	9.4	49.5	19	2	AX131915	Sequence	C 202	9.2	47.4	19	2	CQ801954	Sequence
C 130	9.2	48.4	19	2	BD226459	Method an	C 203	9.2	47.4	19	2	CQ861212	Sequence
C 131	9.2	48.4	19	2	BD226470	Method an	C 204	9.2	47.4	19	2	CQ962863	Sequence
C 132	9.2	48.4	19	2	CQ786254	Sequence	C 205	9.2	47.4	19	2	CQ966178	Sequence
C 133	9.2	48.4	19	2	CQ799886	Sequence	C 206	9.2	47.4	19	2	CQ966206	Sequence
C 134	9.2	48.4	19	2	CQ961307	Sequence	C 207	9.2	47.4	19	2	CQ966387	Sequence
C 135	9.2	48.4	19	2	CQ962958	Sequence	C 208	9.2	47.4	19	2	CQ966415	Sequence
C 136	9.2	48.4	19	2	CQ987750	Sequence	C 209	9.2	47.4	19	2	CQ988332	Sequence
C 137	9.2	48.4	19	2	CQ988075	Sequence	C 210	9.2	47.4	19	2	CQ988456	Sequence
C 138	9.2	48.4	19	2	CQ988158	Sequence	C 211	9.2	47.4	19	2	CS089765	Sequence
C 139	9.2	48.4	19	2	CQ988241	Sequence	C 212	9.2	47.4	19	2	CS089769	Sequence
C 140	9.2	48.4	19	2	CS013271	Sequence	C 213	9.2	47.4	19	2	CS089772	Sequence
C 141	9.2	48.4	19	2	CS014598	Sequence	C 214	9.2	47.4	19	2	CS089927	Sequence
C 142	9.2	48.4	19	2	CS015012	Sequence	C 215	9.2	47.4	19	2	CS090461	Sequence
C 143	9.2	48.4	19	2	CS050332	Sequence	C 216	9.2	47.4	19	2	CS090465	Sequence
C 144	9.2	48.4	19	2	CS093150	Sequence	C 217	9.2	47.4	19	2	CS090468	Sequence
C 145	9.2	48.4	19	2	CS093457	Sequence	C 218	9.2	47.4	19	2	CS090623	Sequence
C 146	9.2	48.4	19	2	CS102052	Sequence	C 219	9.2	47.4	19	2	CS101722	Sequence
C 147	9.2	48.4	19	2	CS102189	Sequence	C 220	9.2	47.4	19	2	CS101845	Sequence
C 148	9.2	48.4	19	2	CS197448	Sequence	C 221	9.2	47.4	19	2	CS129011	Sequence
C 149	9.2	48.4	19	2	CS197449	Sequence	C 222	9.2	47.4	19	2	CS132280	Sequence
C 150	9.2	48.4	19	2	CS197450	Sequence	C 223	9.2	47.4	19	2	CS132418	Sequence
C 151	9.2	48.4	19	2	CS197451	Sequence	C 224	9.2	47.4	19	2	CS197912	Sequence
C 152	9.2	48.4	19	2	CS197452	Sequence	C 225	9.2	47.4	19	2	CS197913	Sequence
C 153	9.2	48.4	19	2	CS197453	Sequence	C 226	9.2	47.4	19	2	CS197914	Sequence
C 154	9.2	48.4	19	2	CS197805	Sequence	C 227	9.2	47.4	19	2	CS199664	Sequence
C 155	9.2	48.4	19	2	CS197811	Sequence	C 228	9.2	47.4	19	2	CS199665	Sequence
C 156	9.2	48.4	19	2	CS199200	Sequence	C 229	9.2	47.4	19	2	CS199666	Sequence
C 157	9.2	48.4	19	2	CS199201	Sequence	C 230	9.2	47.4	19	2	DD174897	THERAPUT
C 158	9.2	48.4	19	2	CS199202	Sequence	C 231	9.2	47.4	19	2	DD174918	THERAPUT
C 159	9.2	48.4	19	2	CS199203	Sequence	C 232	9.2	47.4	19	2	DD174942	THERAPUT
C 160	9.2	48.4	19	2	CS199204	Sequence	C 233	9.2	47.4	19	2	DD174957	THERAPUT
C 161	9.2	48.4	19	2	CS199205	Sequence	C 234	9.2	47.4	19	2	DD174981	THERAPUT
C 162	9.2	48.4	19	2	CS199557	Sequence	C 235	9.2	47.4	19	2	DD175047	THERAPUT
C 163	9.2	48.4	19	2	CS199563	Sequence	C 236	9.2	47.4	19	2	DD175128	THERAPUT
C 164	9.2	48.4	19	2	CS203688	Sequence	C 237	9.2	47.4	19	2	DD175185	THERAPUT



C 238	9	47.4	19	2	DD197645	311	8.8	46.3	19	2	CQ961569	CQ961569 Sequence
C 239	9	47.4	19	2	DD197649	312	8.8	46.3	19	2	CQ961585	CQ961585 Sequence
C 240	9	47.4	19	2	DD197652	313	8.8	46.3	19	2	CQ961634	CQ961634 Sequence
241	9	47.4	19	2	DD197807	314	8.8	46.3	19	2	CQ961648	CQ961648 Sequence
242	9	47.4	19	2	DD198341	315	8.8	46.3	19	2	CQ962331	CQ962331 Sequence
243	9	47.4	19	2	DD198345	316	8.8	46.3	19	2	CQ962336	CQ962336 Sequence
C 244	9	47.4	19	2	DD198348	317	8.8	46.3	19	2	CQ965463	CQ965463 Sequence
C 245	9	47.4	19	2	DD198503	318	8.8	46.3	19	2	CQ965626	CQ965626 Sequence
C 246	9	47.4	19	2	DD202481	319	8.8	46.3	19	2	CQ966716	CQ966716 Sequence
C 247	9	47.4	19	2	DD202805	320	8.8	46.3	19	2	CQ966897	CQ966897 Sequence
C 248	9	47.4	19	2	DD204244	321	8.8	46.3	19	2	CQ96897	CQ96897 Sequence
C 249	9	47.4	19	2	DD204248	322	8.8	46.3	19	2	CS014347	CS014347 Sequence
C 250	9	47.4	19	2	DD204251	323	8.8	46.3	19	2	CS014627	CS014627 Sequence
C 251	9	47.4	19	2	DD204406	324	8.8	46.3	19	2	CS015041	CS015041 Sequence
252	9	47.4	19	2	DD204940	325	8.8	46.3	19	2	CS027812	CS027812 Sequence
253	9	47.4	19	2	DD204944	326	8.8	46.3	19	2	CS028172	CS028172 Sequence
254	9	47.4	19	2	DD204947	327	8.8	46.3	19	2	CS028279	CS028279 Sequence
C 255	9	47.4	19	2	DD204947	328	8.8	46.3	19	2	CS028639	CS028639 Sequence
C 256	9	47.4	19	2	DD205102	329	8.8	46.3	19	2	CS067596	CS067596 Sequence
257	9	47.4	19	2	BD5122	330	8.8	46.3	19	2	CS083317	CS083317 Sequence
258	9	47.4	19	2	BD5126	331	8.8	46.3	19	2	CS092930	CS092930 Sequence
259	9	47.4	19	2	BD5126	332	8.8	46.3	19	2	CS093237	CS093237 Sequence
C 260	9	47.4	19	2	BD5126	333	8.8	46.3	19	2	CS094055	CS094055 Sequence
261	9	47.4	19	2	BD5126	334	8.8	46.3	19	2	CS094155	CS094155 Sequence
262	9	47.4	19	2	BD5126	335	8.8	46.3	19	2	CS096186	CS096186 Sequence
C 263	9	47.4	19	2	BD5126	336	8.8	46.3	19	2	CS096285	CS096285 Sequence
C 264	9	47.4	19	2	BD5126	337	8.8	46.3	19	2	CS101995	CS101995 Sequence
C 265	9	47.4	19	2	BD5126	338	8.8	46.3	19	2	CS102132	CS102132 Sequence
C 266	9	47.4	19	2	BD5126	339	8.8	46.3	19	2	CS105004	CS105004 Sequence
267	9	47.4	19	2	BD5126	340	8.8	46.3	19	2	CS122274	CS122274 Sequence
C 268	9	47.4	19	2	BD5126	341	8.8	46.3	19	2	CS128959	CS128959 Sequence
C 269	9	47.4	19	2	BD5126	342	8.8	46.3	19	2	CS132232	CS132232 Sequence
C 270	9	47.4	19	2	BD5126	343	8.8	46.3	19	2	CS141729	CS141729 Sequence
C 271	9	47.4	19	2	BD5126	344	8.8	46.3	19	2	CS145659	CS145659 Sequence
C 272	9	47.4	19	2	BD5126	345	8.8	46.3	19	2	CS162487	CS162487 Sequence
C 273	9	47.4	19	2	BD5126	346	8.8	46.3	19	2	CS165985	CS165985 Sequence
C 274	9	47.4	19	2	BD5126	347	8.8	46.3	19	2	CS187399	CS187399 Sequence
275	9	47.4	19	2	BD5126	348	8.8	46.3	19	2	CS190942	CS190942 Sequence
C 276	9	47.4	19	2	BD5126	349	8.8	46.3	19	2	CS190943	CS190943 Sequence
C 277	9	47.4	19	2	BD5126	350	8.8	46.3	19	2	CS193706	CS193706 Sequence
278	9	47.4	19	2	BD5126	351	8.8	46.3	19	2	CS193707	CS193707 Sequence
C 279	9	47.4	19	2	BD5126	352	8.8	46.3	19	2	CS204195	CS204195 Sequence
C 280	9	47.4	19	2	BD5126	353	8.8	46.3	19	2	CS250304	CS250304 Sequence
281	9	47.4	19	2	BD5126	354	8.8	46.3	19	2	CS251829	CS251829 Sequence
C 282	9	47.4	19	2	BD5126	355	8.8	46.3	19	2	CS254946	CS254946 Sequence
C 283	9	47.4	19	2	BD5126	356	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 284	9	47.4	19	2	BD5126	357	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 285	9	47.4	19	2	BD5126	358	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 286	9	47.4	19	2	BD5126	359	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 287	9	47.4	19	2	BD5126	360	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 288	9	47.4	19	2	BD5126	361	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 289	9	47.4	19	2	BD5126	362	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 290	9	47.4	19	2	BD5126	363	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 291	9	47.4	19	2	BD5126	364	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 292	9	47.4	19	2	BD5126	365	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 293	9	47.4	19	2	BD5126	366	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 294	9	47.4	19	2	BD5126	367	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 295	9	47.4	19	2	BD5126	368	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 296	9	47.4	19	2	BD5126	369	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 297	9	47.4	19	2	BD5126	370	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 298	9	47.4	19	2	BD5126	371	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 299	9	47.4	19	2	BD5126	372	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 300	9	47.4	19	2	BD5126	373	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 301	9	47.4	19	2	BD5126	374	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 302	9	47.4	19	2	BD5126	375	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 303	9	47.4	19	2	BD5126	376	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 304	9	47.4	19	2	BD5126	377	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 305	9	47.4	19	2	BD5126	378	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 306	9	47.4	19	2	BD5126	379	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 307	9	47.4	19	2	BD5126	380	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 308	9	47.4	19	2	BD5126	381	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 309	9	47.4	19	2	BD5126	382	8.8	46.3	19	2	CS256296	CS256296 Sequence
C 310	9	47.4	19	2	BD5126	383	8.8	46.3	19	2	CS256296	CS256296 Sequence

C 384	8.8	46.3	19	2	AX130374	AX130374 Sequence	C 457	8.6	45.3	19	2	DD204220	DD204220 RNA Inter
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C 386	8.8	46.3	19	2	AX473978	AX473978 Sequence	C 459	8.6	45.3	19	2	DD204410	DD204410 RNA Inter
C 387	8.8	46.3	19	2	AX571906	AX571906 Sequence	C 460	8.6	45.3	19	2	DD204411	DD204411 RNA Inter
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C 393	8.6	45.3	19	2	AR054185	AR054185 Sequence	C 466	8.6	45.3	19	2	133618	133618 Sequence 12
C 394	8.6	45.3	19	2	AR102040	AR102040 Sequence	C 467	8.6	45.3	19	2	AR203420	AR203420 Sequence
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C 396	8.6	45.3	19	2	AR145159	AR145159 Sequence	C 469	8.6	45.3	19	2	AR235571	AR235571 Sequence
C 397	8.6	45.3	19	2	BD016971	BD016971 Method to	C 470	8.6	45.3	19	2	AR236680	AR236680 Sequence
C 398	8.6	45.3	19	2	BD078589	Regulated	C 471	8.6	45.3	19	2	AR242410	AR242410 Sequence
C 399	8.6	45.3	19	2	BD136146	BD136146 Mutated n	C 472	8.6	45.3	19	2	AR293267	AR293267 Sequence
C 400	8.6	45.3	19	2	CQ759465	CQ759465 Sequence	C 473	8.6	45.3	19	2	175965	175965 Sequence 12
C 401	8.6	45.3	19	2	CQ797638	CQ797638 Sequence	C 474	8.6	45.3	19	2	AR442339	AR442339 Sequence
C 402	8.6	45.3	19	2	CQ801941	CQ801941 Sequence	C 475	8.6	45.3	19	2	AR565836	AR565836 Sequence
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C 424	8.6	45.3	19	2	CS102084	CS102084 Sequence	C 497	8.4	44.2	19	2	AR097387	AR097387 Sequence
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C 428	8.6	45.3	19	2	CS178814	CS178814 Sequence	C 501	8.4	44.2	19	2	AR137367	AR137367 Sequence
C 429	8.6	45.3	19	2	CS178831	CS178831 Sequence	C 502	8.4	44.2	19	2	AR156036	AR156036 Sequence
C 430	8.6	45.3	19	2	CS184401	CS184401 Sequence	C 503	8.4	44.2	19	2	AR158133	AR158133 Sequence
C 431	8.6	45.3	19	2	CS197825	CS197825 Sequence	C 504	8.4	44.2	19	2	AX323611	AX323611 Sequence
C 432	8.6	45.3	19	2	CS197826	CS197826 Sequence	C 505	8.4	44.2	19	2	AX337551	AX337551 Sequence
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C 434	8.6	45.3	19	2	CS197828	CS197828 Sequence	C 507	8.4	44.2	19	2	BD000756	BD000756 Chimera 9
C 435	8.6	45.3	19	2	CS197829	CS197829 Sequence	C 508	8.4	44.2	19	2	BD001009	BD001009 Method an
C 436	8.6	45.3	19	2	CS199577	CS199577 Sequence	C 509	8.4	44.2	19	2	BD001438	BD001438 Method an
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C 438	8.6	45.3	19	2	CS199579	CS199579 Sequence	C 511	8.4	44.2	19	2	BD075239	BD075239 Methods f
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C 444	8.6	45.3	19	2	DD177099	DD177099 Verificat	C 517	8.4	44.2	19	2	BD196780	BD196780 Prostatit
C 445	8.6	45.3	19	2	DD180922	DD180922 GENES emc	C 518	8.4	44.2	19	2	BD221967	BD221967 Nucleic a
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C 544	8.4	44.2	19	2	CS089906	Sequence	CS089906	617	8.4	44.2	19	2	E07049	Partial seq
C 545	8.4	44.2	19	2	CS089919	Sequence	CS089919	618	8.4	44.2	19	2	E07073	Probe for H
C 546	8.4	44.2	19	2	CS090602	Sequence	CS090602	619	8.4	44.2	19	2	E32522	Scavenger r
C 547	8.4	44.2	19	2	CS090615	Sequence	CS090615	620	8.4	44.2	19	2	E32540	Scavenger r
C 548	8.4	44.2	19	2	CS092028	Sequence	CS092028	621	8.4	44.2	19	2	E36743	Primer for
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C 551	8.4	44.2	19	2	CS092223	Sequence	CS092223	624	8.4	44.2	19	2	AR202163	Sequence
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C 598	8.4	44.2	19	2	DD198495	RNA Inter	DD198495	671	8.4	44.2	19	2	AR691005	Sequence
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C 600	8.4	44.2	19	2	DD199140	RNA Inter	DD199140	673	8.4	44.2	19	2	AR721559	Sequence
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C 602	8.4	44.2	19	2	DD200633	RNA Inter	DD200633	675	8.4	44.2	19	2	AX037487	Sequence
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## ALIGNMENTS

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VERSION      AR451384.1      GI:42682409
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
TITLE      Antisense IAP nucleic acids and uses thereof
JOURNAL      Patent: US 6673917-A 29 06-JAN-2004;
              University of Ottawa; Ottawa;
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DEFINITION      Sequence 29 from Patent WO20226968.

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VERSION      AX411929.1      GI:21444394
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
AUTHORS      Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
TITLE      Antisense iap nucleic acids and uses thereof
JOURNAL      Patent: WO 0226968-A 29 04-APR-2002;
              University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
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ACCESSION      CS027764
VERSION      CS027764.1      GI:60497314
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
AUTHORS      McSwiggen,J. and Chovvira,B.M.
TITLE      RNA interference mediated inhibition of XIAP gene expression using
JOURNAL      short interfering Nucleic Acid (siNA)
              Patent: WO 2005014811-A 17 17-FEB-2005;
              Sirna Therapeutics, Inc. (US)

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FEATURES
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QY      5      CGGTATCTCCTTCAC 19
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RESULT 4
LOCUS      CS028231      19 bp      RNA      linear      PAT 03-MAR-2005
DEFINITION      Sequence 484 from Patent WO2005014811.
ACCESSION      CS028231
VERSION      CS028231.1      GI:604977781
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
REFERENCE      1

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other sequences; artificial sequences.

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AUTHORS Mcswiggen, J. and Chowrira, B.M.  
TITLE RNA interference mediated inhibition of XIAP gene expression using  
short interfering Nucleic Acid (siNA)  
JOURNAL Patent: WO 2005014811-A 484 17-FEB-2005;  
Sirta Therapeutics, Inc. (US)  
FEATURES Location/Qualifiers  
SOURCE 1..19  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence: siNA antisense region"

ORIGIN  
Query Match 78.9%; Score 15; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGGTATCTCTCTTCAC 19  
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| | | | | | | | | | | | | | | | | | | | |  
Db 1 CGGTATCTCTCTTCAC 15

RESULT 5  
AX923594 19 bp DNA linear PAT 18-DEC-2003  
LOCUS AX923594  
DEFINITION Sequence 29 from Patent WO03080638.  
ACCESSION AX923594  
VERSION AX923594.1 GI:40216610  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
SOURCE  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Lacasse, E., Mcmanus, D. and Durkin, J.P.  
TITLE Antisense iap nucleobase oligomers and uses thereof  
JOURNAL Patent: WO 03080638-A 29 02-OCT-2003;  
Aegera Therapeutics Inc. (CA)  
FEATURES  
SOURCE  
Location/Qualifiers  
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/organism="synthetic construct"  
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of a ribonucleotide, deoxyribonucleotide, or nucleotide  
analog  
n = T or U"

ORIGIN  
Query Match 73.7%; Score 14; DB 2; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.8e+04;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTCAC 19  
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Db 1 CGCAGCGNANCCNNCAC 19

RESULT 6  
AX923672 19 bp DNA linear PAT 18-DEC-2003  
LOCUS AX923672  
DEFINITION Sequence 107 from Patent WO03080638.  
ACCESSION AX923672  
VERSION AX923672.1 GI:40216688  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
SOURCE  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Lacasse, E., Mcmanus, D. and Durkin, J.P.  
TITLE Antisense iap nucleobase oligomers and uses thereof  
JOURNAL Patent: WO 03080638-A 107 02-OCT-2003;  
Aegera Therapeutics Inc. (CA)

FEATURES Location/Qualifiers  
SOURCE 1..19  
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of a ribonucleotide, deoxyribonucleotide, or nucleotide  
analog  
n = T or U"

ORIGIN  
Query Match 73.7%; Score 14; DB 2; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.8e+04;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCTTCAC 19  
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Db 1 CGCAGCGNANCCNNCAC 19

RESULT 7  
BD080793 19 bp DNA linear PAT 27-AUG-2002  
LOCUS BD080793  
DEFINITION Human estrogen receptor beta.  
ACCESSION BD080793  
VERSION BD080793.1 GI:22626396  
KEYWORDS JP 2001510690-A/16.  
SOURCE  
ORGANISM  
FEATURES  
SOURCE  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1 (bases 1 to 19)

REFERENCE  
AUTHORS Denton, R. and Barton, R.  
TITLE Human estrogen receptor beta  
JOURNAL Patent: JP 2001510690-A 16 07-AUG-2001;  
YALE UNIVERSITY  
OS Artificial Sequence  
PN JP 2001510690-A/16  
PD 07-AUG-2001  
PF 28-JUL-1998 JP 2000504163  
PR 28-JUL-1997 US 60/053869, 30-JUL-1997 US 60/054210 PI  
REX DENTON, ROLAND BARON  
PC  
C12N15/09, A61K31/711, A61K38/00, A61K39/395, A61K39/395, A61K45/00, PC  
A61K48/00,  
PC A61P35/00, A61P43/00, C07K14/705, C07K16/20, C12N1/15, C12N1/19, PC  
C12N1/21,  
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, G01N33/15, G01N33/50, PC  
G01N33/53,  
PC G01N33/566, C12N15/00, A61K37/02, C12N5/00  
CC Description of Artificial Sequence: Cloning/PCR primer, primer

CC Key 7 Location/Qualifiers  
FH Key 1..19 /organism="Artificial Sequence".  
FT source  
FT Location/Qualifiers  
1..19  
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/db\_xref="taxon:32630"

ORIGIN  
Query Match 62.1%; Score 11.8; DB 2; Length 19;  
Best Local Similarity 86.7%; Pred. No. 7.8e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGTATCTCTCTTCAC 19  
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Db 2 CAGTAGCTCTCTTCAC 16

RESULT 8  
BD080808

LOCUS BD080808 19 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Novel estrogen receptor beta and iso-type proteins thereof.  
 ACCESSION BD080808  
 VERSION BD080808.1 GI:22626411  
 KEYWORDS JP 2001510691-A/11.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Baron,R., Denton,R., Chambon,P., Dupont,S. and Garnier,J.M.  
 TITLE Novel estrogen receptor beta and iso-type proteins thereof  
 JOURNAL Patent: JP 2001510691-A 11 07-AUG-2001;  
 YALE UNIVERSITY  
 COMMENT OS Artificial Sequence  
 PN JP 2001510691-A/11  
 PD 07-AUG-2001  
 PE 28-JUL-1998 JP 2000504164  
 PR 28-JUL-1997 US 60/053869,30-JUL-1997 US 60/054210 PR  
 28-JUL-1997 US 60/053869,30-JUL-1997 US 60/054210 PI ROLAND  
 BARON,REX DENTON,PIERRE CHAMBON,SONIA  
 DUPONT,JEAN MARIE  
 PI GARNIER  
 PC C12N15/09,A61K31/7088,A61K38/00,A61K39/395,A61K39/395 PC  
 ,A61K39/395,A61K31/00,  
 PC A61K48/00,A61P13/08,A61P19/10,A61P35/00,C07K14/47,C07K14/705,  
 PC C07K16/28,  
 PC C07K16/46,C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/566, PC  
 C12N15/00,  
 PC A61K37/02,A61K43/00,C12N5/00  
 CC Description of Artificial Sequence: Cloning/PCR primer, primer  
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 FT source 1.19 /organism='Artificial Sequence'.  
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 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 CGGTATCTCCTTCAC 19  
 DB 2 CAGTACCTCCTTCAC 16  
 RESULT 9  
 LOCUS CS251594/c 19 bp DNA linear PAT 18-JAN-2006  
 DEFINITION Sequence 161 from Patent WO2005124342.  
 ACCESSION CS251594  
 VERSION CS251594.1 GI:85362134  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Vandeghinste,N.  
 TITLE Methods and means for treatment of osteoarthritis  
 JOURNAL Patent: WO 2005124342-A 161 29-DEC-2005;  
 Galapagos N.V. (BE)  
 FEATURES  
 source 1.19 Location/Qualifiers  
 /organism="synthetic construct"  
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 Query Match 62.1%; Score 11.8; DB 2; Length 19;  
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 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 CGGTATCTCCTTCAC 19  
 DB 2 CAGTACCTCCTTCAC 16

Query Match 62.1%; Score 11.8; DB 2; Length 19;  
 Best Local Similarity 86.7%; Pred. No. 7.8e+05;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 CGGTATCTCCTTCAC 19  
 DB 17 CAGTACCTCCTTCAC 3  
 RESULT 10  
 LOCUS CS094047 19 bp RNA linear PAT 03-JUN-2005  
 DEFINITION Sequence 39 from Patent WO2005045041.  
 ACCESSION CS094047  
 VERSION CS094047.1 GI:66951561  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS McSwiggen,J. and Polisky,B.  
 TITLE RNA interference mediated inhibition of cholesterol ester transfer protein (cetp) gene expression using short interfering nucleic acid (siNA)  
 JOURNAL Patent: WO 2005045041-A 139 19-MAY-2005;  
 Sirna Therapeutics, Inc. (US)  
 FEATURES  
 source 1.19 Location/Qualifiers  
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 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 ATCTCCTTCAC 19  
 DB 6 ATCTCCTTCAC 16  
 RESULT 11  
 LOCUS CS094147 19 bp RNA linear PAT 03-JUN-2005  
 DEFINITION Sequence 139 from Patent WO2005045041.  
 ACCESSION CS094147  
 VERSION CS094147.1 GI:66951661  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS McSwiggen,J. and Polisky,B.  
 TITLE RNA interference mediated inhibition of cholesterol ester transfer protein (cetp) gene expression using short interfering nucleic acid (siNA)  
 JOURNAL Patent: WO 2005045041-A 139 19-MAY-2005;  
 Sirna Therapeutics, Inc. (US)  
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 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 ATCTCCTTCAC 19  
 DB 6 ATCTCCTTCAC 16



Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ATCTCTTCAC 19  
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14 ATCTCTTCAC 4

Db

RESULT 12  
AR295824  
LOCUS AR295824 19 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 7559 from patent US 6537751.  
ACCESSION AR295824  
VERSION AR295824.1 GI:31683108  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.  
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome  
JOURNAL Patent: US 6537751-A 7559 25-MAR-2003;  
Genet S.A.;;  
FRX;

FEATURES  
source Location/Qualifiers  
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ORIGIN

Query Match 57.9%; Score 11; DB 2; Length 19;  
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Qy 7 GATCTCTTC 17  
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Db

RESULT 13  
AR573706/c  
LOCUS AR573706 19 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 3034 from patent US 6770633.  
ACCESSION AR573706  
VERSION AR573706.1 GI:56574598  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Robbins,J.M. and Tritz,R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: US 6770633-A 3034 03-AUG-2004;  
Immusol, Inc.; San Diego, CA  
Location/Qualifiers  
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ORIGIN

Query Match 56.8%; Score 10.8; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 2.8e+06;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGTATCTCCTCA 18  
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17 CGGTCTACTCA 4

Db

RESULT 14  
AR573800  
LOCUS AR573800 19 bp DNA linear PAT 14-DEC-2004

DEFINITION Sequence 3128 from patent US 6770633.  
ACCESSION AR573800  
VERSION AR573800.1 GI:56574692  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Robbins,J.M. and Tritz,R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: US 6770633-A 3128 03-AUG-2004;  
Immusol, Inc.; San Diego, CA  
Location/Qualifiers  
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ORIGIN

Query Match 56.8%; Score 10.8; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 2.8e+06;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGTATCTCCTCA 18  
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6 CAGTTCTCCTCA 19

Db

RESULT 15  
AR573801  
LOCUS AR573801 19 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 3129 from patent US 6770633.  
ACCESSION AR573801  
VERSION AR573801.1 GI:56574693  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Robbins,J.M. and Tritz,R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: US 6770633-A 3129 03-AUG-2004;  
Immusol, Inc.; San Diego, CA  
Location/Qualifiers  
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ORIGIN

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Best Local Similarity 85.7%; Pred. No. 2.8e+06;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGTATCTCCTCA 18  
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5 CAGTTCTCCTCA 18

Db

RESULT 16  
AR573802  
LOCUS AR573802 19 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 3130 from patent US 6770633.  
ACCESSION AR573802  
VERSION AR573802.1 GI:56574694  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Robbins,J.M. and Tritz,R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases

JOURNAL Patent: US 6770633-A 3130 03-AUG-2004;  
Immusol, Inc.; San Diego, CA  
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Best Local Similarity 85.7%; Pred. No. 2.8e+06;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 5 CGGTATCTCCTTCA 18  
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Db 4 CAGTTTCTCCTTCA 17  
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RESULT 17  
AR573803 19 bp DNA linear PAT 14-DEC-2004  
LOCUS  
DEFINITION Sequence 3131 from patent US 6770633.  
ACCESSION AR573803  
VERSION AR573803.1 GI:56574695  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS Robbins,J.M. and Tritz,R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: US 6770633-A 3131 03-AUG-2004;  
Immusol, Inc.; San Diego, CA  
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ORIGIN  
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Best Local Similarity 85.7%; Pred. No. 2.8e+06;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 5 CGGTATCTCCTTCA 18  
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Db 2 CAGTTTCTCCTTCA 15  
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RESULT 18  
AX131816/c 19 bp DNA linear PAT 15-MAY-2001  
LOCUS  
DEFINITION Sequence 3034 from Patent WO0130362.  
ACCESSION AX131816  
VERSION AX131816.1 GI:14138121  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Robbins,J.M. and Tritz,R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: WO 0130362-A 3034 03-MAY-2001;  
IMMUSOL, INC. (US)  
FEATURES  
source  
/organism="Homo sapiens"  
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ORIGIN

Query Match 56.8%; Score 10.8; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 2.8e+06;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 5 CGGTATCTCCTTCA 18  
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Db 17 CGGTCTCTACTTCA 4  
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RESULT 19  
AX131910 19 bp DNA linear PAT 15-MAY-2001  
LOCUS  
DEFINITION Sequence 3128 from Patent WO0130362.  
ACCESSION AX131910  
VERSION AX131910.1 GI:14138215  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Robbins,J.M. and Tritz,R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: WO 0130362-A 3128 03-MAY-2001;  
IMMUSOL, INC. (US)  
FEATURES  
source  
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ORIGIN  
Query Match 56.8%; Score 10.8; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 2.8e+06;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 5 CGGTATCTCCTTCA 18  
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Db 6 CAGTTTCTCCTTCA 19  
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RESULT 20  
AX131911 19 bp DNA linear PAT 15-MAY-2001  
LOCUS  
DEFINITION Sequence 3129 from Patent WO0130362.  
ACCESSION AX131911  
VERSION AX131911.1 GI:14138216  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Robbins,J.M. and Tritz,R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: WO 0130362-A 3129 03-MAY-2001;  
IMMUSOL, INC. (US)  
FEATURES  
source  
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/note="Cyclin A1 ribozyme binding site"  
ORIGIN  
Query Match 56.8%; Score 10.8; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 2.8e+06;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 5 CGGTATCTCCTTCA 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 6 CAGTTTCTCCTTCA 19  
| | | | | | | | | | | | | | | | | | | | | |  
RESULT 20  
AX131911 19 bp DNA linear PAT 15-MAY-2001  
LOCUS  
DEFINITION Sequence 3129 from Patent WO0130362.  
ACCESSION AX131911  
VERSION AX131911.1 GI:14138216  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Robbins,J.M. and Tritz,R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: WO 0130362-A 3129 03-MAY-2001;  
IMMUSOL, INC. (US)  
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/db\_xref="taxon:9606"  
/note="Cyclin A1 ribozyme binding site"  
ORIGIN

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGTATCTCCTTCA 18  
Db 5 CAGTTTCTCCTTCA 18

RESULT 21  
AX131912  
LOCUS  
DEFINITION Sequence 3130 from Patent WO0130362.  
ACCESSION AX131912  
VERSION AX131912.1 GI:14138217  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Robbins J.M. and Tritz R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: WO 0130362-A 3130 03-MAY-2001;  
IMMUSOL, INC. (US)  
FEATURES  
source location/Qualifiers  
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/organism="Homo sapiens"  
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/note="Cyclin A1 ribozyme binding site"

ORIGIN  
Query Match 56.8%; Score 10.8; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 2.8e+06;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGTATCTCCTTCA 18  
Db 4 CAGTTTCTCCTTCA 17

RESULT 22  
AX131913  
LOCUS  
DEFINITION Sequence 3131 from Patent WO0130362.  
ACCESSION AX131913  
VERSION AX131913.1 GI:14138218  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Robbins J.M. and Tritz R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: WO 0130362-A 3131 03-MAY-2001;  
IMMUSOL, INC. (US)  
FEATURES  
source location/Qualifiers  
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/note="Cyclin A1 ribozyme binding site"

ORIGIN  
Query Match 56.8%; Score 10.8; DB 2; Length 19;  
Best Local Similarity 85.7%; Pred. No. 2.8e+06;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGTATCTCCTTCA 18  
Db 5 CGGTATCTCCTTCA 18

Db 2 CAGTTTCTCCTTCA 15

RESULT 23  
CO824220  
LOCUS  
DEFINITION Sequence 73 from Patent EP1428893.  
ACCESSION CO824220  
VERSION CO824220.1 GI:49021193  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Sprecher, E. and Bergman, R.  
TITLE Methods of and compositions for modulating hair growth via p-cadherin modulators  
JOURNAL Patent: EP 1428893-A 73 16-JUN-2004;  
Sprecher, Eli (IL); Bergman, Reuven (IL)  
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source location/Qualifiers  
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Best Local Similarity 76.5%; Pred. No. 3.6e+06;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CACGTATCTCCTTCA 19  
Db 3 CGCGGCGAGCTGCTTCA 19

RESULT 24  
CS171759  
LOCUS  
DEFINITION Sequence 5004 from Patent EP1580263.  
ACCESSION CS171759  
VERSION CS171759.1 GI:77156429  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Ilegai, T.  
TITLE Full-length cDNA sequences  
JOURNAL Patent: EP 1580263-A 5004 28-SEP-2005;  
Research Association for Biotech nology (JP)  
FEATURES  
source location/Qualifiers  
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/organism="unidentified"  
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/db\_xref="taxon:32644"  
/note="Description of Artificial Sequence: an artificially synthesized primer se q uence"

ORIGIN  
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Best Local Similarity 76.5%; Pred. No. 3.6e+06;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CACGTATCTCCTTCA 19  
Db 1 CACTGATTTTCTTCA 17

RESULT 25  
E54494/c  
LOCUS  
E54494 19 bp DNA linear PAT 27-AUG-2002

DEFINITION Heat-resistant lysine biosynthesis enzyme gene of thermophilic  
 Corynebacterium.  
 ACCESSION E54494  
 VERSION E54494.1 GI:22553551  
 KEYWORDS JP 2001120270-A/18.  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Itaya,M., Kimura,E., Kawara,Y. and Sugimoto,S.  
 TITLE Heat-resistant lysine biosynthesis enzyme gene of thermophilic  
 JOURNAL coryneform bacterium  
 COMMENT Patent: JP 2001120270-A 18 08-MAY-2001;  
 AJINOMOTO CO INC  
 OS Artificial Sequence  
 PN JP 2001120270-A/18  
 PD 08-MAY-2001  
 PP 01-NOV-1999 JP 1999311148  
 P1 MINORU ITAYA,EICHIRO KIMURA,YOSHIO KAWARA,SHINICHI SUGIMOTO PC  
 C12N15/09/(C12N15/09,C12R1:15),C12N15/00,C12R1:15) CC  
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QY 2 GCAGGTATCTCCTTCA 18  
 DB 17 GTACGGCATCGCCTACA 1

RESULT 26  
 AR297589/c 19 bp DNA linear PAT 12-JUN-2003  
 LOCUS AR297589  
 DEFINITION Sequence 9324 from patent US 6537751.  
 ACCESSION AR297589  
 VERSION AR297589.1 GI:31684873  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.  
 TITLE Biallelic markers for use in constructing a high density  
 JOURNAL disequilibrium map of the human genome  
 Patent: US 6537751-A 9324 25-MAR-2003;  
 Genetec S.A.;  
 FRX;  
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QY 3 CACGGTATCTCCTTCA 19  
 DB 19 CACAGTCTCTTTTCAC 3

RESULT 27  
 AX117403

LOCUS AX117403 19 bp DNA linear PAT 11-MAY-2001  
 DEFINITION Sequence 2526 from Patent WO0129262.  
 ACCESSION AX117403  
 VERSION AX117403.1 GI:14034354  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Picoult-Newburg,L. and Pohl,M.  
 TITLE Genotyping reagents, kits and methods of use thereof  
 JOURNAL Patent: WO 0129262-A 2526 26-APR-2001;  
 Orchid Biosciences, Inc. (US)  
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Query Match 55.8%; Score 10.6; DB 2; Length 19;  
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QY 3 CACGGTATCTCCTTCA 19  
 DB 1 CAGGGTTTCACCTTCCC 17

RESULT 28  
 AX751584 19 bp DNA linear PAT 20-JUN-2003  
 LOCUS AX751584  
 DEFINITION Sequence 5 from Patent WO03034072.  
 ACCESSION AX751584  
 VERSION AX751584.1 GI:32133863  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Wilson,D.I., Hearn,T. and Walker,M.  
 TITLE Diagnosis and therapy of conditions involving ALMS1  
 JOURNAL Patent: WO 03034072-A 5 24-APR-2003;  
 UNIVERSITY OF SOUTHAMPTON (GB)  
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QY 2 GCAGGTATCTCCTTCA 18  
 DB 1 GCGCGTTTCTCTCGTCA 17

RESULT 29  
 AX837880 19 bp DNA linear PAT 15-DEC-2003  
 LOCUS AX837880  
 DEFINITION Sequence 5004 from Patent EP1347046.  
 ACCESSION AX837880  
 VERSION AX837880.1 GI:39921572  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified  
 REFERENCE 1 unclassified sequences.

AUTHORS Isegai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y.

TITLE Full-length cDNA sequences

JOURNAL Patent: EP 1347046-A 5004 24-SEP-2003; Research Association for Biotechnology (JP)

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ORIGIN

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Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 CACGATATCTCCTTCAC 19  
| | | | | | | | | | | | | | | | | | | | |  
1 CACTGATTTTCTTCAC 17

RESULT 30  
LOCUS CS246174 19 bp DNA linear PAT 09-JAN-2006  
DEFINITION Sequence 113 from Patent WO2005119262.  
ACCESSION CS246174  
VERSION CS246174.1 GI:84660126  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
OTHER SEQUENCES; artificial sequences.

REFERENCE  
AUTHORS Merckliere, P. G.  
TITLE Methods, compositions and compound assays for inhibiting amyloid-beta protein production  
JOURNAL Patent: WO 2005119262-A 113 15-DEC-2005; Galapagos Genomics N.V. (BE)  
FEATURES  
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1. 19  
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Query Match 54.7%; Score 10.4; DB 2; Length 19;  
Best Local Similarity 91.7%; Pred. No. 4.6e+06;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 GGTATCTCCTTC 17  
| | | | | | | | | | | | | | | | | | | | |  
1 GGATCTCCTTC 12

Db 1 GGATCTCCTTC 12

RESULT 31  
LOCUS AR293205 19 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 4940 from patent US 6537751.  
ACCESSION AR293205  
VERSION AR293205.1 GI:31680489  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
OTHER SEQUENCES; Unclassified.

REFERENCE  
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.  
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome  
JOURNAL Patent: US 6537751-A 4940 25-MAR-2003;

Genet S. A.;;  
FRX;  
Location/Qualifiers  
1. 19  
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ORIGIN

Query Match 54.7%; Score 10.4; DB 2; Length 19;  
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Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 7 GTATCTCCTTCA 18  
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2 GTATCTACTTCA 13

Db 2 GTATCTACTTCA 13

RESULT 32  
LOCUS AR294484 19 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 6219 from patent US 6537751.  
ACCESSION AR294484  
VERSION AR294484.1 GI:31681768  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
OTHER SEQUENCES; Unclassified.

REFERENCE  
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.  
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome  
JOURNAL Patent: US 6537751-A 6219 25-MAR-2003; Genet S. A.;;  
FRX;  
Location/Qualifiers  
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Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 8 TATCTCCTTCAC 19  
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4 TATCTACTTCAC 15

Db 4 TATCTACTTCAC 15

RESULT 33  
LOCUS AR533333 19 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 18 from patent US 6730500.  
ACCESSION AR533333  
VERSION AR533333.1 GI:53922961  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
OTHER SEQUENCES; Unclassified.

REFERENCE  
AUTHORS Lok, S.  
TITLE Methods for generating a continuous nucleotide sequence from noncontiguous nucleotide sequences  
JOURNAL Patent: US 6730500-A 18 04-MAY-2004; ZymoGenetics, Inc.; Seattle, WA  
FEATURES  
source  
1. 19  
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/mol\_type="genomic DNA"

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Best Local Similarity 91.7%; Pred. No. 4.6e+06;

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Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 ACGTATCTCCT 15
Db 18 AAGGTATCTCCT 7

RESULT 34
AR573804
LOCUS AR573804 19 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 3132 from patent US 6770653.
ACCESSION AR573804
VERSION AR573804.1 GI:56574696
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: US 6770653-A 3132 03-AUG-2004;
IMMUSOL, Inc.; San Diego, CA
FEATURES
source
1.19
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Best Local Similarity 91.7%; Pred. No. 4.6e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTATCTCCTCA 18
Db 1 GTTCTCTCTCA 12

RESULT 35
AX131914
LOCUS AX131914 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3132 from Patent WO0130362.
ACCESSION AX131914
VERSION AX131914.1 GI:14138219
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 19)
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 3132 03-MAY-2001;
IMMUSOL, INC. (US)
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Db 1 GTTCTCTCTCA 12

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RESULT 36
BD244859/c
LOCUS BD244859 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide primer capable of making the non-specific double strand formation unstable.
ACCESSION BD244859
VERSION BD244859.1 GI:33054629
KEYWORDS JP 2002532063-A/4.
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Pelletier,J. and Das,M.
TITLE Oligonucleotide primer capable of making the non-specific double strand formation unstable
JOURNAL Patent: JP 2002532063-A 4 02-OCT-2002;
MCGILL UNIVERSITY
COMMENT OS Artificial Sequence
PN JP 2002532063-A/4
PD 02-OCT-2002
PR 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JBERRY PELLETIER, MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key
FT source
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FEATURES
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Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 CACGATCTCCTTC 17
Db 15 CACAGCATTTCTCCTC 1

RESULT 37
CS128821/c
LOCUS CS128821 19 bp DNA linear PAT 02-AUG-2005
DEFINITION Sequence 2 from Patent WO2005063983.
ACCESSION CS128821
VERSION CS128821.1 GI:71790688
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 19)
AUTHORS van Rompaey,L.J.
TITLE Patent: WO 2005063983-A 2 14-JUL-2005;
JOURNAL Galapagos Genomics N.V. (BB)
FEATURES
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Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 CGGTATCTCCTTCA 19
Db 1 CGGTATCTCCTTCA 19

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Db 16 CAGCAGCTCTTCAC 2

RESULT 38  
LOCUS CS132095/c 19 bp DNA linear PAT 02-AUG-2005  
DEFINITION Sequence 4 from Patent WO2005063976.  
ACCESSION CS132095  
VERSION CS132095.1 GI:71795131  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
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/db\_xref="taxon:32630"  
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Best Local Similarity 80.0%; Pred. No. 5.9e+06;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGGTATCTCTTCAC 19  
Db 16 CAGCAGCTCTTCAC 2

RESULT 39  
LOCUS CS197806 19 bp RNA linear PAT 08-DEC-2005  
DEFINITION Sequence 1329 from Patent WO2005105995.  
ACCESSION CS197806  
VERSION CS197806.1 GI:83413293  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
JOURNAL  
FEATURES  
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Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTT 16  
Db 5 GCACGGTATCTCCTT 19

RESULT 40  
LOCUS CS197807 19 bp RNA linear PAT 08-DEC-2005  
DEFINITION Sequence 1330 from Patent WO2005105995.  
ACCESSION CS197807  
VERSION CS197807.1 GI:83413294

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
JOURNAL  
FEATURES  
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Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCCTT 16  
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Job time : 1006.67 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: August 10, 2006, 07:08:17 ; Search time 981 Seconds  
(without alignments)  
1238.533 Million cell updates/sec

Title: US-10-636-065-29

Perfect score: 19

Sequence: 1 cgcacggatccctccac 19

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2541152

Minimum DB seq length: 0

Maximum DB seq length: 70

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

GenEmbl:\*  
1: gb env:\*  
2: gb pat:\*  
3: gb ph:\*  
4: gb pl:\*  
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6: gb pr:\*  
7: gb pr:\*  
8: gb pr:\*  
9: gb pr:\*  
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11: gb pr:\*  
12: gb pr:\*  
13: gb pr:\*  
14: gb pr:\*  
15: gb pr:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARYS

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	2	AR451384 Sequence
2	19	100.0	19	2	AX411929 Sequence
3	18	94.7	23	2	AR103283 Sequence
4	15.4	81.1	54	2	AR559550 Sequence
5	15	78.9	19	2	CS027764 Sequence
6	15	78.9	19	2	CS028231 Sequence
7	14	73.7	19	2	AX923594 Sequence
8	14	73.7	19	2	AX923672 Sequence
9	13.8	72.6	59	2	AR536378 Sequence
10	13.8	72.6	59	2	AR536378 Sequence
11	13.4	70.5	37	2	AR537934 Sequence
12	13.4	70.5	37	2	AR537934 Sequence
13	13.4	70.5	40	5	S80712 gamma delta
14	13.4	69.5	60	2	CS0541032 Sequence
15	13.2	69.5	20	2	AR311923 Sequence
16	13.2	69.5	29	2	AR721266 Sequence
17	13.2	69.5	42	2	AR925902 Sequence
18	13.2	69.5	56	2	AR526230 Sequence
			65	2	CS051296 Sequence

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C 20	12.8	67.4	22	2	AR569453	AR569453 Sequence
C 21	12.8	67.4	22	2	AX005818	AX005818 Sequence
C 22	12.8	67.4	23	2	BD074493	BD074493 Genetic r
C 23	12.8	67.4	23	2	AR569455	AR569455 Sequence
C 24	12.8	67.4	23	2	AX005820	AX005820 Sequence
C 25	12.8	67.4	52	2	AR580727	AR580727 Sequence
C 26	12.6	66.3	30	2	BD000514	BD000514 Method fo
C 27	12.6	66.3	30	2	DD159756	DD159756 Method fo
C 28	12.6	66.3	34	2	A06937	A06937 F. domestica
C 29	12.6	66.3	35	2	CQ970331	CQ970331 Sequence
C 30	12.6	66.3	35	2	CQ970340	CQ970340 Sequence
C 31	12.6	66.3	39	2	BD195709	BD195709 In vivo u
C 32	12.6	66.3	39	2	BD232001	BD232001 Methode a
C 33	12.6	66.3	39	2	AR282802	AR282802 Sequence
C 34	12.6	66.3	50	2	AR682667	AR682667 Sequence
C 35	12.6	66.3	60	2	CQ536153	CQ536153 Sequence
C 36	12.6	66.3	65	2	CQ557963	CQ557963 Sequence
C 37	12.4	65.3	21	2	BD194418	BD194418 Secretary
C 38	12.4	65.3	21	2	AR297198	AR297198 Secretary
C 39	12.4	65.3	24	2	CQ853550	CQ853550 Sequence
C 40	12.4	65.3	27	2	CQ853552	CQ853552 Sequence
C 41	12.4	65.3	29	2	AR614221	AR614221 Sequence
C 42	12.4	65.3	35	2	BD074489	BD074489 Genetic r
C 43	12.4	65.3	35	2	AR569451	AR569451 Sequence
C 44	12.4	65.3	35	2	AX005816	AX005816 Sequence
C 45	12.4	65.3	47	2	AR288581	AR288581 Sequence
C 46	12.4	65.3	65	2	CQ560131	CQ560131 Sequence
C 47	12.2	64.2	21	2	AR264310	AR264310 Sequence
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C 49	12.2	64.2	24	2	AR124725	AR124725 Sequence
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C 51	12.2	64.2	26	2	BD096366	BD096366 Wtl Inter
C 52	12.2	64.2	26	2	BD103725	BD103725 A detecti
C 53	12.2	64.2	26	2	BD136223	BD136223 Method fo
C 54	12.2	64.2	26	2	BD267502	BD267502 New metat
C 55	12.2	64.2	47	2	BD134418	BD134418 Productio
C 56	12.2	64.2	47	2	AX798079	AX798079 Sequence
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C 58	12.2	64.2	49	2	AX952538	AX952538 Sequence
C 59	12.2	64.2	50	2	AR681411	AR681411 Sequence
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C 61	12.2	64.2	60	2	CQ540565	CQ540565 Sequence
C 62	12.2	64.2	60	2	CQ544799	CQ544799 Sequence
C 63	12.2	64.2	65	2	CQ556637	CQ556637 Sequence
C 64	12.2	64.2	68	2	AR523001	AR523001 Sequence
C 65	12.2	64.2	68	2	AR027476	AR027476 Sequence
C 66	12.2	64.2	68	2	AR082686	AR082686 Sequence
C 67	12.2	64.2	70	2	AR131323	AR131323 Sequence
C 68	12.2	64.2	70	2	DD206809	DD206809 Methods a
C 69	12.2	63.2	39	2	AR443166	AR443166 Sequence
C 70	12.2	63.2	39	2	CS120079	CS120079 Sequence
C 71	12.2	63.2	41	2	CS120295	CS120295 Sequence
C 72	12.2	63.2	41	2	AR109087	AR109087 Sequence
C 73	12.2	63.2	41	2	AR200742	AR200742 Sequence
C 74	12.2	63.2	51	2	AX483415	AX483415 Sequence
C 75	12.2	63.2	53	2	CQ007472	CQ007472 Sequence
C 76	12.2	63.2	53	2	AR590028	AR590028 Sequence
C 77	12.2	63.2	65	2	CQ555655	CQ555655 Sequence
C 78	11.8	62.1	16	2	A08781	A08781 reverse com
C 79	11.8	62.1	16	2	E32722	E32722 Small tripl
C 80	11.8	62.1	16	2	AX000278	AX000278 Sequence
C 81	11.8	62.1	19	2	BD080793	BD080793 Human est
C 82	11.8	62.1	19	2	BD080808	BD080808 Novel est
C 83	11.8	62.1	19	2	CS251594	CS251594 Sequence
C 84	11.8	62.1	20	2	A08780	A08780 Nucleotide
C 85	11.8	62.1	20	2	AR565776	AR565776 Sequence
C 86	11.8	62.1	20	2	AX009199	AX009199 Sequence
C 87	11.8	62.1	21	2	E14408	E14408 Primer. 7/1
C 88	11.8	62.1	26	2	AR078530	AR078530 Sequence
C 89	11.8	62.1	27	2	AR143841	AR143841 Sequence
C 90	11.8	62.1	27	2	BD140898	BD140898 Method fo
C 91	11.8	62.1	27	2	AR585210	AR585210 Sequence

92 11.8 62.1 31 2 AR232074  
 C 93 11.8 62.1 41 2 AX516947  
 C 94 11.8 62.1 41 2 AX519458  
 C 95 11.8 62.1 44 2 A08788  
 C 96 11.8 62.1 44 2 A08788  
 C 97 11.8 62.1 44 2 A08789  
 C 98 11.8 62.1 44 2 A08789  
 C 99 11.8 62.1 45 2 A01999  
 100 11.8 62.1 45 2 A06445

## ALIGNMENTS

RESULT 1  
 AR451384  
 LOCUS AR451384 19 bp DNA linear PAT 20-FEB-2004  
 DEFINITION Sequence 29 from patent US 6673917.  
 ACCESSION AR451384  
 VERSION AR451384.1 GI:42682409  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE  
 AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.  
 TITLE Antisense iAP nucleic acids and uses thereof  
 JOURNAL Patent: US 6673917-A 29 06-JUN-2004;  
 University of Ottawa; Ottawa;  
 CAX;

FEATURES  
 source 1..19  
 Location/Qualifiers  
 /organism="unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 85;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCTTCAC 19  
 |||||  
 Db 1 CGCAGGTATCTCTTCAC 19

RESULT 2  
 AX411929  
 LOCUS AX411929 19 bp DNA linear PAT 14-JUN-2002  
 DEFINITION Sequence 29 from Patent WO0226968.  
 ACCESSION AX411929  
 VERSION AX411929.1 GI:21444394  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 other sequences; artificial sequences.

REFERENCE  
 AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.  
 TITLE Antisense iap nucleic acids and uses thereof  
 JOURNAL Patent: WO 0226968-A 29 04-APR-2002;  
 University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)  
 Location/Qualifiers  
 1..19  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="based on Homo sapiens"

## FEATURES

## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 85;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCTTCAC 19

Db |||||  
 1 CGCAGGTATCTCTTCAC 19

RESULT 3  
 AR103283  
 LOCUS AR103283 23 bp DNA linear PAT 14-FEB-2001  
 DEFINITION Sequence 3 from patent US 6087173.  
 ACCESSION AR103283  
 VERSION AR103283.1 GI:12814871  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE  
 AUTHORS Bennett,C.,Frank., Ackermann,E.J. and Cowsett,L.M.  
 TITLE Antisense modulation of X-linked inhibitor of apoptosis expression  
 JOURNAL Patent: US 6087173-A 3 11-JUL-2000;  
 Location/Qualifiers  
 1..23  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Query Match 94.7%; Score 18; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCTTCAC 19  
 |||||  
 Db 1 GCACGGTATCTCTTCAC 18

RESULT 4  
 AR559550  
 LOCUS AR559550 54 bp DNA linear PAT 08-OCT-2004  
 DEFINITION Sequence 5 from patent US 6750052.  
 ACCESSION AR559550  
 VERSION AR559550.1 GI:53969031  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE  
 AUTHORS Shinohara,T., Singh,D. and Chylack,L.T. Jr.  
 TITLE Lens epithelial cell derived growth factor  
 JOURNAL Patent: US 6750052-A 5 15-JUN-2004;  
 The Brigham and Women's Hospital, Inc.; Boston, MA  
 Location/Qualifiers  
 1..54  
 /organism="unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

Query Match 81.1%; Score 15.4; DB 2; Length 54;  
 Best Local Similarity 94.1%; Pred. No. 6.7e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGTATCTCTTCAC 19  
 |||||  
 Db 48 CACGGTATCTCTTCAC 32

RESULT 5  
 CS027764/c  
 LOCUS CS027764 19 bp RNA linear PAT 03-MAR-2005  
 DEFINITION Sequence 17 from Patent WO2005014811.  
 ACCESSION CS027764  
 VERSION CS027764.1 GI:60497314  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Mcswiggen,J. and Chowrira,B.M.  
TITLE RNA interference mediated inhibition of XIAP gene expression using short interfering Nucleic Acid (siNA)  
JOURNAL Patent: WO 2005014811-A 17 17-FEB-2005;  
Sirta Therapeutics, Inc. (US)  
FEATURES Location/Qualifiers  
SOURCE 1..19  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence: Target Sequence/siNA sense region"

ORIGIN  
Query Match 78.9%; Score 15; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCAC 19  
|||||  
19 CGGTATCTCCTTCAC 5

Db 19 CGGTATCTCCTTCAC 5

RESULT 6  
LOCUS CS028231 19 bp RNA  
DEFINITION Sequence 484 from Patent WO2005014811.  
ACCESSION CS028231  
VERSION CS028231.1 GI:60497781  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Mcswiggen,J. and Chowrira,B.M.  
TITLE RNA interference mediated inhibition of XIAP gene expression using short interfering Nucleic Acid (siNA)  
JOURNAL Patent: WO 2005014811-A 484 17-FEB-2005;  
Sirta Therapeutics, Inc. (US)  
FEATURES Location/Qualifiers  
SOURCE 1..19  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence: siNA antisense region"

ORIGIN  
Query Match 78.9%; Score 15; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGGTATCTCCTTCAC 19  
|||||  
1 CGGTATCTCCTTCAC 15

Db 1 CGGTATCTCCTTCAC 15

RESULT 7  
LOCUS AX923594 19 bp DNA  
DEFINITION Sequence 29 from Patent WO03080638.  
ACCESSION AX923594  
VERSION AX923594.1 GI:40216610  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Lacasse,E., Mcmann,D. and Durkin,J.P.  
TITLE Antisense 1ap nucleobase oligomers and uses thereof  
JOURNAL Patent: WO 03080638-A 29 02-OCT-2003;  
Aegera Therapeutics Inc. (CA)

FEATURES Location/Qualifiers  
SOURCE 1..19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="based on Homo sapiens. Each nucleobase may be part of a ribonucleotide, deoxyribonucleotide, or nucleotide analog  
n = T or U"

ORIGIN  
Query Match 73.7%; Score 14; DB 2; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.8e+04;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGCACGGTATCTCCTTCAC 19  
|||||  
1 CGCACGGTATCTCCTTCAC 19

Db 1 CGCACGGTATCTCCTTCAC 19

RESULT 9  
LOCUS AR356378 59 bp DNA  
DEFINITION Sequence 2496 from patent US 6593114.  
ACCESSION AR356378  
VERSION AR356378.1 GI:33762462  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 59)  
AUTHORS Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and Rosen,C.A.  
TITLE Staphylococcus aureus polynucleotides and sequences  
JOURNAL Patent: US 6593114-A 2496 15-JUL-2003;  
Human Genome Sciences, Inc.; Rockville, MD  
FEATURES Location/Qualifiers  
SOURCE 1..59

ORIGIN /organism="unknown"  
/mol\_type="genomic DNA"

Query Match 72.6%; Score 13.8; DB 2; Length 59;  
Best Local Similarity 88.2%; Pred. No. 5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCCTTC 17  
14 CGCAGCGATTTCTTC 30

RESULT 10  
ARS37934  
LOCUS Sequence 2496 from patent US 6737248.  
DEFINITION ARS37934  
ACCESSION ARS37934  
VERSION ARS37934.1 GI:53929151  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1.59  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 72.6%; Score 13.8; DB 2; Length 59;  
Best Local Similarity 88.2%; Pred. No. 5e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGCAGCGTATCTCCTTC 17  
14 CGCAGCGATTTCTTC 30

RESULT 11  
I24033  
LOCUS Sequence 15 from patent US 5541110.  
DEFINITION I24033  
ACCESSION I24033  
VERSION I24033.1 GI:1603903  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1.37  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 70.5%; Score 13.4; DB 2; Length 37;  
Best Local Similarity 93.3%; Pred. No. 9e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGATATCTCCTTC 17  
1 CATGATATCTCCTTC 15

RESULT 12  
S80712  
LOCUS 40 bp DNA linear PRI 07-MAY-1993  
DEFINITION gamma delta T cell antigen receptor delta-chain [V delta 2-J delta 1 junction] [human, peripheral blood, Genomic, 40 nt].  
ACCESSION S80712  
VERSION S80712.1 GI:244924  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REMARK  
FEATURES  
source  
1.40  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
1.40  
/gene="gamma delta T cell antigen receptor delta-chain"

Query Match 70.5%; Score 13.4; DB 5; Length 40;  
Best Local Similarity 93.3%; Pred. No. 8.9e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGATATCTCCTTC 17  
5 CACGATATCACCCTTC 19

RESULT 13  
CQ541032  
LOCUS Sequence 10667 from Patent WO0210449.  
DEFINITION CQ541032  
ACCESSION CQ541032  
VERSION CQ541032.1 GI:41507296  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1.60  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 70.5%; Score 13.4; DB 2; Length 60;  
Best Local Similarity 93.3%; Pred. No. 8.3e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGGATATCTCCTTCAC 19  
27 CTGATATCTCCTTCAC 13

**RESULT 14**  
**LOCUS** AR311923/c 20 bp DNA linear PAT 12-JUN-2003  
**DEFINITION** Sequence 2460 from patent US 6559294.  
**ACCESSION** AR311923  
**VERSION** AR311923.1 GI:31705349  
**KEYWORDS**  
**SOURCE** Unknown.  
**ORGANISM** Unclassified.  
**REFERENCE** 1 (bases 1 to 20)  
**AUTHORS** Griffiths, R., Holseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,  
**TITLE** Chlamydia pneumoniae polynucleotides and uses thereof  
**JOURNAL** Patent: US 6559294-A 2460 06-MAY-2003;  
**Genet. S.A.;**  
**FRX;**  
**FEATURES** location/Qualifiers  
**source** 1..20  
/mol\_type="genomic DNA"  
**ORIGIN**  
**Query Match** 69.5%; Score 13.2; DB 2; Length 20;  
**Best Local Similarity** 83.3%; Pred. No. 1.3e+05;  
**Matches** 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
**QY** 2 GCACGGTATCTCTTCAC 19  
|||||  
18 GCACGTATCTCCATCAC 1  
**Db**  
**RESULT 15**  
**LOCUS** AR721266 29 bp DNA linear PAT 07-OCT-2005  
**DEFINITION** Sequence 9 from patent US 6946294.  
**ACCESSION** AR721266  
**VERSION** AR721266.1 GI:77372750  
**KEYWORDS**  
**SOURCE** Unknown.  
**ORGANISM** Unclassified.  
**REFERENCE** 1 (bases 1 to 29)  
**AUTHORS** Kang, J.-G., Yun, J., Song, P.-S. and Park, C.-M.  
**TITLE** Transgenic plant transformed with a transcriptionally controlled  
tumor protein (TCTP) gene  
**JOURNAL** Patent: US 6946294-A 9 20-SBP-2005;  
**Kunho Petrochemical Co., Seoul;**  
**KRX;**  
**FEATURES** location/Qualifiers  
**source** 1..29  
/mol\_type="genomic DNA"  
**ORIGIN**  
**Query Match** 69.5%; Score 13.2; DB 2; Length 29;  
**Best Local Similarity** 83.3%; Pred. No. 1.2e+05;  
**Matches** 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
**QY** 1 CGCAGGTATCTCTTCA 18  
|||||  
9 CGCAGTTGATCTCTTCA 26  
**Db**  
**RESULT 16**  
**LOCUS** AX925902 42 bp DNA linear PAT 19-DEC-2003  
**DEFINITION** Sequence 4 from Patent EPI352966.  
**ACCESSION** AX925902  
**VERSION** AX925902.1 GI:40244706  
**KEYWORDS**

**SOURCE** synthetic construct  
**ORGANISM** synthetic construct  
other sequences; artificial sequences.  
**REFERENCE** 1  
**AUTHORS** Hara, Y.C., Izui, H.C., Asano, T.C., Watanabe, Y.C. and Nakamatsu  
**TITLE** Teiyoshi, C.T.  
**JOURNAL** Method for producing L-amino acid  
Patent: EP 1352966-A 4 15-OCT-2003;  
**Ajinomoto Co., Inc. (JP)**  
**FEATURES** location/Qualifiers  
**source** 1..42  
/mol\_type="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence: primer"  
**ORIGIN**  
**Query Match** 69.5%; Score 13.2; DB 2; Length 42;  
**Best Local Similarity** 83.3%; Pred. No. 1.1e+05;  
**Matches** 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
**QY** 1 CGCAGGTATCTCTTCA 18  
|||||  
2 CGCAGGTATCTCTTCA 19  
**Db**  
**RESULT 17**  
**LOCUS** AR526230 56 bp DNA linear PAT 22-SBP-2004  
**DEFINITION** Sequence 31190 from patent US 6703491.  
**ACCESSION** AR526230  
**VERSION** AR526230.1 GI:52461718  
**KEYWORDS**  
**SOURCE** Unknown.  
**ORGANISM** Unclassified.  
**REFERENCE** 1 (bases 1 to 56)  
**AUTHORS** Homburger, S.A., Ebens, A.J. Jr., Erickson, C.S., Francis-Lang, H.L.,  
**TITLE** Margolis, J.S., Reddy, B.P., Ruddy, D.A. and Buchman, A.R.  
**JOURNAL** Drosophila sequences  
Patent: US 6703491-A 31190 09-MAR-2004;  
**Exelixis, Inc.; South San Francisco, CA**  
**FEATURES** location/Qualifiers  
**source** 1..56  
/mol\_type="genomic DNA"  
**ORIGIN**  
**Query Match** 69.5%; Score 13.2; DB 2; Length 56;  
**Best Local Similarity** 83.3%; Pred. No. 1.1e+05;  
**Matches** 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
**QY** 1 CGCAGGTATCTCTTCA 18  
|||||  
4 CGCAGCGCATCGCATCA 21  
**Db**  
**RESULT 18**  
**LOCUS** CO531296 65 bp DNA linear PAT 30-JAN-2004  
**DEFINITION** Sequence 931 from Patent WO0210449.  
**ACCESSION** CO531296  
**VERSION** CO531296.1 GI:41497560  
**KEYWORDS**  
**SOURCE** Rattus norvegicus (Norway rat)  
**ORGANISM** Rattus norvegicus  
**REFERENCE** 1  
**AUTHORS** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
**TITLE** Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Rattus.  
1 Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Paigler, S.  
Oligonucleotide library for detecting rna transcripts and splice  
variants that populate a transcriptome

JOURNAL Patent: WO 0210449-A 931 07-FEB-2002;  
Compugen Inc. (US)  
FEATURES Location/Qualifiers  
source 1..65  
/organism="Rattus norvegicus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10116"  
ORIGIN  
Query Match 69.5%; Score 13.2; DB 2; Length 65;  
Best Local Similarity 83.3%; Pred. No. 1e+05; Mismatches 3; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 CGCAGCGTATCTCTTCA 18  
| | | | | | | | | | | | | | | | | | | | | |  
| | | | | | | | | | | | | | | | | | | | | |  
Db 39 CGCAAGAGATCTCTTCA 56  
RESULT 19  
BD074491 22 bp DNA linear PAT 27-AUG-2002  
LOCUS Genetic regulation of plant growth and development.  
DEFINITION BD074491 GI:22620094  
ACCESSION BD074491.1  
VERSION JP 2001514893-A/16.  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Herbert,N.P., Richards,D.E. and Pen,J.  
TITLE Genetic regulation of plant growth and development  
JOURNAL Patent: JP 2001514893-A 16 18-SEP-2001;  
PLANT BIOSCIENCE LTD  
COMMENT OS Artificial Sequence  
PN JP 2001514893-A/16  
PD 18-SEP-2001 JP 2000509838  
PR 07-AUG-1998 JP 2000509838  
PI NICHOLAS PAUL HERBERT,DONALD ERNEST RICHARDS,JINLON PEN PC  
C12N5/09,A01H5/00,C07K14/415,C12N1/15,C12N1/19,C12N1/21 PC  
C12N5/10,C12N5/10,PC  
C12P21/02,C12Q1/68,C12N15/00,C12N5/00,C12N5/00 CC  
Description of Artificial Sequence: Primer  
FH Key Location/Qualifiers  
FT source 1..22  
Location/Qualifiers  
FEATURES Location/Qualifiers  
source 1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 67.4%; Score 12.8; DB 2; Length 22;  
Best Local Similarity 87.5%; Pred. No. 2.1e+05; Mismatches 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 4 ACGGTATCTCTTCA 19  
| | | | | | | | | | | | | | | | | | | | | |  
| | | | | | | | | | | | | | | | | | | | | |  
Db 19 ACGGTATCTCTTCA 4  
RESULT 20  
AR569453 22 bp DNA linear PAT 14-DEC-2004  
LOCUS AR569453  
DEFINITION Sequence 27 from patent US 6762348.  
ACCESSION AR569453  
VERSION AR569453.1  
KEYWORDS GI:56570004  
SOURCE Unknown.  
ORGANISM Unknown.  
COMMENT Unclassified.  
REFERENCE 1 (bases 1 to 22)

AUTHORS Harberd,N.P., Richards,D.E. and Peng,J.  
TITLE Genetic control of plant growth and development  
JOURNAL Patent: US 6762348-A 27 13-JUL-2004;  
Pioneer Hi-Bred International, Inc.; Johnston, IA;  
WOX;  
FEATURES Location/Qualifiers  
source 1..22  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 67.4%; Score 12.8; DB 2; Length 22;  
Best Local Similarity 87.5%; Pred. No. 2.1e+05; Mismatches 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 4 ACGGTATCTCTTCA 19  
| | | | | | | | | | | | | | | | | | | | | |  
| | | | | | | | | | | | | | | | | | | | | |  
Db 19 ACGGTATCTCTTCA 4  
RESULT 21  
AX005818 22 bp DNA linear PAT 24-AUG-2000  
LOCUS AX005818/c  
DEFINITION Sequence 27 from Patent WO9909174.  
ACCESSION AX005818  
VERSION AX005818.1  
KEYWORDS GI:9928814  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Harberd,N.P. and Peng,J.  
TITLE Genetic control of plant growth and development  
JOURNAL Patent: WO 9909174-A 27 25-FEB-1999;  
HARBERD NICHOLAS PAUL (GB); PENG JINLON (GB)  
COMMENT Location/Qualifiers  
source 1..22  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"  
ORIGIN  
Query Match 67.4%; Score 12.8; DB 2; Length 22;  
Best Local Similarity 87.5%; Pred. No. 2.1e+05; Mismatches 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 4 ACGGTATCTCTTCA 19  
| | | | | | | | | | | | | | | | | | | | | |  
| | | | | | | | | | | | | | | | | | | | | |  
Db 19 ACGGTATCTCTTCA 4  
RESULT 22  
BD074493 23 bp DNA linear PAT 27-AUG-2002  
LOCUS BD074493  
DEFINITION Genetic regulation of plant growth and development.  
ACCESSION BD074493  
VERSION BD074493.1  
KEYWORDS GI:22620096  
JP 2001514893-A/18.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Herbert,N.P., Richards,D.E. and Pen,J.  
TITLE Genetic regulation of plant growth and development  
JOURNAL Patent: JP 2001514893-A 18 18-SEP-2001;  
PLANT BIOSCIENCE LTD  
COMMENT OS Artificial Sequence  
PN JP 2001514893-A/18  
PD 18-SEP-2001 JP 2000509838  
PR 07-AUG-1998 JP 2000509838  
PI NICHOLAS PAUL HERBERT,DONALD ERNEST RICHARDS,JINLON PEN PC

Accession	Source	Location/Qualifiers
C12N25/09, C12N15/00, C07K14/415, C12N1/15, C12N1/19, C12N1/21	PC	
C12N5/10, C12N5/10.	PC	
C12P21/02, C12Q1/68, C12N15/00, C12N5/00, C12N5/00	CC	
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LOCUS	AR569455	23 bp	DNA	
DEFINITION	Sequence 29 from patent US 6782348.		linear	
ACCESSION	AR569455			
VERSION	AR569455.1	GI:5657006		
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ORGANISM	Unknown.			

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RESULT 24			
LOCUS	AX005820		
DEFINITION	Sequence 29 from Patent WO9309174.	23 bp	DNA
ACCESSION	AX005820		linear
VERSION	AX005820.1	GI:9928816	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	Harberd,N.P. and Peng,J.		
TITLE	Genetic control of plant growth and development		
JOURNAL	Patent: WO 9909174-A 29 25-FEB-1999;		
	HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)		
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LOCUS	AR580727	52 bp	DNA	linear	PAT 15-DEC-2004
DEFINITION	Sequence 26 from patent US 6790444.				
ACCESSION	AR580727				
VERSION	AR580727.1	GI:56611237			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 52)				
AUTHORS	Le,J., Vilcek,J., Daddona,P., Ghayeb,J., Knight,D. and Siegel,S.				
TITLE	Anti-TNF antibodies and peptides of human necrosis factor				
JOURNAL	Patent: US 6790444-A 26 14-SBP-2004;				
	New York University Medical Center and Centocor, Inc.; New York, NY				
FEATURES	Location/Qualifiers				
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RESULT 26				
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LOCUS	BD000514	30 bp	DNA	linear
DEFINITION	Method for screening G protein-coupled receptor ligand and method for expression cloning G protein-coupled receptor.			
ACCESSION	BD000514			
				PAT 31-JAN-2002

RESULT	26
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LOCUS	BD000514
DEFINITION	BD000514 30 bp DNA linear PAT 31-JAN-2002
ACCESSION	Method for screening G protein-coupled receptor ligand and method
VERSION	for expression cloning G protein-coupled receptor.
KEYWORDS	BD000514 GI:18623627
SOURCE	JP 2000354500-A/2.
ORGANISM	synthetic construct
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	other sequences; artificial sequences.
REFERENCE	1. (bases 1 to 30)
AUTHORS	Naito,T., Saito,Y. and Morita,M.
TITLE	Method for screening G protein-coupled receptor ligand and method
JOURNAL	for expression cloning G protein-coupled receptor
	Patent : JP 2000354500-A 2 26-DEC-2000;
	JAPAN TOBACCO INC
COMMENT	OS Artificial Sequence
	PN JP 2000354500-A/2
	PD 26-DEC-2000
	PF 12-APR-2000 JP 200011313
	PR
PI	TAKAYUKI NAITO,YUTAKA SAITO,MITSUHIRO MORITA
PC	C12D1/68,C07K14/47,C07K14/705,C12N5/10,C12N15/09,C12P21/02, PC
	C12Q1/02,
PC	C12N1/66,G01N33/15,G01N33/50,G01N33/50,G01N33/566,G01N33/68//
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QY
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RESULT 27
DD159756          30 bp      DNA      linear      PAT 23-NOV-2005
LOCUS             DD159756
DEFINITION        Method for Screening Ligands of G-Protein Coupled Receptor and
ACCESSION         DD159756
VERSION           DD159756.1 GI:83959486
KEYWORDS
SOURCE            JP 2005118050-A/2.
ORGANISM          synthetic construct
                  other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 30)
AUTHORS           Saito,Y., Naito,T. and Morita,M.
TITLE             Method for Screening Ligands of G-Protein Coupled Receptor and
JOURNAL           Expression Cloning Method for G-Protein Coupled Receptor
                  Patent: JP 2005118050-A 2 12-MAY-2005;
                  Japan Tobacco Inc
COMMENT           OS Artificial Sequence
                  PN JP 2005118050-A/2
                  PD 12-MAY-2005
                  PF 07-DEC-2004 JP 2004353501
                  PI yutaka saito,takayuki naito,mitsunori morita
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8 CGCAGCGTCTCTCTTCAC 26

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A06937          34 bp      DNA      linear      PAT 04-OCT-1993
LOCUS             A06937
DEFINITION        F.domesticus c-fes/fps gene, exon 1.
ACCESSION         A06937
VERSION           A06937.1 GI:488944
KEYWORDS
SOURCE            Felis catus (cat)
ORGANISM          Felis catus
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
                  Felinae; Felis.
REFERENCE
1 (bases 1 to 34)
AUTHORS           Van de Ven,W.U.M., Roebroek,A.J.M. and Schalcken,J.A.
TITLE             Recombinant DNA and cDNA, mRNA, protein, antibodies, and a method

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of detecting tumor cells
JOURNAL           Patent: EP 0246709-A 4 25-NOV-1987;
                  Stichting Katholieke Universiteit
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QY
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LOCUS             CQ970331
DEFINITION        Sequence 2 from Patent WO2004046720.
ACCESSION         CQ970331
VERSION           CQ970331.1 GI:56744102
KEYWORDS
SOURCE            synthetic construct
                  other sequences; artificial sequences.
ORGANISM          synthetic construct
REFERENCE
1
AUTHORS           Elismark,P., Furebyring,C., Ohlin,M. and Borrebaeck,C.
TITLE             Methods for identifying members of specific binding pairs
JOURNAL           Patent: WO 2004046720-A 2 03-JUN-2004;
                  Alligator Bioscience AB (SE)
FEATURES
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DEFINITION        Sequence 11 from Patent WO2004046720.
ACCESSION         CQ970340
VERSION           CQ970340.1 GI:56744111
KEYWORDS
SOURCE            synthetic construct
                  other sequences; artificial sequences.
ORGANISM          synthetic construct
REFERENCE
1
AUTHORS           Elismark,P., Furebyring,C., Ohlin,M. and Borrebaeck,C.
TITLE             Methods for identifying members of specific binding pairs
JOURNAL           Patent: WO 2004046720-A 11 03-JUN-2004;
                  Alligator Bioscience AB (SE)
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ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Wohlgenuth,J., Fry,K., Woodward,R. and Ly,N.  
TITLE Methods and compositions for diagnosing or monitoring auto immune  
and chronic inflammatory diseases  
JOURNAL Patent: US 6905827-A 2096 14-JUN-2005;  
Expression Diagnostics, Inc.; So. San Francisco, CA  
FEATURES  
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DB 49 CTCACGTCTCTCTCTCAC 31  
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LOCUS COS36153 60 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 5788 from Patent WO0210449.  
ACCESSION COS36153  
VERSION COS36153.1 GI:41502417  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
TITLE Oligonucleotide library for detecting rna transcripts and splice  
variants that populate a transcritpome  
JOURNAL Patent: WO 0210449-A 5788 07-FEB-2002;  
Compugen Inc. (US)  
FEATURES  
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QY 1 CGCAGCGTATCTCTCTCAC 19  
DB 25 CCCACGATATCTGCTCAC 43  
RESULT 36  
LOCUS COS57963/c 65 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 27598 from Patent WO0210449.  
ACCESSION COS57963  
VERSION COS57963.1 GI:41524390  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
REFERENCE 1  
AUTHORS Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
ACCESSION AR297198

AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
TITLE Oligonucleotide library for detecting rna transcripts and splice  
variants that populate a transcritpome  
JOURNAL Patent: WO 0210449-A 27598 07-FEB-2002;  
Compugen Inc. (US)  
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LOCUS BD194418 21 bp DNA linear PAT 17-JUL-2003  
DEFINITION Secretory proteins and polynucleotides encoding the same.  
ACCESSION BD194418  
VERSION BD194418.1 GI:33004159  
KEYWORDS JP 2002509722-A/13.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Jacobs,K., McCoy,J.M., Lavallie,E.R., Racie,L.A.C., Evans,C.,  
Metberg,D., Treacy,M., Agostino,M.J. and Li,R.J.S.  
TITLE Secretory proteins and polynucleotides encoding the same  
JOURNAL Patent: JP 2002509722-A 13 02-APR-2002;  
GENETICS INSTITUTE INC  
COMMENT  
PN JP 2002509722-A/13  
PD 02-APR-2002  
PF 30-MAR-1999 JP 2000541293  
PR 31-MAR-1998 US 60/080110, 29-MAR-1999 US 09/280591 PI  
KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A COULINS PI  
RACIE,  
PI CHERYL EVANS,DAVID MERBERG,MAURICE TREACY,MICHAEL J AGOSTINO,  
PI ROBERT J STEININGER II  
PC CI2N15/09,C07K7/00,C07K14/00,C07K14/435,CI2N5/10,CI2N15/00, PC  
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DEFINITION Sequence 8933 from patent US 6537751.  
ACCESSION AR297198

VERSION AR297198.1 GI:31684482  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.  
TITLE Biallelic markers for use in constructing a high density  
disequilibrium map of the human genome  
JOURNAL Patent: US 6537751-A 8933 25-MAR-2003;  
Genet S.A.;;  
FRX;  
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ACCESSION CQ853550  
VERSION CQ853550.1 GI:51509753  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Cuello, C., Saragovi, U., du Ruisseau, P., Gold, P., Bernard, N. and  
Moffett, S.  
TITLE Prostate cancer diagnosis and treatment  
JOURNAL Patent: WO 2004067570-A 15 12-AUG-2004;  
Proscan RX Pharma (CA)  
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Db  
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CQ853552 27 bp DNA linear PAT 23-AUG-2004  
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DEFINITION Sequence 17 from Patent WO2004067570.  
ACCESSION CQ853552  
VERSION CQ853552.1 GI:51509755  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Cuello, C., Saragovi, U., du Ruisseau, P., Gold, P., Bernard, N. and  
Moffett, S.

TITLE Prostate cancer diagnosis and treatment  
JOURNAL Patent: WO 2004067570-A 17 12-AUG-2004;  
Proscan RX Pharma (CA)  
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#### SUMMARIES

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4	10.8	56.8	19	US-09-696-791-3128	Sequence 3128, Ap
5	10.8	56.8	19	US-09-696-791-3129	Sequence 3129, Ap
6	10.8	56.8	19	US-09-696-791-3130	Sequence 3130, Ap
7	10.8	56.8	19	US-09-696-791-3131	Sequence 3131, Ap
8	10.6	55.8	19	US-09-422-978-9324	Sequence 9324, Ap
9	10.4	54.7	19	US-09-422-978-9940	Sequence 9940, Ap
10	10.4	54.7	19	US-09-422-978-6219	Sequence 6219, Ap
11	10.4	54.7	19	US-09-938-077-18	Sequence 18, Appl
12	10.4	54.7	19	US-09-696-791-3132	Sequence 3132, Ap
13	10	52.6	19	US-08-182-619-2	Sequence 2, Appl
14	10	52.6	19	US-08-310-535A-2	Sequence 2, Appl
15	10	52.6	19	US-08-838-844-2	Sequence 2, Appl
16	10	52.6	19	US-08-851-350-26	Sequence 26, Appl
17	10	52.6	19	US-08-924-287A-26	Sequence 26, Appl
18	9.8	51.6	19	US-08-117-952-739	Sequence 739, Appl
19	9.8	51.6	19	US-08-549-004A-3	Sequence 3, Appl
20	9.8	51.6	19	US-09-051-982A-3	Sequence 3, Appl
21	9.8	51.6	19	US-08-815-795-2	Sequence 2, Appl
22	9.8	51.6	19	US-09-422-978-5993	Sequence 5993, Ap
23	9.8	51.6	19	US-10-130-158A-9	Sequence 9, Appl

C 24	9.8	51.6	19	US-10-130-158A-10	Sequence 10, Appl
C 25	9.6	50.5	19	US-09-108-006C-28	Sequence 28, Appl
C 26	9.6	50.5	19	US-09-422-978-7112	Sequence 7112, Ap
C 27	9.6	50.5	19	US-09-688-188B-74	Sequence 74, Appl
C 28	9.6	50.5	19	US-09-291-417D-74	Sequence 74, Appl
C 29	9.6	50.5	19	US-09-544-398B-169	Sequence 169, App
C 30	9.6	50.5	19	US-09-543-771B-169	Sequence 169, App
C 31	9.6	50.5	19	US-10-032-495A-20	Sequence 20, Appl
C 32	9.4	49.5	19	US-09-696-791-3133	Sequence 3133, Ap
C 33	9.4	49.5	19	US-09-747-385-7	Sequence 7, Appl
C 34	9.2	48.4	19	US-09-506-729-1	Sequence 1, Appl
C 35	9.2	48.4	19	US-09-422-978-5154	Sequence 5154, Ap
C 36	9.2	48.4	19	US-09-973-132-2	Sequence 2, Appl
C 37	9.2	48.4	19	US-09-696-791-1137	Sequence 1137, Ap
C 38	9.2	48.4	19	US-09-696-791-1138	Sequence 1138, Ap
C 39	9.2	48.4	19	US-09-696-791-1429	Sequence 1429, Ap
C 40	9.2	48.4	19	US-09-696-791-1430	Sequence 1430, Ap
C 41	9.2	48.4	19	US-09-696-791-1430	Sequence 1430, Ap
C 42	9.2	48.4	19	5217865-10	Patent No. 5217865
C 43	9.2	48.4	19	5475095-10	Patent No. 5475095
C 44	9	47.4	19	US-08-086-915-9	Sequence 9, Appl
C 45	9	47.4	19	US-08-769-601-3	Sequence 3, Appl
C 46	9	47.4	19	US-08-825-558-9	Sequence 9, Appl
C 47	9	47.4	19	US-08-300-928C-34	Sequence 34, Appl
C 48	9	47.4	19	US-08-430-944D-34	Sequence 34, Appl
C 49	9	47.4	19	US-08-430-014-34	Sequence 34, Appl
C 50	9	47.4	19	US-08-431-184-34	Sequence 34, Appl
C 51	9	47.4	19	US-08-836-352A-9	Sequence 9, Appl
C 52	9	47.4	19	US-09-338-907-554	Sequence 554, App
C 53	9	47.4	19	US-09-218-207-554	Sequence 9, Appl
C 54	9	47.4	19	US-09-112-611-9	Sequence 9, Appl
C 55	9	47.4	19	US-09-422-978-4426	Sequence 4426, Ap
C 56	9	47.4	19	US-09-696-791-2439	Sequence 2439, Ap
C 57	9	47.4	19	US-09-696-791-2946	Sequence 2946, Ap
C 58	9	47.4	19	US-10-258-828-3	Sequence 3, Appl
C 59	8.8	46.3	19	US-07-767-135-4	Sequence 4, Appl
C 60	8.8	46.3	19	US-08-190-711-1	Sequence 1, Appl
C 61	8.8	46.3	19	US-08-241-853-34	Sequence 34, Appl
C 62	8.8	46.3	19	US-08-433-854-49	Sequence 49, Appl
C 63	8.8	46.3	19	US-08-174-745A-49	Sequence 49, Appl
C 64	8.8	46.3	19	US-08-246-583-13	Sequence 13, Appl
C 65	8.8	46.3	19	US-08-132-168B-6	Sequence 6, Appl
C 66	8.8	46.3	19	US-08-399-986B-19	Sequence 19, Appl
C 67	8.8	46.3	19	US-08-493-754A-19	Sequence 19, Appl
C 68	8.8	46.3	19	US-08-195-947-49	Sequence 49, Appl
C 69	8.8	46.3	19	US-08-850-917-34	Sequence 34, Appl
C 70	8.8	46.3	19	US-08-450-905B-77	Sequence 77, Appl
C 71	8.8	46.3	19	US-08-433-885-49	Sequence 49, Appl
C 72	8.8	46.3	19	US-08-951-648-10	Sequence 10, Appl
C 73	8.8	46.3	19	US-08-433-908B-49	Sequence 49, Appl
C 74	8.8	46.3	19	US-07-982-759P-77	Sequence 77, Appl
C 75	8.8	46.3	19	US-09-338-907-495	Sequence 495, App
C 76	8.8	46.3	19	US-08-410-614-49	Sequence 49, Appl
C 77	8.8	46.3	19	US-09-218-207-495	Sequence 495, App
C 78	8.8	46.3	19	US-09-328-750A-6	Sequence 6, Appl
C 79	8.8	46.3	19	US-09-636-791A-24	Sequence 24, Appl
C 80	8.8	46.3	19	US-09-422-978-5152	Sequence 5152, Ap
C 81	8.8	46.3	19	US-09-422-978-7626	Sequence 7626, Ap
C 82	8.8	46.3	19	US-09-696-791-1136	Sequence 1136, Ap
C 83	8.8	46.3	19	US-09-696-791-1591	Sequence 1591, Ap
C 84	8.8	46.3	19	US-09-696-791-1592	Sequence 1592, Ap
C 85	8.6	45.3	19	US-08-444-994-1	Sequence 1, Appl
C 86	8.6	45.3	19	US-08-244-189-4	Sequence 4, Appl
C 87	8.6	45.3	19	US-08-452-262-12	Sequence 12, Appl
C 88	8.6	45.3	19	US-08-734-550-12	Sequence 12, Appl
C 89	8.6	45.3	19	US-08-656-586-10	Sequence 10, Appl
C 90	8.6	45.3	19	US-09-138-024-1	Sequence 1, Appl
C 91	8.6	45.3	19	US-08-881-784-38	Sequence 38, Appl
C 92	8.6	45.3	19	US-09-292-768-39	Sequence 39, Appl
C 93	8.6	45.3	19	US-09-522-800-7	Sequence 7, Appl
C 94	8.6	45.3	19	US-09-103-975B-111	Sequence 111, App
C 95	8.6	45.3	19	US-09-037-990B-78	Sequence 78, Appl
C 96	8.6	45.3	19	US-08-637-732A-29	Sequence 29, Appl
C 96	8.6	45.3	19	US-09-504-358-36	Sequence 36, Appl

C 97	8.6	45.3	19	3	US-09-404-066-1	Sequence 1, Appl1	170	8.4	44.2	19	3	US-09-902-563-41	Sequence 41, Appl1
C 98	8.6	45.3	19	3	US-09-531-000-70	Sequence 70, Appl1	171	8.4	44.2	19	3	US-10-176-255-12	Sequence 12, Appl1
C 99	8.6	45.3	19	3	US-09-954-314-36	Sequence 36, Appl1	C 172	8.4	44.2	19	3	US-10-197-280B-11	Sequence 31, Appl1
C 100	8.6	45.3	19	3	US-08-820-479-6	Sequence 6, Appl1	C 173	8.4	44.2	19	3	US-10-071-179-107	Sequence 107, App
C 101	8.6	45.3	19	3	US-09-573-322-1	Sequence 1, Appl1	C 174	8.4	44.2	19	3	US-09-693-333-144	Sequence 144, App
C 102	8.6	45.3	19	3	US-09-422-978-5002	Sequence 5002, Ap	C 175	8.4	44.2	19	3	US-09-697-123B-25	Sequence 25, App
C 103	8.6	45.3	19	3	US-09-47-391-240	Sequence 240, App	C 176	8.4	44.2	19	3	US-09-923-327A-6	Sequence 6, Appl1
C 104	8.6	45.3	19	3	US-09-358-321C-52	Sequence 52, Appl1	C 177	8.4	44.2	19	4	US-10-428-826-11	Sequence 141, App
C 105	8.6	45.3	19	3	US-09-696-791-174	Sequence 174, App	C 178	8.4	44.2	19	5	US-10-032-495A-9	Sequence 9, Appl1
C 106	8.6	45.3	19	3	US-09-696-791-1018	Sequence 1018, Ap	C 179	8.4	44.2	19	7	PCT-US95-08605-11	Sequence 11, Appl1
C 107	8.6	45.3	19	3	US-09-696-791-1019	Sequence 1019, Ap	C 180	8.2	43.2	19	2	US-08-110-294A-44	Sequence 44, Appl1
C 108	8.6	45.3	19	3	US-09-696-791-1020	Sequence 1020, Ap	C 181	8.2	43.2	19	2	US-08-389-926-44	Sequence 44, Appl1
C 109	8.6	45.3	19	3	US-10-230-562-36	Sequence 36, Appl1	C 182	8.2	43.2	19	2	US-08-532-727A-6	Sequence 6, Appl1
C 110	8.6	45.3	19	3	US-09-959-120B-26	Sequence 26, Appl1	C 183	8.2	43.2	19	2	US-08-743-637B-68	Sequence 68, Appl1
C 111	8.6	45.3	19	7	PCT-US94-06331A-3	Sequence 3, Appl1	C 184	8.2	43.2	19	3	US-08-526-840B-68	Sequence 68, Appl1
C 112	8.6	45.3	19	7	PCT-US96-07528-12	Sequence 12, Appl1	C 185	8.2	43.2	19	3	US-08-960-760-84	Sequence 84, Appl1
C 113	8.4	44.2	19	2	US-08-388-381-11	Sequence 11, Appl1	C 186	8.2	43.2	19	3	US-08-960-760-122	Sequence 122, App
C 114	8.4	44.2	19	2	US-08-420-244-3	Sequence 3, Appl1	C 187	8.2	43.2	19	3	US-09-311-260-63	Sequence 63, Appl1
C 115	8.4	44.2	19	2	US-08-166-664-14	Sequence 14, Appl1	C 188	8.2	43.2	19	3	US-09-516-989-6	Sequence 488, App
C 116	8.4	44.2	19	2	US-08-313-185-19	Sequence 19, Appl1	C 189	8.2	43.2	19	3	US-09-073-898-84	Sequence 84, Appl1
C 117	8.4	44.2	19	2	US-08-849-536A-7	Sequence 7, Appl1	C 190	8.2	43.2	19	3	US-09-338-907-473	Sequence 473, App
C 118	8.4	44.2	19	3	US-08-765-626-11	Sequence 11, Appl1	C 191	8.2	43.2	19	3	US-09-338-907-488	Sequence 488, App
C 119	8.4	44.2	19	3	US-09-292-071-12	Sequence 12, Appl1	C 192	8.2	43.2	19	3	US-08-797-358B-5	Sequence 5, Appl1
C 120	8.4	44.2	19	3	US-09-082-614A-19	Sequence 19, Appl1	C 193	8.2	43.2	19	3	US-09-218-207-473	Sequence 473, App
C 121	8.4	44.2	19	3	US-09-432-069A-12	Sequence 12, Appl1	C 194	8.2	43.2	19	3	US-09-218-207-488	Sequence 488, App
C 122	8.4	44.2	19	3	US-09-418-721-112	Sequence 112, App	C 195	8.2	43.2	19	3	US-09-561-989-6	Sequence 6, Appl1
C 123	8.4	44.2	19	3	US-09-050-159-112	Sequence 112, App	C 196	8.2	43.2	19	3	US-09-422-978-4088	Sequence 4088, Ap
C 124	8.4	44.2	19	3	US-09-050-159-114	Sequence 114, App	C 197	8.2	43.2	19	3	US-09-422-978-6464	Sequence 6464, Ap
C 125	8.4	44.2	19	3	US-09-061-769A-9	Sequence 9, Appl1	C 198	8.2	43.2	19	3	US-09-422-978-7129	Sequence 7129, Ap
C 126	8.4	44.2	19	3	US-08-478-316-93	Sequence 93, Appl1	C 199	8.2	43.2	19	3	US-09-556-377A-10	Sequence 10, Appl1
C 127	8.4	44.2	19	3	US-09-338-907-395	Sequence 395, App	C 200	8.2	43.2	19	3	US-09-526-193A-135	Sequence 135, App
C 128	8.4	44.2	19	3	US-09-218-207-395	Sequence 395, App	C 201	8.2	43.2	19	3	US-09-982-212-40	Sequence 40, Appl1
C 129	8.4	44.2	19	3	US-09-534-607-20	Sequence 20, Appl1	C 202	8.2	43.2	19	3	US-09-850-351A-84	Sequence 84, Appl1
C 130	8.4	44.2	19	3	US-08-420-672-13	Sequence 13, Appl1	C 203	8.2	43.2	19	3	US-09-850-351A-122	Sequence 122, App
C 131	8.4	44.2	19	3	US-09-019-793A-93	Sequence 93, Appl1	C 204	8.2	43.2	19	3	US-09-747-391-50	Sequence 50, Appl1
C 132	8.4	44.2	19	3	US-09-345-882-107	Sequence 107, App	C 205	8.2	43.2	19	3	US-09-747-391-51	Sequence 51, Appl1
C 133	8.4	44.2	19	3	US-09-442-143A-41	Sequence 41, Appl1	C 206	8.2	43.2	19	3	US-09-747-391-130	Sequence 130, App
C 134	8.4	44.2	19	3	US-09-387-341-199	Sequence 199, App	C 207	8.2	43.2	19	3	US-09-747-391-135	Sequence 135, App
C 135	8.4	44.2	19	3	US-09-328-750A-7	Sequence 7, Appl1	C 208	8.2	43.2	19	3	US-08-401-192-3	Sequence 3, Appl1
C 136	8.4	44.2	19	3	US-09-767-013-12	Sequence 12, Appl1	C 209	8.2	43.2	19	3	US-09-696-791-175	Sequence 175, App
C 137	8.4	44.2	19	3	US-09-545-686-31	Sequence 31, Appl1	C 210	8.2	43.2	19	3	US-09-696-791-1139	Sequence 1139, Ap
C 138	8.4	44.2	19	3	US-09-475-947A-99	Sequence 99, Appl1	C 211	8.2	43.2	19	3	US-09-696-791-1431	Sequence 1431, Ap
C 139	8.4	44.2	19	3	US-09-775-947A-100	Sequence 100, App	C 212	8.2	43.2	19	3	US-09-696-791-1721	Sequence 1721, Ap
C 140	8.4	44.2	19	3	US-09-588-995A-85	Sequence 85, Appl1	C 213	8.2	43.2	19	3	US-09-696-791-1722	Sequence 1722, Ap
C 141	8.4	44.2	19	3	US-09-999-201B-20	Sequence 20, Appl1	C 214	8.2	43.2	19	3	US-09-696-791-123	Sequence 123, Ap
C 142	8.4	44.2	19	3	US-09-422-978-3958	Sequence 3958, Ap	C 215	8.2	43.2	19	3	US-09-696-791-1830	Sequence 1830, Ap
C 143	8.4	44.2	19	3	US-09-422-978-4936	Sequence 4936, Ap	C 216	8.2	43.2	19	3	US-09-696-791-2254	Sequence 2254, Ap
C 144	8.4	44.2	19	3	US-09-422-978-6771	Sequence 6771, Ap	C 217	8.2	43.2	19	3	US-09-696-791-2255	Sequence 2255, Ap
C 145	8.4	44.2	19	3	US-09-422-978-6771	Sequence 6771, Ap	C 218	8.2	43.2	19	3	US-09-696-791-2256	Sequence 2256, Ap
C 146	8.4	44.2	19	3	US-09-422-978-6995	Sequence 6995, Ap	C 219	8.2	43.2	19	3	US-09-696-791-3042	Sequence 3042, Ap
C 147	8.4	44.2	19	3	US-09-422-978-7741	Sequence 7741, Ap	C 220	8.2	43.2	19	3	US-09-696-791-3043	Sequence 3043, Ap
C 148	8.4	44.2	19	3	US-09-422-978-10354	Sequence 10354, A	C 221	8.2	43.2	19	3	US-09-696-791-3044	Sequence 3044, Ap
C 149	8.4	44.2	19	3	US-09-422-978-11231	Sequence 11231, A	C 222	8.2	43.2	19	3	US-09-071-881-11	Sequence 11, Appl1
C 150	8.4	44.2	19	3	US-09-422-978-11468	Sequence 11468, A	C 223	8.2	43.2	19	3	US-10-131-827-8825	Sequence 8825, Ap
C 151	8.4	44.2	19	3	US-09-992-072-12	Sequence 12, Appl1	C 224	8.2	43.2	19	4	US-09-977-868-40	Sequence 40, Appl1
C 152	8.4	44.2	19	3	US-09-908-500A-22	Sequence 22, Appl1	C 225	8.2	43.2	19	5	US-10-131-831-8825	Sequence 8825, Ap
C 153	8.4	44.2	19	3	US-09-747-391-16	Sequence 16, Appl1	C 226	8.2	43.2	19	5	US-10-032-495A-24	Sequence 24, Appl1
C 154	8.4	44.2	19	3	US-10-281-673A-20	Sequence 20, Appl1	C 227	8.2	43.2	19	2	US-08-127-954-23	Sequence 23, Appl1
C 155	8.4	44.2	19	3	US-08-401-192-4	Sequence 4, Appl1	C 228	8.2	43.2	19	2	US-08-152-482-5	Sequence 5, Appl1
C 156	8.4	44.2	19	3	US-09-696-791-449	Sequence 449, App	C 229	8.2	43.2	19	2	US-08-748-591-21	Sequence 21, Appl1
C 157	8.4	44.2	19	3	US-09-696-791-450	Sequence 450, App	C 230	8.2	43.2	19	2	US-08-779-341-5	Sequence 5, Appl1
C 158	8.4	44.2	19	3	US-09-696-791-451	Sequence 451, App	C 231	8.2	43.2	19	2	US-08-544-577-5	Sequence 5, Appl1
C 159	8.4	44.2	19	3	US-09-696-791-452	Sequence 452, App	C 232	8.2	43.2	19	2	US-08-833-883-17	Sequence 17, Appl1
C 160	8.4	44.2	19	3	US-09-696-791-453	Sequence 453, App	C 233	8.2	43.2	19	2	US-08-833-883-37	Sequence 37, Appl1
C 161	8.4	44.2	19	3	US-09-696-791-454	Sequence 454, App	C 234	8.2	43.2	19	2	US-08-444-481D-2	Sequence 2, Appl1
C 162	8.4	44.2	19	3	US-09-696-791-455	Sequence 455, App	C 235	8.2	43.2	19	2	US-08-833-877-17	Sequence 17, Appl1
C 163	8.4	44.2	19	3	US-09-696-791-1274	Sequence 1274, Ap	C 236	8.2	43.2	19	2	US-08-833-877-37	Sequence 37, Appl1
C 164	8.4	44.2	19	3	US-09-696-791-1275	Sequence 1275, Ap	C 237	8.2	43.2	19	2	US-08-779-342-5	Sequence 5, Appl1
C 165	8.4	44.2	19	3	US-09-696-791-1276	Sequence 1276, Ap	C 238	8.2	43.2	19	3	US-08-282-197C-3	Sequence 3, Appl1
C 166	8.4	44.2	19	3	US-09-696-791-1898	Sequence 1898, Ap	C 239	8.2	43.2	19	3	US-08-665-259-53	Sequence 53, Appl1
C 167	8.4	44.2	19	3	US-09-696-791-2116	Sequence 2116, Ap	C 240	8.2	43.2	19	3	US-09-035-190-5	Sequence 5, Appl1
C 168	8.4	44.2	19	3	US-09-696-791-3142	Sequence 3142, Ap	C 241	8.2	43.2	19	3	US-08-762-500-53	Sequence 53, Appl1
C 169	8.4	44.2	19	3	US-09-601-326-141	Sequence 141, App	C 242	8.2	43.2	19	3	US-08-895-707-19	Sequence 19, Appl1

C 243	8	42.1	19	3	US-09-191-099-13	Sequence 13, Appl	316	7.8	41.1	19	2	US-08-440-740A-43	Sequence 43, Appl
244	8	42.1	19	3	US-09-108-099-5	Sequence 5, Appl	C 317	7.8	41.1	19	2	US-08-223-355-14	Sequence 14, Appl
245	8	42.1	19	3	US-09-108-100-5	Sequence 5, Appl	C 318	7.8	41.1	19	2	US-09-097-562C-43	Sequence 3, Appl
C 246	8	42.1	19	3	US-09-407-818-10	Sequence 10, Appl	319	7.8	41.1	19	2	US-08-344-153C-43	Sequence 2, Appl
C 247	8	42.1	19	3	US-08-943-571-7	Sequence 7, Appl	C 320	7.8	41.1	19	2	US-08-696-900-2	Sequence 2, Appl
248	8	42.1	19	3	US-09-316-349-5	Sequence 4, Appl	321	7.8	41.1	19	2	US-08-955-138-39	Sequence 3, Appl
249	8	42.1	19	3	US-09-115-475-4	Sequence 4, Appl	322	7.8	41.1	19	3	US-08-982-845B-43	Sequence 4, Appl
250	8	42.1	19	3	US-09-387-341-198	Sequence 198, Appl	C 323	7.8	41.1	19	3	US-08-445-643B-18	Sequence 18, Appl
C 251	8	42.1	19	3	US-09-661-711A-23	Sequence 23, Appl	C 324	7.8	41.1	19	3	US-08-445-644C-18	Sequence 18, Appl
C 252	8	42.1	19	3	US-09-422-978-5106	Sequence 5106, Appl	325	7.8	41.1	19	3	US-08-991-525B-43	Sequence 43, Appl
C 253	8	42.1	19	3	US-09-422-978-5969	Sequence 6969, Appl	326	7.8	41.1	19	3	US-09-085-759-43	Sequence 43, Appl
C 254	8	42.1	19	3	US-09-422-978-7989	Sequence 7989, Appl	327	7.8	41.1	19	3	US-09-128-956-43	Sequence 43, Appl
C 255	8	42.1	19	3	US-09-422-978-10081	Sequence 10081, A	C 328	7.8	41.1	19	3	US-09-192-657A-10	Sequence 10, Appl
256	8	42.1	19	3	US-09-422-978-11399	Sequence 11399, A	C 329	7.8	41.1	19	3	US-09-192-657B-14	Sequence 14, Appl
257	8	42.1	19	3	US-09-650-229-5	Sequence 5, Appl	C 330	7.8	41.1	19	3	US-09-342-479-2	Sequence 2, Appl
C 258	8	42.1	19	3	US-09-982-212-34	Sequence 34, Appl	C 331	7.8	41.1	19	3	US-09-300-672-16	Sequence 16, Appl
C 259	8	42.1	19	3	US-09-261-104-12	Sequence 12, Appl	332	7.8	41.1	19	3	US-09-117-525-9	Sequence 9, Appl
C 260	8	42.1	19	3	US-09-796-081-1	Sequence 1, Appl	333	7.8	41.1	19	3	US-09-009-490A-43	Sequence 43, Appl
C 261	8	42.1	19	3	US-09-796-081-2	Sequence 2, Appl	334	7.8	41.1	19	3	US-09-468-738A-15	Sequence 15, Appl
C 262	8	42.1	19	3	US-09-630-202-5	Sequence 5, Appl	335	7.8	41.1	19	3	US-09-326-186B-98	Sequence 98, Appl
263	8	42.1	19	3	US-09-688-078-18	Sequence 18, Appl	C 336	7.8	41.1	19	3	US-09-563-826-5	Sequence 5, Appl
264	8	42.1	19	3	US-09-672-717-37	Sequence 37, Appl	C 337	7.8	41.1	19	3	US-09-504-358-46	Sequence 46, Appl
265	8	42.1	19	3	US-09-032-438C-23	Sequence 23, Appl	C 338	7.8	41.1	19	3	US-09-395-345-30	Sequence 30, Appl
C 266	8	42.1	19	3	US-08-983-605-55	Sequence 55, Appl	339	7.8	41.1	19	3	US-09-513-007-6	Sequence 6, Appl
C 267	8	42.1	19	3	US-09-696-791-526	Sequence 526, Appl	340	7.8	41.1	19	3	US-09-940-019-15	Sequence 15, Appl
268	8	42.1	19	3	US-09-696-791-1277	Sequence 1277, Appl	341	7.8	41.1	19	3	US-09-555-889A-5	Sequence 5, Appl
269	8	42.1	19	3	US-09-696-791-1278	Sequence 1278, Appl	C 342	7.8	41.1	19	3	US-09-434-408-16	Sequence 16, Appl
270	8	42.1	19	3	US-09-696-791-1279	Sequence 1281, Appl	C 343	7.8	41.1	19	3	US-08-044-857B-18	Sequence 18, Appl
271	8	42.1	19	3	US-09-696-791-2181	Sequence 2181, Appl	C 344	7.8	41.1	19	3	US-09-954-314-46	Sequence 46, Appl
272	8	42.1	19	3	US-09-696-791-2182	Sequence 2182, Appl	345	7.8	41.1	19	3	US-09-940-037A-15	Sequence 15, Appl
273	8	42.1	19	3	US-09-696-791-2680	Sequence 2680, Appl	346	7.8	41.1	19	3	US-09-540-257B-22	Sequence 22, Appl
274	8	42.1	19	3	US-09-696-791-2681	Sequence 2681, Appl	347	7.8	41.1	19	3	US-09-649-747-53	Sequence 53, Appl
275	8	42.1	19	3	US-09-696-791-2682	Sequence 2682, Appl	C 348	7.8	41.1	19	3	US-09-422-978-395A	Sequence 395A, Appl
276	8	42.1	19	3	US-09-696-791-3148	Sequence 3148, Appl	C 349	7.8	41.1	19	3	US-09-422-978-4067	Sequence 4067, Appl
277	8	42.1	19	3	US-09-696-791-3149	Sequence 3149, Appl	C 350	7.8	41.1	19	3	US-09-422-978-4813	Sequence 4813, Appl
278	8	42.1	19	3	US-09-696-791-3150	Sequence 3150, Appl	C 351	7.8	41.1	19	3	US-09-422-978-4832	Sequence 4832, Appl
279	8	42.1	19	3	US-09-696-791-3151	Sequence 3151, Appl	352	7.8	41.1	19	3	US-09-422-978-5785	Sequence 5785, Appl
280	8	42.1	19	3	US-09-696-791-3152	Sequence 3152, Appl	C 353	7.8	41.1	19	3	US-09-422-978-6717	Sequence 6717, Appl
281	8	42.1	19	3	US-09-696-791-3508	Sequence 3508, Appl	C 354	7.8	41.1	19	3	US-09-422-978-8141	Sequence 8141, Appl
C 282	8	42.1	19	3	US-07-720-435A-8	Sequence 8, Appl	C 355	7.8	41.1	19	3	US-09-422-978-8368	Sequence 8368, Appl
C 283	8	42.1	19	3	US-09-720-435A-13	Sequence 13, Appl	356	7.8	41.1	19	3	US-09-422-978-8368	Sequence 10583, A
C 284	8	42.1	19	3	US-09-269-446D-74	Sequence 74, Appl	C 357	7.8	41.1	19	3	US-09-422-978-10141	Sequence 10141, A
285	8	42.1	19	3	US-09-479-040-18	Sequence 18, Appl	C 358	7.8	41.1	19	3	US-09-614-614-14	Sequence 10, Appl
286	8	42.1	19	3	US-09-984-037-3	Sequence 3, Appl	C 359	7.8	41.1	19	3	US-09-356-806-100	Sequence 100, Appl
287	8	42.1	19	3	US-09-959-716-14	Sequence 14, Appl	C 360	7.8	41.1	19	3	US-09-356-806-101	Sequence 101, Appl
C 288	8	42.1	19	3	US-09-814-252-10	Sequence 10, Appl	361	7.8	41.1	19	3	US-09-434-840-28	Sequence 28, Appl
C 289	8	42.1	19	3	US-09-814-257-10	Sequence 10, Appl	C 362	7.8	41.1	19	3	US-09-831-642-10	Sequence 10, Appl
C 290	8	42.1	19	4	US-09-310-844C-34	Sequence 34, Appl	C 363	7.8	41.1	19	3	US-09-747-391-241	Sequence 241, Appl
C 291	8	42.1	19	4	US-09-977-668-34	Sequence 34, Appl	C 364	7.8	41.1	19	3	US-09-672-717-28	Sequence 28, Appl
292	8	42.1	19	5	US-10-032-495A-6	Sequence 6, Appl	C 365	7.8	41.1	19	3	US-09-303-013-4	Sequence 4, Appl
293	8	42.1	19	5	US-10-032-495A-14	Sequence 14, Appl	C 366	7.8	41.1	19	3	US-09-533-149-5	Sequence 5, Appl
294	8	42.1	19	5	US-10-032-495A-19	Sequence 19, Appl	367	7.8	41.1	19	3	US-09-634-960A-28	Sequence 28, Appl
295	8	42.1	19	7	PCT-US94-13041-5	Sequence 5, Appl	368	7.8	41.1	19	3	US-09-634-960A-29	Sequence 29, Appl
296	8	42.1	19	7	PCT-US95-02865-5	Sequence 5, Appl	369	7.8	41.1	19	3	US-09-696-791-176	Sequence 176, Appl
297	8	42.1	19	10	5217865-9	Patent No. 5217865	C 370	7.8	41.1	19	3	US-09-696-791-401	Sequence 439, Appl
298	8	42.1	19	10	5475095-9	Patent No. 5475095	C 371	7.8	41.1	19	3	US-09-696-791-801	Sequence 801, Appl
299	7.8	41.1	19	2	US-08-063-167A-43	Sequence 43, Appl	C 372	7.8	41.1	19	3	US-09-696-791-802	Sequence 802, Appl
300	7.8	41.1	19	2	US-08-315-695-13	Sequence 13, Appl	373	7.8	41.1	19	3	US-09-696-791-1854	Sequence 1854, Appl
301	7.8	41.1	19	2	US-08-007-997A-43	Sequence 43, Appl	374	7.8	41.1	19	3	US-09-696-791-1855	Sequence 1855, Appl
302	7.8	41.1	19	2	US-08-411-020-36	Sequence 36, Appl	C 375	7.8	41.1	19	3	US-09-696-791-1902	Sequence 1902, Appl
303	7.8	41.1	19	2	US-08-411-020-56	Sequence 56, Appl	C 376	7.8	41.1	19	3	US-09-696-791-2005	Sequence 2005, Appl
304	7.8	41.1	19	2	US-08-411-020-58	Sequence 58, Appl	C 377	7.8	41.1	19	3	US-09-696-791-2154	Sequence 2154, Appl
305	7.8	41.1	19	2	US-08-446-530-3	Sequence 3, Appl	C 378	7.8	41.1	19	3	US-09-696-791-2154	Sequence 2155, Appl
306	7.8	41.1	19	2	US-08-832-883-28	Sequence 28, Appl	C 379	7.8	41.1	19	3	US-09-696-791-2155	Sequence 2155, Appl
307	7.8	41.1	19	2	US-08-410-779B-58	Sequence 58, Appl	380	7.8	41.1	19	3	US-09-696-791-2247	Sequence 2247, Appl
308	7.8	41.1	19	2	US-08-410-779B-58	Sequence 68, Appl	381	7.8	41.1	19	3	US-09-696-791-2476	Sequence 2476, Appl
309	7.8	41.1	19	2	US-08-410-779B-84	Sequence 84, Appl	382	7.8	41.1	19	3	US-09-696-791-2478	Sequence 2478, Appl
310	7.8	41.1	19	2	US-08-410-779B-100	Sequence 100, Appl	C 383	7.8	41.1	19	3	US-09-696-791-2581	Sequence 2581, Appl
311	7.8	41.1	19	2	US-08-410-779B-122	Sequence 122, Appl	C 384	7.8	41.1	19	3	US-09-696-791-2582	Sequence 2582, Appl
312	7.8	41.1	19	2	US-08-410-779B-130	Sequence 130, Appl	C 385	7.8	41.1	19	3	US-09-696-791-2583	Sequence 2583, Appl
C 313	7.8	41.1	19	2	US-08-331-389A-10	Sequence 10, Appl	C 386	7.8	41.1	19	3	US-09-696-791-2584	Sequence 2584, Appl
C 314	7.8	41.1	19	2	US-08-331-389A-14	Sequence 14, Appl	C 387	7.8	41.1	19	3	US-09-696-791-3075	Sequence 3075, Appl
315	7.8	41.1	19	2	US-08-832-877-28	Sequence 28, Appl	C 388	7.8	41.1	19	3	US-09-696-791-3143	Sequence 3143, Appl

c 389	7.8	41.1	19	3	US-09-696-791-3326	Sequence 3326, Ap	462	7.6	40.0	19	3	US-09-696-791-403	Sequence 403, App
c 390	7.8	41.1	19	3	US-09-696-791-3744	Sequence 3744, Ap	c 463	7.6	40.0	19	3	US-09-696-791-774	Sequence 774, App
c 391	7.8	41.1	19	3	US-09-696-791-3745	Sequence 3745, Ap	c 464	7.6	40.0	19	3	US-09-696-791-775	Sequence 775, App
c 392	7.8	41.1	19	3	US-09-696-791-3746	Sequence 3746, Ap	c 465	7.6	40.0	19	3	US-09-696-791-1676	Sequence 1676, Ap
c 393	7.8	41.1	19	3	US-09-696-791-3747	Sequence 3747, Ap	c 466	7.6	40.0	19	3	US-09-696-791-1677	Sequence 1677, Ap
c 394	7.8	41.1	19	3	US-09-696-791-3748	Sequence 3748, Ap	c 467	7.6	40.0	19	3	US-09-696-791-1678	Sequence 1678, Ap
c 395	7.8	41.1	19	3	US-10-730-562-46	Sequence 46, Appl	c 468	7.6	40.0	19	3	US-09-696-791-1828	Sequence 2033, Ap
c 396	7.8	41.1	19	3	US-10-071-411A-17	Sequence 17, Appl	c 469	7.6	40.0	19	3	US-09-696-791-2013	Sequence 2588, Ap
c 397	7.8	41.1	19	3	US-09-627-1658-18	Sequence 18, Appl	c 470	7.6	40.0	19	3	US-09-696-791-2588	Sequence 3920, Ap
c 398	7.8	41.1	19	3	US-09-982-262C-43	Sequence 43, Appl	c 471	7.6	40.0	19	3	US-09-696-791-3960	Sequence 3968, Ap
c 399	7.8	41.1	19	3	US-09-647-501-24	Sequence 24, Appl	c 472	7.6	40.0	19	3	US-09-696-791-3969	Sequence 3969, Ap
c 400	7.8	41.1	19	3	US-09-882-434A-6	Sequence 6, Appl1	c 473	7.6	40.0	19	3	US-09-720-435A-9	Sequence 9, Appl1
c 401	7.8	41.1	19	3	US-10-199-945A-18	Sequence 18, Appl	c 474	7.6	40.0	19	3	US-09-719-737-14	Sequence 14, Appl1
c 402	7.8	41.1	19	3	US-09-830-902-70	Sequence 70, Appl	c 475	7.6	40.0	19	3	US-09-850-514-1	Sequence 1, Appl1
c 403	7.8	41.1	19	3	US-09-832-424-10	Sequence 10, Appl	c 476	7.6	40.0	19	3	US-09-502-498C-133	Sequence 133, App
c 404	7.8	41.1	19	3	US-09-970-532-6	Sequence 6, Appl1	c 477	7.6	40.0	19	3	US-09-502-498C-134	Sequence 134, App
c 405	7.8	41.1	19	3	US-09-935-338-183	Sequence 183, App	c 478	7.6	40.0	19	3	US-09-865-807-33	Sequence 33, Appl
c 406	7.8	41.1	19	3	US-09-935-338-200	Sequence 200, App	c 479	7.6	40.0	19	3	US-09-735-271-1440	Sequence 1440, Ap
c 407	7.8	41.1	19	4	US-09-855-309-15	Sequence 15, Appl	c 480	7.6	40.0	19	3	US-09-807-201-23	Sequence 23, Appl
c 408	7.8	41.1	19	5	US-09-543-679A-1394	Sequence 1394, Ap	c 481	7.6	40.0	19	3	US-09-502-424C-133	Sequence 133, App
c 409	7.8	41.1	19	7	PCT-US93-08101-43	Sequence 43, Appl	c 482	7.6	40.0	19	3	US-09-502-424C-134	Sequence 134, App
c 410	7.8	41.1	19	7	PCT-US94-03437-18	Sequence 18, Appl	c 483	7.6	40.0	19	3	US-09-508-377-57	Sequence 57, Appl
c 411	7.8	41.1	19	7	PCT-US95-04477-58	Sequence 58, Appl	c 484	7.6	40.0	19	4	US-10-270-861-29	Sequence 29, Appl
c 412	7.8	41.1	19	7	PCT-US95-04477-68	Sequence 68, Appl	c 485	7.6	40.0	19	4	US-09-977-868-3314	Sequence 33, Appl
c 413	7.8	41.1	19	7	PCT-US95-04477-84	Sequence 84, Appl	c 486	7.6	40.0	19	5	US-09-947-868-3314	Sequence 1514, Ap
c 414	7.8	41.1	19	7	PCT-US95-04477-100	Sequence 100, App	c 487	7.6	40.0	19	7	PCT-US95-05265-38	Sequence 38, Appl
c 415	7.8	41.1	19	7	PCT-US95-04477-122	Sequence 122, App	c 488	7.4	38.9	19	2	US-08-242-664-11	Sequence 11, Appl
c 416	7.8	41.1	19	7	PCT-US95-04477-130	Sequence 130, App	c 489	7.4	38.9	19	2	US-08-223-177A-78	Sequence 78, Appl
c 417	7.6	40.0	19	2	US-08-235-503B-38	Sequence 38, Appl	c 490	7.4	38.9	19	2	US-08-199-152-1	Sequence 1, Appl1
c 418	7.6	40.0	19	2	US-08-105-168B-12	Sequence 12, Appl	c 491	7.4	38.9	19	2	US-08-266-414-9	Sequence 9, Appl1
c 419	7.6	40.0	19	2	US-08-358-782D-3	Sequence 3, Appl1	c 492	7.4	38.9	19	2	US-08-631-200-47	Sequence 47, Appl
c 420	7.6	40.0	19	2	US-08-445-289B-14	Sequence 14, Appl	c 493	7.4	38.9	19	2	US-08-450-257-66	Sequence 66, Appl
c 421	7.6	40.0	19	2	US-08-564-860A-3	Sequence 3, Appl1	c 494	7.4	38.9	19	2	US-08-450-257-67	Sequence 67, Appl
c 422	7.6	40.0	19	2	US-08-698-948-12	Sequence 12, Appl	c 495	7.4	38.9	19	2	US-08-484-138-11	Sequence 11, Appl
c 423	7.6	40.0	19	2	US-08-117-952-98	Sequence 98, Appl	c 496	7.4	38.9	19	2	US-08-450-246-66	Sequence 66, Appl
c 424	7.6	40.0	19	2	US-08-764-527A-3	Sequence 3, Appl1	c 497	7.4	38.9	19	2	US-08-450-246-67	Sequence 67, Appl
c 425	7.6	40.0	19	2	US-08-910-367-7	Sequence 7, Appl1	c 498	7.4	38.9	19	2	US-08-450-098-66	Sequence 66, Appl
c 426	7.6	40.0	19	2	US-08-519-547A-2	Sequence 2, Appl1	c 499	7.4	38.9	19	2	US-08-450-098-67	Sequence 67, Appl
c 427	7.6	40.0	19	2	US-09-013-114-3	Sequence 3, Appl1	c 500	7.4	38.9	19	2	US-08-229-145-23	Sequence 23, Appl
c 428	7.6	40.0	19	3	US-09-133-934-10	Sequence 10, Appl	c 501	7.4	38.9	19	2	US-08-462-305-18	Sequence 18, Appl
c 429	7.6	40.0	19	3	US-09-014-416-54	Sequence 54, Appl	c 502	7.4	38.9	19	2	US-08-171-718-82	Sequence 82, Appl
c 430	7.6	40.0	19	3	US-09-050-159-27	Sequence 27, Appl	c 503	7.4	38.9	19	2	US-08-582-539-29	Sequence 29, Appl
c 431	7.6	40.0	19	3	US-09-288-586-7	Sequence 7, Appl1	c 504	7.4	38.9	19	2	US-08-451-233-66	Sequence 66, Appl
c 432	7.6	40.0	19	3	US-08-836-261A-40	Sequence 40, Appl	c 505	7.4	38.9	19	2	US-08-451-233-67	Sequence 67, Appl
c 433	7.6	40.0	19	3	US-09-290-577-33	Sequence 33, Appl	c 506	7.4	38.9	19	2	US-08-450-236-66	Sequence 66, Appl
c 434	7.6	40.0	19	3	US-09-338-907-535	Sequence 535, App	c 507	7.4	38.9	19	2	US-08-450-236-67	Sequence 67, Appl
c 435	7.6	40.0	19	3	US-09-297-535-22	Sequence 22, Appl	c 508	7.4	38.9	19	2	US-08-912-976-28	Sequence 28, Appl
c 436	7.6	40.0	19	3	US-09-290-452-32	Sequence 33, Appl	c 509	7.4	38.9	19	2	US-08-812-779B-76	Sequence 76, Appl
c 437	7.6	40.0	19	3	US-09-290-338-33	Sequence 33, Appl	c 510	7.4	38.9	19	2	US-08-410-779B-92	Sequence 92, Appl
c 438	7.6	40.0	19	3	US-09-218-207-535	Sequence 535, App	c 511	7.4	38.9	19	2	US-08-829-553-47	Sequence 47, Appl
c 439	7.6	40.0	19	3	US-09-342-681C-81	Sequence 81, Appl	c 512	7.4	38.9	19	2	US-08-267-803B-71	Sequence 71, Appl
c 440	7.6	40.0	19	3	US-09-531-000-40	Sequence 40, Appl	c 513	7.4	38.9	19	2	US-08-331-389A-22	Sequence 22, Appl
c 441	7.6	40.0	19	3	US-09-291-129-6	Sequence 6, Appl1	c 514	7.4	38.9	19	2	US-08-633-501-12	Sequence 12, Appl
c 442	7.6	40.0	19	3	US-09-290-000-33	Sequence 33, Appl	c 515	7.4	38.9	19	2	US-08-633-501-106	Sequence 106, App
c 443	7.6	40.0	19	3	US-09-422-978-4222	Sequence 4222, Ap	c 516	7.4	38.9	19	2	US-08-757-653-11	Sequence 118, Appl
c 444	7.6	40.0	19	3	US-09-422-978-5276	Sequence 5276, Ap	c 517	7.4	38.9	19	2	US-08-607-384A-26	Sequence 26, Appl
c 445	7.6	40.0	19	3	US-09-422-978-6102	Sequence 6102, Ap	c 518	7.4	38.9	19	2	US-08-593-345B-4	Sequence 4, Appl1
c 446	7.6	40.0	19	3	US-09-422-978-6782	Sequence 6782, Ap	c 519	7.4	38.9	19	2	US-08-922-267A-47	Sequence 47, Appl1
c 447	7.6	40.0	19	3	US-09-422-978-7450	Sequence 7450, Ap	c 520	7.4	38.9	19	2	US-08-173-489C-28	Sequence 28, Appl
c 448	7.6	40.0	19	3	US-09-422-978-8701	Sequence 8701, Ap	c 521	7.4	38.9	19	2	US-08-882-083-12	Sequence 12, Appl
c 449	7.6	40.0	19	3	US-09-422-978-9149	Sequence 9149, Ap	c 522	7.4	38.9	19	2	US-08-936-707A-47	Sequence 47, Appl
c 450	7.6	40.0	19	3	US-09-422-978-9763	Sequence 9763, Ap	c 523	7.4	38.9	19	2	US-08-613-417A-18	Sequence 18, Appl
c 451	7.6	40.0	19	3	US-09-422-978-10748	Sequence 10748, Ap	c 524	7.4	38.9	19	2	US-08-936-706A-47	Sequence 47, Appl
c 452	7.6	40.0	19	3	US-09-422-978-11405	Sequence 11405, A	c 525	7.4	38.9	19	2	US-08-690-495-33	Sequence 33, Appl
c 453	7.6	40.0	19	3	US-09-954-594A-33	Sequence 33, Appl	c 526	7.4	38.9	19	2	US-08-532-777A-2	Sequence 2, Appl1
c 454	7.6	40.0	19	3	US-09-982-212-33	Sequence 33, Appl	c 527	7.4	38.9	19	2	US-08-587-332B-4	Sequence 4, Appl1
c 455	7.6	40.0	19	3	US-09-261-104-11	Sequence 11, Appl	c 528	7.4	38.9	19	2	US-08-558-107-12	Sequence 12, Appl
c 456	7.6	40.0	19	3	US-09-747-391-105	Sequence 105, App	c 529	7.4	38.9	19	2	US-08-690-494-33	Sequence 33, Appl
c 457	7.6	40.0	19	3	US-09-672-717-46	Sequence 46, Appl	c 530	7.4	38.9	19	2	US-08-475-634D-12	Sequence 12, Appl
c 458	7.6	40.0	19	3	US-09-672-717-120	Sequence 120, App	c 531	7.4	38.9	19	2	US-08-756-386-54	Sequence 54, Appl
c 459	7.6	40.0	19	3	US-08-401-192-4	Sequence 4, Appl1	c 532	7.4	38.9	19	2	US-08-743-637B-67	Sequence 67, Appl
c 460	7.6	40.0	19	3	US-09-763-590-23	Sequence 23, Appl	c 533	7.4	38.9	19	2	US-08-823-516-43	Sequence 43, Appl
c 461	7.6	40.0	19	3	US-09-696-791-219	Sequence 219, App	c 534	7.4	38.9	19	3	US-08-526-840B-67	Sequence 67, Appl



535	7.4	38.9	19	3	US-08-682-853A-54	Sequence 54, App1	608	7.4	38.9	19	3	US-09-422-978-4894	Sequence 4894, Ap
C 536	7.4	38.9	19	3	US-08-594-452-18	Sequence 18, App1	C 609	7.4	38.9	19	3	US-09-422-978-4919	Sequence 4919, Ap
C 537	7.4	38.9	19	3	US-08-578-686C-17	Sequence 17, App1	C 610	7.4	38.9	19	3	US-09-422-978-5133	Sequence 5133, Ap
538	7.4	38.9	19	3	US-09-044-946-12	Sequence 12, App1	611	7.4	38.9	19	3	US-09-422-978-5350	Sequence 5350, Ap
539	7.4	38.9	19	3	US-09-044-946-106	Sequence 106, App1	C 612	7.4	38.9	19	3	US-09-422-978-5491	Sequence 5491, Ap
C 540	7.4	38.9	19	3	US-08-281-203-13	Sequence 13, App1	C 613	7.4	38.9	19	3	US-09-422-978-5595	Sequence 5595, Ap
C 541	7.4	38.9	19	3	US-09-248-203-47	Sequence 47, App1	C 614	7.4	38.9	19	3	US-09-422-978-6132	Sequence 6132, Ap
C 542	7.4	38.9	19	3	US-08-485-942A-39	Sequence 39, App1	C 615	7.4	38.9	19	3	US-09-422-978-6518	Sequence 6518, Ap
C 543	7.4	38.9	19	3	US-09-094-405-20	Sequence 20, App1	C 616	7.4	38.9	19	3	US-09-422-978-6991	Sequence 6991, Ap
544	7.4	38.9	19	3	US-08-478-087-82	Sequence 82, App1	C 617	7.4	38.9	19	3	US-09-422-978-7108	Sequence 7108, Ap
545	7.4	38.9	19	3	US-08-777-266A-98	Sequence 98, App1	C 618	7.4	38.9	19	3	US-09-422-978-7342	Sequence 7342, Ap
C 546	7.4	38.9	19	3	US-08-660-645A-47	Sequence 47, App1	C 619	7.4	38.9	19	3	US-09-422-978-7368	Sequence 7368, Ap
547	7.4	38.9	19	3	US-08-759-038-54	Sequence 54, App1	C 620	7.4	38.9	19	3	US-09-422-978-7861	Sequence 7861, Ap
548	7.4	38.9	19	3	US-08-855-372B-84	Sequence 84, App1	C 621	7.4	38.9	19	3	US-09-422-978-8354	Sequence 8354, Ap
549	7.4	38.9	19	3	US-08-758-314-54	Sequence 54, App1	C 622	7.4	38.9	19	3	US-09-422-978-8928	Sequence 8928, Ap
550	7.4	38.9	19	3	US-09-058-489-52	Sequence 52, App1	C 623	7.4	38.9	19	3	US-09-422-978-9226	Sequence 9226, Ap
C 551	7.4	38.9	19	3	US-09-258-408-18	Sequence 18, App1	C 624	7.4	38.9	19	3	US-09-422-978-9228	Sequence 9228, A
552	7.4	38.9	19	3	US-09-044-908-12	Sequence 12, App1	C 625	7.4	38.9	19	3	US-09-308-825A-54	Sequence 54, App1
553	7.4	38.9	19	3	US-09-044-908-106	Sequence 106, App1	C 626	7.4	38.9	19	3	US-09-399-217-33	Sequence 33, App1
C 554	7.4	38.9	19	3	US-09-488-214A-39	Sequence 39, App1	C 627	7.4	38.9	19	3	US-09-356-806-49	Sequence 49, App1
C 555	7.4	38.9	19	3	US-08-488-208A-39	Sequence 39, App1	C 628	7.4	38.9	19	3	US-09-356-806-71	Sequence 71, App1
C 556	7.4	38.9	19	3	US-09-196-132-18	Sequence 18, App1	C 629	7.4	38.9	19	3	US-09-728-265-33	Sequence 33, App1
C 557	7.4	38.9	19	3	US-09-243-539-12	Sequence 12, App1	C 630	7.4	38.9	19	3	US-09-814-986-47	Sequence 47, App1
C 558	7.4	38.9	19	3	US-09-144-112-17	Sequence 17, App1	C 631	7.4	38.9	19	3	US-09-547-267-47	Sequence 47, App1
C 559	7.4	38.9	19	3	US-09-192-657A-22	Sequence 22, App1	C 632	7.4	38.9	19	3	US-09-582-212-32	Sequence 32, App1
C 560	7.4	38.9	19	3	US-09-378-528-4	Sequence 4, App1	C 633	7.4	38.9	19	3	US-08-210-143C-22	Sequence 22, App1
561	7.4	38.9	19	3	US-09-406-071-47	Sequence 47, App1	C 634	7.4	38.9	19	3	US-09-456-122B-2	Sequence 2, App1
C 562	7.4	38.9	19	3	US-09-546-969-47	Sequence 47, App1	C 635	7.4	38.9	19	3	US-09-747-391-11	Sequence 11, App1
C 563	7.4	38.9	19	3	US-08-962-690-37	Sequence 37, App1	C 636	7.4	38.9	19	3	US-09-495-714C-90	Sequence 90, App1
C 564	7.4	38.9	19	3	US-09-262-773-22	Sequence 22, App1	C 637	7.4	38.9	19	3	US-09-655-778A-118	Sequence 118, App
565	7.4	38.9	19	3	US-09-385-377-9	Sequence 9, App1	C 638	7.4	38.9	19	3	US-09-672-717-43	Sequence 43, App1
C 566	7.4	38.9	19	3	US-09-038-637-82	Sequence 82, App1	C 639	7.4	38.9	19	3	US-09-672-717-132	Sequence 132, App
C 567	7.4	38.9	19	3	US-09-038-637-147	Sequence 147, App1	C 640	7.4	38.9	19	3	US-09-672-717-172	Sequence 172, App
C 568	7.4	38.9	19	3	US-09-052-333A-50	Sequence 50, App1	C 641	7.4	38.9	19	3	US-09-672-717-181	Sequence 181, App
570	7.4	38.9	19	3	US-09-338-907-419	Sequence 419, App1	C 642	7.4	38.9	19	3	US-09-920-923B-26	Sequence 26, App1
571	7.4	38.9	19	3	US-09-338-907-431	Sequence 431, App1	C 643	7.4	38.9	19	3	US-09-940-244-43	Sequence 43, App1
C 572	7.4	38.9	19	3	US-08-803-346-51	Sequence 51, App1	C 644	7.4	38.9	19	3	US-09-333-145-54	Sequence 54, App1
C 573	7.4	38.9	19	3	US-08-803-346-51	Sequence 51, App1	C 645	7.4	38.9	19	3	US-08-983-605-120	Sequence 120, App
C 574	7.4	38.9	19	3	US-09-439-616-3	Sequence 3, App1	C 646	7.4	38.9	19	3	US-08-983-605-120	Sequence 120, App
C 575	7.4	38.9	19	3	US-08-483-211A-39	Sequence 39, App1	C 647	7.4	38.9	19	3	US-09-696-791-35	Sequence 35, App1
C 576	7.4	38.9	19	3	US-08-235-403-67	Sequence 67, App1	C 648	7.4	38.9	19	3	US-09-696-791-155	Sequence 55, App1
C 577	7.4	38.9	19	3	US-08-235-403-67	Sequence 67, App1	C 649	7.4	38.9	19	3	US-09-696-791-266	Sequence 266, App
C 578	7.4	38.9	19	3	US-08-895-981-18	Sequence 18, App1	C 650	7.4	38.9	19	3	US-09-696-791-267	Sequence 267, App
C 579	7.4	38.9	19	3	US-09-564-805-105	Sequence 105, App1	C 651	7.4	38.9	19	3	US-09-696-791-308	Sequence 308, App
581	7.4	38.9	19	3	US-09-218-207-419	Sequence 419, App1	C 652	7.4	38.9	19	3	US-09-696-791-438	Sequence 438, App
C 582	7.4	38.9	19	3	US-09-218-207-431	Sequence 431, App1	C 653	7.4	38.9	19	3	US-09-696-791-546	Sequence 546, App
C 583	7.4	38.9	19	3	US-08-337-120A-20	Sequence 20, App1	C 654	7.4	38.9	19	3	US-09-696-791-705	Sequence 705, App
C 584	7.4	38.9	19	3	US-08-337-120A-20	Sequence 20, App1	C 655	7.4	38.9	19	3	US-09-696-791-706	Sequence 706, App
C 585	7.4	38.9	19	3	US-08-468-223A-39	Sequence 39, App1	C 656	7.4	38.9	19	3	US-09-696-791-707	Sequence 707, App
586	7.4	38.9	19	3	US-08-520-946-118	Sequence 118, App1	C 657	7.4	38.9	19	3	US-09-696-791-1288	Sequence 1288, App
C 587	7.4	38.9	19	3	US-08-294-312B-24	Sequence 24, App1	C 658	7.4	38.9	19	3	US-09-696-791-1338	Sequence 1338, App
C 588	7.4	38.9	19	3	US-08-458-831A-39	Sequence 39, App1	C 659	7.4	38.9	19	3	US-09-696-791-1671	Sequence 1671, Ap
C 589	7.4	38.9	19	3	US-09-531-000-7	Sequence 7, App1	C 660	7.4	38.9	19	3	US-09-696-791-1673	Sequence 1673, Ap
592	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 661	7.4	38.9	19	3	US-09-696-791-1943	Sequence 1943, Ap
C 593	7.4	38.9	19	3	US-09-531-000-8	Sequence 8, App1	C 662	7.4	38.9	19	3	US-09-696-791-2216	Sequence 2216, Ap
C 594	7.4	38.9	19	3	US-08-187-757D-22	Sequence 22, App1	C 663	7.4	38.9	19	3	US-09-696-791-2217	Sequence 2217, Ap
C 595	7.4	38.9	19	3	US-09-221-013A-15	Sequence 15, App1	C 664	7.4	38.9	19	3	US-09-696-791-2218	Sequence 2218, Ap
C 596	7.4	38.9	19	3	US-09-221-013A-25	Sequence 25, App1	C 665	7.4	38.9	19	3	US-09-696-791-2219	Sequence 2219, Ap
C 597	7.4	38.9	19	3	US-09-588-995A-97	Sequence 97, App1	C 666	7.4	38.9	19	3	US-09-696-791-2334	Sequence 2334, Ap
C 598	7.4	38.9	19	3	US-09-642-952-2	Sequence 2, App1	C 667	7.4	38.9	19	3	US-09-696-791-2335	Sequence 2335, Ap
C 599	7.4	38.9	19	3	US-09-386-816C-10	Sequence 10, App1	C 668	7.4	38.9	19	3	US-09-696-791-2532	Sequence 2532, Ap
C 600	7.4	38.9	19	3	US-09-386-816C-12	Sequence 12, App1	C 669	7.4	38.9	19	3	US-09-696-791-2852	Sequence 2852, Ap
C 601	7.4	38.9	19	3	US-09-206-551-9	Sequence 9, App1	C 670	7.4	38.9	19	3	US-09-696-791-3076	Sequence 3076, Ap
603	7.4	38.9	19	3	US-09-422-978-4634	Sequence 4634, Ap	C 671	7.4	38.9	19	3	US-09-696-791-3106	Sequence 3106, Ap
C 604	7.4	38.9	19	3	US-09-422-978-4712	Sequence 4712, Ap	C 672	7.4	38.9	19	3	US-09-696-791-3349	Sequence 3349, Ap
C 605	7.4	38.9	19	3			C 673	7.4	38.9	19	3		
C 606	7.4	38.9	19	3			C 674	7.4	38.9	19	3		
607	7.4	38.9	19	3			C 675	7.4	38.9	19	3		

681	7.4	38.9	19	3	US-09-696-791-3414	Sequence 3414, Ap	c 754	7.2	37.9	19	2	US-08-549-045-12	Sequence 12, Appl
682	7.4	38.9	19	3	US-09-696-791-3415	Sequence 3415, Ap	c 755	7.2	37.9	19	2	US-08-650-125-8	Sequence 8, Appl
683	7.4	38.9	19	3	US-09-696-791-3416	Sequence 3416, Ap	c 756	7.2	37.9	19	2	US-08-795-006A-8	Sequence 8, Appl
684	7.4	38.9	19	3	US-09-696-791-3417	Sequence 3417, Ap	c 757	7.2	37.9	19	2	US-08-270-581-5	Sequence 5, Appl
685	7.4	38.9	19	3	US-09-696-791-3418	Sequence 3418, Ap	c 758	7.2	37.9	19	2	US-08-485-688-44	Sequence 44, Appl
c 686	7.4	38.9	19	3	US-09-696-791-3449	Sequence 3449, Ap	c 759	7.2	37.9	19	2	US-08-450-905B-155	Sequence 155, App
687	7.4	38.9	19	3	US-09-696-791-3488	Sequence 3488, Ap	c 760	7.2	37.9	19	2	US-08-716-718-7	Sequence 44, Appl
688	7.4	38.9	19	3	US-09-696-791-3489	Sequence 3489, Ap	c 761	7.2	37.9	19	2	US-08-476-021A-44	Sequence 44, Appl
689	7.4	38.9	19	3	US-09-696-791-3490	Sequence 3490, Ap	c 762	7.2	37.9	19	2	US-08-743-200-25	Sequence 25, Appl
690	7.4	38.9	19	3	US-09-696-791-3491	Sequence 3491, Ap	c 763	7.2	37.9	19	2	US-08-914-512-12	Sequence 12, Appl
691	7.4	38.9	19	3	US-09-696-791-3509	Sequence 3509, Ap	c 764	7.2	37.9	19	2	US-08-478-608B-44	Sequence 44, Appl
692	7.4	38.9	19	3	US-09-696-791-3510	Sequence 3510, Ap	c 765	7.2	37.9	19	2	US-08-282-197C-19	Sequence 19, Appl
693	7.4	38.9	19	3	US-09-696-791-3511	Sequence 3511, Ap	c 766	7.2	37.9	19	2	US-08-690-495-36	Sequence 36, Appl
694	7.4	38.9	19	3	US-09-696-791-3512	Sequence 3512, Ap	c 767	7.2	37.9	19	2	US-08-912-129A-83	Sequence 83, Appl
c 695	7.4	38.9	19	3	US-09-696-791-3583	Sequence 3583, Ap	c 768	7.2	37.9	19	2	US-08-912-129A-83	Sequence 83, Appl
696	7.4	38.9	19	3	US-09-696-791-3743	Sequence 3743, Ap	c 769	7.2	37.9	19	2	US-08-690-494-36	Sequence 36, Appl
697	7.4	38.9	19	3	US-09-696-791-3876	Sequence 3876, Ap	c 770	7.2	37.9	19	2	US-08-849-021-75	Sequence 75, Appl
698	7.4	38.9	19	3	US-09-696-791-3877	Sequence 3877, Ap	c 771	7.2	37.9	19	2	US-09-212-771-3	Sequence 3, Appl
699	7.4	38.9	19	3	US-09-696-791-3878	Sequence 3878, Ap	c 772	7.2	37.9	19	2	US-08-690-184-2	Sequence 2, Appl
700	7.4	38.9	19	3	US-09-696-791-3879	Sequence 3879, Ap	c 773	7.2	37.9	19	3	US-08-485-942A-81	Sequence 81, Appl
c 701	7.4	38.9	19	3	US-09-696-791-3921	Sequence 3921, Ap	c 774	7.2	37.9	19	3	US-07-982-759F-155	Sequence 155, App
c 702	7.4	38.9	19	3	US-09-835-370-19	Sequence 19, Appl	c 775	7.2	37.9	19	3	US-08-881-784-28	Sequence 28, Appl
703	7.4	38.9	19	3	US-09-404-448-3	Sequence 3, Appl	c 776	7.2	37.9	19	3	US-08-787-091-10	Sequence 10, Appl
704	7.4	38.9	19	3	US-10-320-176-10	Sequence 10, Appl	c 777	7.2	37.9	19	3	US-08-488-214A-81	Sequence 81, Appl
705	7.4	38.9	19	3	US-10-320-176-12	Sequence 12, Appl	c 778	7.2	37.9	19	3	US-08-488-208A-81	Sequence 81, Appl
706	7.4	38.9	19	3	US-09-90-700-18	Sequence 18, Appl	c 779	7.2	37.9	19	3	US-09-291-823-2	Sequence 2, Appl
707	7.4	38.9	19	3	US-09-434-382-105	Sequence 105, App	c 780	7.2	37.9	19	3	US-08-938-669A-11	Sequence 11, Appl
708	7.4	38.9	19	3	US-10-309-438-33	Sequence 33, Appl	c 781	7.2	37.9	19	3	US-08-161-674B-17	Sequence 17, Appl
709	7.4	38.9	19	3	US-09-381-212-43	Sequence 43, Appl	c 782	7.2	37.9	19	3	US-09-184-073-8	Sequence 8, Appl
710	7.4	38.9	19	3	US-10-081-806-54	Sequence 54, Appl	c 783	7.2	37.9	19	3	US-09-292-768-29	Sequence 29, Appl
c 711	7.4	38.9	19	3	US-09-928-796-3	Sequence 3, Appl	c 784	7.2	37.9	19	3	US-09-050-159-56	Sequence 56, Appl
c 712	7.4	38.9	19	3	US-09-623-828C-15	Sequence 15, Appl	c 785	7.2	37.9	19	3	US-09-050-159-83	Sequence 83, Appl
c 713	7.4	38.9	19	3	US-09-646-533D-34	Sequence 34, Appl	c 786	7.2	37.9	19	3	US-08-856-963-6	Sequence 6, Appl
c 714	7.4	38.9	19	3	US-09-835-371-19	Sequence 19, Appl	c 787	7.2	37.9	19	3	US-08-856-963-10	Sequence 10, Appl
715	7.4	38.9	19	3	US-09-713-601A-43	Sequence 43, Appl	c 788	7.2	37.9	19	3	US-08-856-963-18	Sequence 18, Appl
c 716	7.4	38.9	19	3	US-09-793-146-17	Sequence 17, Appl	c 789	7.2	37.9	19	3	US-08-856-963-22	Sequence 22, Appl
717	7.4	38.9	19	3	US-09-693-333-169	Sequence 169, App	c 790	7.2	37.9	19	3	US-08-476-423A-44	Sequence 44, Appl
c 718	7.4	38.9	19	4	US-10-98-816-2	Sequence 2, Appl	c 791	7.2	37.9	19	3	US-08-833-624-20	Sequence 20, Appl
c 719	7.4	38.9	19	4	US-09-310-844C-32	Sequence 32, Appl	c 792	7.2	37.9	19	3	US-09-338-907-476	Sequence 476, App
c 720	7.4	38.9	19	4	US-09-977-868-32	Sequence 32, Appl	c 793	7.2	37.9	19	3	US-09-483-211A-81	Sequence 81, Appl
c 721	7.4	38.9	19	4	US-10-114-908-28	Sequence 28, Appl	c 794	7.2	37.9	19	3	US-09-457-708-9	Sequence 9, Appl
722	7.4	38.9	19	4	US-10-114-908-213	Sequence 213, App	c 795	7.2	37.9	19	3	US-09-218-207-476	Sequence 476, App
723	7.4	38.9	19	4	US-10-114-908-214	Sequence 214, App	c 796	7.2	37.9	19	3	US-08-488-223A-81	Sequence 81, Appl
c 724	7.4	38.9	19	4	US-10-222-825-17	Sequence 17, Appl	c 797	7.2	37.9	19	3	US-09-438-836A-7	Sequence 7, Appl
c 725	7.4	38.9	19	5	US-10-125-001-7	Sequence 7, Appl	c 798	7.2	37.9	19	3	US-09-319-648-14	Sequence 14, Appl
726	7.4	38.9	19	5	US-09-982-667-54	Sequence 54, Appl	c 799	7.2	37.9	19	3	US-09-319-648-41	Sequence 41, Appl
c 728	7.4	38.9	19	5	US-09-818-943-6	Sequence 6, Appl	c 800	7.2	37.9	19	3	US-09-144-367-44	Sequence 44, Appl
729	7.4	38.9	19	7	PCT-US91-03680-9	Sequence 9, Appl	c 801	7.2	37.9	19	3	US-09-470-443-87	Sequence 87, Appl
c 730	7.4	38.9	19	7	PCT-US95-04477-76	Sequence 76, Appl	c 802	7.2	37.9	19	3	US-09-319-648-4	Sequence 4, Appl
731	7.4	38.9	19	7	PCT-US95-04477-92	Sequence 92, Appl	c 803	7.2	37.9	19	3	US-09-319-648-14	Sequence 14, Appl
732	7.4	38.9	19	7	PCT-US95-06379-11	Sequence 11, Appl	c 804	7.2	37.9	19	3	US-09-319-648-41	Sequence 41, Appl
733	7.4	38.9	19	9	US-09-798-641-33	Sequence 33, Appl	c 805	7.2	37.9	19	3	US-09-150-661-4	Sequence 4, Appl
c 734	7.2	37.9	19	10	5262866-12	Patent No. 5262866	c 806	7.2	37.9	19	3	US-09-146-893-5	Sequence 5, Appl
c 735	7.2	37.9	19	2	US-07-689-008-10	Sequence 10, Appl	c 807	7.2	37.9	19	3	US-08-488-223A-81	Sequence 81, Appl
c 736	7.2	37.9	19	2	US-07-661-378A-3	Sequence 3, Appl	c 808	7.2	37.9	19	3	US-09-306-828-11	Sequence 11, Appl
c 737	7.2	37.9	19	2	US-08-093-884-1	Sequence 1, Appl	c 809	7.2	37.9	19	3	US-09-216-393B-278	Sequence 278, App
c 738	7.2	37.9	19	2	US-08-093-884-2	Sequence 2, Appl	c 810	7.2	37.9	19	3	US-09-578-634A-1	Sequence 1, Appl
739	7.2	37.9	19	2	US-08-093-884-3	Sequence 3, Appl	c 811	7.2	37.9	19	3	US-09-661-596A-42	Sequence 42, Appl
c 740	7.2	37.9	19	2	US-07-932-379A-10	Sequence 22, Appl	c 812	7.2	37.9	19	3	US-09-422-978-4453	Sequence 4453, Ap
c 741	7.2	37.9	19	2	US-08-379-295-10	Sequence 10, Appl	c 813	7.2	37.9	19	3	US-09-422-978-4539	Sequence 4539, Ap
c 742	7.2	37.9	19	2	US-08-379-296-7	Sequence 7, Appl	c 814	7.2	37.9	19	3	US-09-422-978-4653	Sequence 4653, Ap
c 743	7.2	37.9	19	2	US-08-244-309-10	Sequence 10, Appl	c 815	7.2	37.9	19	3	US-09-422-978-4917	Sequence 4917, Ap
c 744	7.2	37.9	19	2	US-08-379-081B-136	Sequence 10, Appl	c 816	7.2	37.9	19	3	US-09-422-978-4951	Sequence 4951, Ap
745	7.2	37.9	19	2	US-08-379-081B-137	Sequence 136, App	c 817	7.2	37.9	19	3	US-09-422-978-5022	Sequence 5022, Ap
746	7.2	37.9	19	2	US-08-276-919-15	Sequence 137, App	c 818	7.2	37.9	19	3	US-09-422-978-5543	Sequence 5543, Ap
c 747	7.2	37.9	19	2	US-08-456-923-5	Sequence 15, Appl	c 819	7.2	37.9	19	3	US-09-422-978-6003	Sequence 6003, Ap
748	7.2	37.9	19	2	US-08-379-078-136	Sequence 136, Appl	c 820	7.2	37.9	19	3	US-09-422-978-6312	Sequence 6312, Ap
749	7.2	37.9	19	2	US-08-379-078-137	Sequence 137, Appl	c 821	7.2	37.9	19	3	US-09-422-978-7349	Sequence 7349, Ap
c 750	7.2	37.9	19	2	US-08-300-265-7	Sequence 7, Appl	c 822	7.2	37.9	19	3	US-09-422-978-7558	Sequence 7558, Ap
c 751	7.2	37.9	19	2	US-08-599-252-12	Sequence 12, Appl	c 823	7.2	37.9	19	3	US-09-422-978-7772	Sequence 7772, Ap
c 752	7.2	37.9	19	2	US-08-436-074-12	Sequence 12, Appl	c 824	7.2	37.9	19	3	US-09-422-978-8852	Sequence 8852, Ap
c 753	7.2	37.9	19	2	US-08-776-088-20	Sequence 20, Appl	c 825	7.2	37.9	19	3	US-09-422-978-9519	Sequence 9519, Ap
							c 826	7.2	37.9	19	3	US-09-422-978-10099	Sequence 10099, A

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C 838	7.2	37.9	19	3	US-09-831-642-26	Sequence 26, Appl	C 911	7.2	37.9	19	4	US-10-116-949A-87	Sequence 87, Appl
C 839	7.2	37.9	19	3	US-09-027-258-7	Sequence 7, Appl	912	7.2	37.9	19	5	US-09-825-993-3	Sequence 3, Appl
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842	7.2	37.9	19	3	US-09-825-923-6	Sequence 6, Appl	915	7.2	37.9	19	5	US-09-543-679A-1677	Sequence 1677, Ap
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C 997	7	36.8	19	2	US-09-213-768-5	Sequence 5, Appl
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C 999	7	36.8	19	2	US-09-289-368-5	Sequence 5, Appl
C 1000	7	36.8	19	4	US-10-099-322-295	Sequence 295, Appl

## ALIGNMENTS

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RESULT 1
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; Patent No. 6673817
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thercof
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; US-09-672-717-29
OTHER INFORMATION: based on Homo sapiens

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	Best Local Similarity	100.0%	Pred. No. 1.7;		
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; Sequence 7559, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel

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? APPLICANT: Blumenfeld, Marta
? APPLICANT: Chumakov, Ilya
? TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
? FILE REFERENCE: GENSET.020CPI
? CURRENT APPLICATION NUMBER: US/09/422,978
? CURRENT FILING DATE: 1999-10-20
? EARLIER APPLICATION NUMBER: US 09/298,850
? EARLIER FILING DATE: 1999-04-21
? EARLIER APPLICATION NUMBER: US 60/109,732
? EARLIER FILING DATE: 1998-11-23
? EARLIER APPLICATION NUMBER: US 60/082,614
? EARLIER FILING DATE: 1998-04-21
? NUMBER OF SEQ ID NOS: 11796
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? TYPE: DNA
? ORGANISM: Homo Sapiens
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? LOCATION: 1..19
? OTHER INFORMATION: upstream amplification primer 99-7945 for SEQ 3625,
US-09-422-978-7559

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Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-696-791-3034/c
; Sequence 3034, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Titz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3034
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cyclin A1 ribozyme binding site
; US-09-696-791-3034

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; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Triller, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407

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CURRENT APPLICATION NUMBER: US/09/696,791  
CURRENT FILING DATE: 2000-10-25  
NUMBER OF SEQ ID NOS: 4523  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3128  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Cyclin A1 ribozyme binding site  
US-09-696-791-3128

Query Match 56.8%; Score 10.8; DB 3; Length 19;  
Best Local Similarity 85.7%; Pred. No. 3.2e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 5  
US-09-696-791-3129  
Sequence 3129, Application US/09696791  
Patent No. 6770633  
GENERAL INFORMATION:  
APPLICANT: Robbins, Joan M.  
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 480124.407  
CURRENT APPLICATION NUMBER: US/09/696,791  
CURRENT FILING DATE: 2000-10-25  
NUMBER OF SEQ ID NOS: 4523  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3129  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Cyclin A1 ribozyme binding site  
US-09-696-791-3129

Query Match 56.8%; Score 10.8; DB 3; Length 19;  
Best Local Similarity 85.7%; Pred. No. 3.2e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 6  
US-09-696-791-3130  
Sequence 3130, Application US/09696791  
Patent No. 6770633  
GENERAL INFORMATION:  
APPLICANT: Robbins, Joan M.  
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 480124.407  
CURRENT APPLICATION NUMBER: US/09/696,791  
CURRENT FILING DATE: 2000-10-25  
NUMBER OF SEQ ID NOS: 4523  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3130  
LENGTH: 19  
TYPE: DNA  
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FEATURE:  
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US-09-696-791-3130

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Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 7  
US-09-696-791-3131  
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Patent No. 6770633  
GENERAL INFORMATION:  
APPLICANT: Robbins, Joan M.  
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 480124.407  
CURRENT APPLICATION NUMBER: US/09/696,791  
CURRENT FILING DATE: 2000-10-25  
NUMBER OF SEQ ID NOS: 4523  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3131  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Cyclin A1 ribozyme binding site  
US-09-696-791-3131

Query Match 56.8%; Score 10.8; DB 3; Length 19;  
Best Local Similarity 85.7%; Pred. No. 3.2e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 2 CAGTTTCTCCTTCA 15

RESULT 8  
US-09-422-978-9324/C  
Sequence 9324, Application US/09422978  
Patent No. 6537751  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marca  
APPLICANT: Chumakov, Ilya  
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
FILE REFERENCE: GENSET.020CP1  
CURRENT APPLICATION NUMBER: US/09/422,978  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: US 09/298,850  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 60/109,732  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 9324  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 1..19  
OTHER INFORMATION: downstream amplification primer 99-25005 for SEQ 1459, in compleme  
US-09-422-978-9324

Query Match 55.8%; Score 10.6; DB 3; Length 19;  
Best Local Similarity 76.5%; Pred. No. 4e+04;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CACGATCTCTTTCAC 19  
Db 19 CACAGTCTCTTTTCAC 3

## RESULT 9

US-09-422-978-4940  
; Sequence 4940, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marla  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET 020CPI  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; EARLIER FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 4940  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..19  
; OTHER INFORMATION: upstream amplification primer 99-18826 for SEQ 1006,  
US-09-422-978-4940

Query Match 54.7%; Score 10.4; DB 3; Length 19;  
Best Local Similarity 91.7%; Pred. No. 5.1e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTATCTCTTCA 18  
Db 2 GTATCTACTTCA 13

## RESULT 10

US-09-422-978-6219  
; Sequence 6219, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marla  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET 020CPI  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; EARLIER FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 6219  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..19  
; OTHER INFORMATION: upstream amplification primer 99-10173 for SEQ 2285,  
US-09-422-978-6219

Query Match 54.7%; Score 10.4; DB 3; Length 19;  
Best Local Similarity 91.7%; Pred. No. 5.1e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TATCTCTTTCAC 19  
Db 4 TATCTACTTTCAC 15

## RESULT 11

US-09-938-077-18/c  
; Sequence 18, Application US/09938077  
; Patent No. 6730500  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; TITLE OF INVENTION: Methods for Generating a Continuous  
; FILE REFERENCE: Nucleotide Sequence from No. 6730500contiguous Nucleotide Sequen  
; Patent No. 6730500  
; FILE REFERENCE: 00-68  
; CURRENT APPLICATION NUMBER: US/09/938,077  
; CURRENT FILING DATE: 2001-08-23  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Illustrative nucleotide sequence.  
US-09-938-077-18

Query Match 54.7%; Score 10.4; DB 3; Length 19;  
Best Local Similarity 91.7%; Pred. No. 5.1e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACGTATCTCCT 15  
Db 18 AAGGTATCTCCT 7

## RESULT 12

US-09-696-791-3132  
; Sequence 3132, Application US/09696791  
; Patent No. 6770633  
; GENERAL INFORMATION:  
; APPLICANT: Robbins, Joan M.  
; APPLICANT: Tritz, Richard  
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE  
; FILE REFERENCE: 480124.407  
; CURRENT APPLICATION NUMBER: US/09/696,791  
; CURRENT FILING DATE: 2000-10-25  
; NUMBER OF SEQ ID NOS: 4523  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3132  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Cyclin A1 ribozyme binding site  
US-09-696-791-3132

Query Match 54.7%; Score 10.4; DB 3; Length 19;  
Best Local Similarity 91.7%; Pred. No. 5.1e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTATCTCTTCA 18  
Db 1 GTTCTCTTCA 12

## RESULT 13

US-08-182-619-2

Sequence 2, Application US/08182619  
Patent No. 5484710  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Miyashita, Toshiyuki  
APPLICANT: Harigai, Masayoshi  
APPLICANT: Hanada, Motoi  
TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING  
TITLE OF INVENTION: AGENTS THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN  
CELL DEATH  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,619  
FILING DATE: 14-JAN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9867  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-182-619-2

Query Match 52.6%; Score 10; DB 2; Length 19;  
Best Local Similarity 72.2%; Pred. No. 8.2e+04;  
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GCACGATATCTCCTTCAC 19  
Db 2 GCACCTGAGCGCCTTCAC 19

RESULT 14  
US-08-330-535A-2  
Sequence 2, Application US/08330535A  
Patent No. 5659024  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Miyashita, Toshiyuki  
APPLICANT: Harigai, Masayoshi  
APPLICANT: Hanada, Motoi  
TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS  
TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL  
DEATH  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/330,535A  
FILING DATE: 27-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/182,619  
FILING DATE: 14-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 1174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-330-535A-2

Query Match 52.6%; Score 10; DB 2; Length 19;  
Best Local Similarity 72.2%; Pred. No. 8.2e+04;  
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GCACGATATCTCCTTCAC 19  
Db 2 GCACCTGAGCGCCTTCAC 19

RESULT 15  
US-08-838-844-2  
Sequence 2, Application US/08838844  
Patent No. 5908750  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Miyashita, Toshiyuki  
APPLICANT: Harigai, Masayoshi  
APPLICANT: Hanada, Motoi  
TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS  
TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL  
DEATH  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,844  
FILING DATE: 11-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/182,619  
FILING DATE: 14-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,535  
FILING DATE: 27-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 2520  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-838-844-2

Query Match 52.6%; Score 10; DB 2; Length 19;  
Best Local Similarity 72.2%; Pred. No. 8.2e+04;  
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GCACGGTATCTCCTTAC 19  
Db 2 GCACCTGAGCGCCTTAC 19

RESULT 16  
US-08-851-350-26  
Sequence 26, Application US/08851350  
Patent No. 6057122  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
TITLE OF INVENTION: NOVEL ANTITUMORIC PEPTIDES,  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,350  
FILING DATE: 05-MAY-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Casuto, Dianne  
REGISTRATION NUMBER: 40,943  
REFERENCE/DOCKET NUMBER: 5940.US.P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-938-3137  
TELEFAX: 847-938-2623  
TEXT:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-851-350-26

Query Match 52.6%; Score 10; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.2e+04;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 TATCTCCTTC 17

Db 8 TATCTCCTTC 17

RESULT 17  
US-08-924-287A-26  
Sequence 26, Application US/08924287A  
Patent No. 669838  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
TITLE OF INVENTION: NOVEL ANTITUMORIC PEPTIDES,  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS FOR INHIBITING  
FILE REFERENCE: 5940.US.P3  
CURRENT APPLICATION NUMBER: US/08/924,287A  
CURRENT FILING DATE: 1997-09-05  
PRIOR APPLICATION NUMBER: US 08/851,350  
PRIOR FILING DATE: 1997-05-05  
PRIOR APPLICATION NUMBER: US 08/832,087  
PRIOR FILING DATE: 1997-04-03  
PRIOR APPLICATION NUMBER: US 08/643,219  
PRIOR FILING DATE: 1996-05-03  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PET3P-ATG Primer  
US-08-924-287A-26

Query Match 52.6%; Score 10; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.2e+04;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TATCTCCTTC 17  
Db 8 TATCTCCTTC 17

RESULT 18  
US-08-117-952-739  
Sequence 739, Application US/08117952  
Patent No. 5851760  
GENERAL INFORMATION:  
APPLICANT: Evans, Glen A.  
APPLICANT: Smith, Michael W.  
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE  
TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES  
NUMBER OF SEQUENCES: 797  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,952  
FILING DATE: 07-SEP-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/078,471  
FILING DATE: 15-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Relfer, Stephen E.



REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9423  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 739:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Oligonucleotide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-117-952-739

Query Match 51.6%; Score 9.8; DB 2; Length 19;  
Best Local Similarity 84.6%; Pred. No. 1e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5 GGTATCTCCTTC 17  
Db 3 CGTATCTCCTTC 15

RESULT 19  
US-08-549-004A-3/c  
Sequence 3, Application US/08549004A  
Patent No. 5869101  
GENERAL INFORMATION:  
APPLICANT: PENDERGAST, ANN MARIE  
APPLICANT: DAI, ZONGHAN  
TITLE OF INVENTION: ABL-INTERACTOR PROTEIN  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/549,004A  
FILING DATE: 27-OCT-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1579-103  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-549-004A-3

Query Match 51.6%; Score 9.8; DB 2; Length 19;  
Best Local Similarity 84.6%; Pred. No. 1e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Oy 6 GGTATCTCCTTCA 18  
Db 13 GGTATCTTCA 1

RESULT 20  
US-09-051-982A-3/c  
Sequence 3, Application US/09051982A  
Patent No. 6255074  
GENERAL INFORMATION:  
APPLICANT: PENDERGAST, ANN MARIE  
APPLICANT: DAI, ZONGHAN  
TITLE OF INVENTION: ABL-INTERACTOR PROTEIN  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/051,982A  
FILING DATE: 08-JUL-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1579-193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-051-982A-3

Query Match 51.6%; Score 9.8; DB 3; Length 19;  
Best Local Similarity 84.6%; Pred. No. 1e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 6 GGTATCTCCTTCA 18  
Db 13 GGTATCTTCA 1

RESULT 21  
US-08-815-795-2/c  
Sequence 2, Application US/08815795  
Patent No. 6271205  
GENERAL INFORMATION:  
APPLICANT: ROSS, ALONZO H.  
APPLICANT: RECHT, LAWRENCE D.  
APPLICANT: LACHYANKAR, MAHESH B.  
TITLE OF INVENTION: CANCER TREATMENT BY EXPRESSION OF  
TITLE OF INVENTION: DIFFERENTIATION FACTOR RECEPTOR  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: LAPPIN & KUSMER  
STREET: 200 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/815,795  
FILING DATE: 514  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/310,287  
FILING DATE: 21-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: McDaniel, Patricia A.  
REGISTRATION NUMBER: 33,194  
REFERENCE/DOCKET NUMBER: WOZM-010C1P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-330-1300  
TELEFAX: 617-330-1311  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHEICAL: NO  
ANTI-SENSE: YES  
US-08-815-795-2

Query Match 51.6%; Score 9.8; DB 3; Length 19;  
Best Local Similarity 84.6%; Pred. No. 1e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTATCTCCTTCAC 19  
DB 19 GTCTCTCTTCTC 7

RESULT 22  
US-09-422-978-5993  
Sequence 5993, Application US/09422978  
Patent No. 6537751  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marla  
FILE REFERENCE: Chumakov, Ilya  
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
FILE REFERENCE: GENSET 020CP1  
CURRENT APPLICATION NUMBER: US/09/422,978  
PRIOR FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: US 09/298,850  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 60/109,732  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 5993  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 1..19  
OTHER INFORMATION: upstream amplification primer 99-8289 for SEQ 2059,  
US-09-422-978-5993

Query Match 51.6%; Score 9.8; DB 3; Length 19;  
Best Local Similarity 84.6%; Pred. No. 1e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGATCTCCTTCA 18  
DB 2 GGATTTACTTCA 14

RESULT 23  
US-10-130-158A-9  
Sequence 9, Application US/10130158A  
Patent No. 6844179  
GENERAL INFORMATION:  
APPLICANT: NAKANISHI, Atsushi  
APPLICANT: MORITA, Shigeru  
FILE OF INVENTION: No. 6844179e1 protein and its DNA  
FILE REFERENCE: 2670USOP  
CURRENT APPLICATION NUMBER: US/10/130,158A  
PRIOR FILING DATE: 2002-05-14  
PRIOR APPLICATION NUMBER: PCT/JP00/0805  
PRIOR FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: JP 11-324467  
PRIOR FILING DATE: 1999-11-15  
NUMBER OF SEQ ID NOS: 18  
SEQ ID NO 9  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
US-10-130-158A-9

Query Match 51.6%; Score 9.8; DB 3; Length 19;  
Best Local Similarity 84.6%; Pred. No. 1e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTATCTCCTTCAC 19  
DB 5 GCATTTCTTCTC 17

RESULT 24  
US-10-130-158A-10/c  
Sequence 10, Application US/10130158A  
Patent No. 6844179  
GENERAL INFORMATION:  
APPLICANT: NAKANISHI, Atsushi  
APPLICANT: MORITA, Shigeru  
FILE OF INVENTION: No. 6844179e1 protein and its DNA  
FILE REFERENCE: 2670USOP  
CURRENT APPLICATION NUMBER: US/10/130,158A  
PRIOR FILING DATE: 2002-05-14  
PRIOR APPLICATION NUMBER: PCT/JP00/0805  
PRIOR FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: JP 11-324467  
PRIOR FILING DATE: 1999-11-15  
NUMBER OF SEQ ID NOS: 18  
SEQ ID NO 10  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
US-10-130-158A-10

Query Match 51.6%; Score 9.8; DB 3; Length 19;  
Best Local Similarity 84.6%; Pred. No. 1e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CACGGTATCTCCT 15  
DB 17 CACGGACCTCTCT 5

RESULT 25  
US-09-108-006C-28/c  
Sequence 28, Application US/09108006C  
Patent No. 6524613  
GENERAL INFORMATION:  
APPLICANT: Steer, Clifford J.

```

; Kren, Betsy T.
; Bandyopadhyay, Paramita
; Roy-Chowdhury, Jayanta
; TITLE OF INVENTION: Hepatocellular Chimeraplaecy
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kimeragen, Inc.
; STREET: 300 Pheasant Run
; CITY: Newtown
; STATE: PA
; COUNTRY: USA
; ZIP: 18940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,006C
; FILING DATE: 30-Jun-1992
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,288
; FILING DATE: 30-APR-1997
; APPLICATION NUMBER: 60/054,837
; FILING DATE: 05-AUG-1997
; APPLICATION NUMBER: 60/064,996
; FILING DATE: 10-NOV-1997
; APPLICATION NUMBER: 60/074,497
; FILING DATE: 12-FEB-1998
; APPLICATION NUMBER: PCT US 98/08834
; FILING DATE: 30-APR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedel, Thomas
; REGISTRATION NUMBER: 29258
; REFERENCE/DOCKET NUMBER: 7991-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-504-4444
; TELEFAX: 215-504-4545
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-108-006C-28

Query Match 50.5%; Score 9.6; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCTT 16
DB 17 CCCCACATCTCTT 2

RESULT 26
US-09-422-978-7112
; Sequence 7112, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
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; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7112
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-24190 for SEQ 3178.
US-09-422-978-7112

Query Match 50.5%; Score 9.6; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ACGGTATCTCTTCAC 19
DB 4 AGGAGTCTCTCCAC 19

RESULT 27
US-09-688-188B-74/C
; Sequence 74, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOMMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-688-188B-74

Query Match 50.5%; Score 9.6; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCTT 16
DB 16 CGCAGCGCATGTCCTT 1

RESULT 28
US-09-291-417D-74/C
; Sequence 74, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOMMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
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NUMBER OF SEQ ID NOS: 155  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 74  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-291-417D-74

Query Match 50.5%; Score 9.6; DB 3; Length 19;  
Best Local Similarity 75.0%; Pred. No. 1.3e+05;  
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCACGGTATCTCTTC 16  
DB 16 GCCCTGAATCCTTC 1

RESULT 29  
US-09-544-398B-169/C  
Sequence 169, Application US/09544398B  
Patent No. 6770461  
GENERAL INFORMATION:  
APPLICANT: Carnelli, John P.  
APPLICANT: Little, Randall D.  
APPLICANT: Recker, Robert R.  
APPLICANT: Johnson, Mark L.  
TITLE OF INVENTION: High bone mass gene of 11q13.3  
FILE REFERENCE: 032796-013  
CURRENT APPLICATION NUMBER: US/09/544,398B  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: US 09/229,319  
PRIOR FILING DATE: 1999-01-13  
PRIOR APPLICATION NUMBER: US 60/071,449  
PRIOR FILING DATE: 1998-01-13  
PRIOR APPLICATION NUMBER: US 60/105,511  
NUMBER OF SEQ ID NOS: 641  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 169  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-544-398B-169

Query Match 50.5%; Score 9.6; DB 3; Length 19;  
Best Local Similarity 75.0%; Pred. No. 1.3e+05;  
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCTTC 17  
DB 19 GCCCTGAATCCTTC 4

RESULT 30  
US-09-543-771B-169/C  
Sequence 169, Application US/09543771B  
Patent No. 6780609  
GENERAL INFORMATION:  
APPLICANT: Carnelli, John P.  
APPLICANT: Little, Randall D.  
APPLICANT: Recker, Robert R.  
APPLICANT: Johnson, Mark L.  
TITLE OF INVENTION: High bone mass gene of 11q13.3  
FILE REFERENCE: 032796-014  
CURRENT APPLICATION NUMBER: US/09/543,771B  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 09/229,319  
PRIOR FILING DATE: 1999-01-13  
PRIOR APPLICATION NUMBER: US 60/071,449  
PRIOR FILING DATE: 1998-01-13  
PRIOR APPLICATION NUMBER: US 60/105,511

PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 641  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 169  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-543-771B-169

Query Match 50.5%; Score 9.6; DB 3; Length 19;  
Best Local Similarity 75.0%; Pred. No. 1.3e+05;  
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GCACGGTATCTCTTC 17  
DB 19 GCCCTGAATCCTTC 4

RESULT 31  
US-10-032-495A-20  
Sequence 20, Application US/10032495A  
Patent No. 7030292  
GENERAL INFORMATION:  
APPLICANT: YAN, WEN LIANG  
TITLE OF INVENTION: METHOD FOR PRODUCING A POPULATION OF HOMOZYGOUS STEM  
TITLE OF INVENTION: CELLS HAVING A PRE-SELECTED IMMUNOTYPE AND/OR GENOTYPE.  
TITLE OF INVENTION: CELLS SUITABLE FOR TRANSPLANT DERIVED THEREFROM, AND  
TITLE OF INVENTION: MATERIALS AND METHODS USING SAME  
FILE REFERENCE: 0249-000205  
CURRENT APPLICATION NUMBER: US/10/032,495A  
CURRENT FILING DATE: 2002-01-02  
PRIOR APPLICATION NUMBER: 60/258,881  
PRIOR FILING DATE: 2001-01-02  
NUMBER OF SEQ ID NOS: 86  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 20  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Probe  
US-10-032-495A-20

Query Match 50.5%; Score 9.6; DB 5; Length 19;  
Best Local Similarity 75.0%; Pred. No. 1.3e+05;  
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCACGGTATCTCTTC 16  
DB 3 GCACGGACTCTCTT 18

RESULT 32  
US-09-696-791-3133  
Sequence 3133, Application US/09696791  
Patent No. 6770633  
GENERAL INFORMATION:  
APPLICANT: Robbins, Joan M.  
APPLICANT: Tiltz, Richard  
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: SKIN AND EYE DISEASES  
FILE REFERENCE: 480124.407  
CURRENT APPLICATION NUMBER: US/09/696,791  
CURRENT FILING DATE: 2000-10-25  
NUMBER OF SEQ ID NOS: 4523  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3133  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Cyclin A1 ribozyme binding site  
US-09-696-791-3133

Query Match 49.5%; Score 9.4; DB 3; Length 19;  
Best Local Similarity 90.9%; Pred. No. 1.7e+05;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCTTCA 18  
Db 1 TTTCTCTTCA 11

RESULT 33  
US-09-747-385-7/c  
Sequence 7, Application US/09747385

Patent No. 6962990  
GENERAL INFORMATION:  
APPLICANT: Attarian, Gwynne  
APPLICANT: Podkaminer, Kara K.  
APPLICANT: Yoder, Sean C.  
APPLICANT: Kinder Haake, Susan A.  
TITLE OF INVENTION: Pseudocarcinoma Nucleic Acids, Plasmids and Vectors  
FILE REFERENCE: 023078-099810US  
CURRENT APPLICATION NUMBER: US/09/747,385  
CURRENT FILING DATE: 2000-12-22  
PRIOR FILING DATE: 1999-12-27  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 7  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:rlx  
US-09-747-385-7

Query Match 49.5%; Score 9.4; DB 4; Length 19;  
Best Local Similarity 90.9%; Pred. No. 1.7e+05;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 ATCTCTTAC 19  
Db 15 ATCTCTTAC 5

RESULT 34  
US-09-506-729-1/c  
Sequence 1, Application US/09506729

Patent No. 6365352  
GENERAL INFORMATION:  
APPLICANT: Yerramilli, Subrahmanyam V.  
APPLICANT: Prashar, Yatindra  
APPLICANT: Newberger, Peter  
APPLICANT: Goguen, Jon  
APPLICANT: Weisman, Sherman M.  
TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN  
FILE OF INVENTION: GRANULOCYTIC CELLS  
FILE REFERENCE: 44921-5016-US  
CURRENT APPLICATION NUMBER: US/09/506,729  
CURRENT FILING DATE: 2000-02-18  
EARLIER APPLICATION NUMBER: PCT/US98/17284  
EARLIER FILING DATE: 1998-08-21  
EARLIER APPLICATION NUMBER: 60/056,844  
EARLIER FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-506-729-1

Query Match 48.4%; Score 9.2; DB 3; Length 19;  
Best Local Similarity 78.6%; Pred. No. 2.2e+05;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGGATCTCTTCA 18  
Db 17 CGGATCTCTTCA 4

RESULT 35

US-09-422-978-5154  
Sequence 5154, Application US/09422978  
Patent No. 6537751  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Chumakov, Ilya  
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
FILE REFERENCE: GENSSET.020CP1  
CURRENT APPLICATION NUMBER: US/09/422,978  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: US 09/298,850  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 60/109,732  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 5154  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 1..19  
OTHER INFORMATION: upstream amplification primer 99-22087 for SEQ 1220,  
US-09-422-978-5154

Query Match 48.4%; Score 9.2; DB 3; Length 19;  
Best Local Similarity 78.6%; Pred. No. 2.2e+05;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GGATCTCTTAC 19  
Db 1 GGATCTCTTAC 14

RESULT 36  
US-09-973-132-2  
Sequence 2, Application US/09973132

Patent No. 6593092  
GENERAL INFORMATION:  
APPLICANT: Wu, H.  
APPLICANT: Merchant, B.T.  
TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION  
FILE REFERENCE: 6687-US.P1  
CURRENT APPLICATION NUMBER: US/09/973,132  
CURRENT FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 09/542,718  
PRIOR FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FastSeq for windows Version 4.0  
SEQ ID NO 2  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic fragments  
US-09-973-132-2

Query Match 48.4%; Score 9.2; DB 3; Length 19;

Best Local Similarity 78.6%; Pred. No. 2.2e+05;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 ACGGATCTCCTTC 17  
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Db 2 ACGGAGCGCTTC 15

RESULT 37  
US-09-696-791-1137

; Sequence 1137, Application US/09696791

; Patent No. 6770633

; GENERAL INFORMATION:

; APPLICANT: Robbins, Joan M.

; APPLICANT: Tritz, Richard

; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE

; FILE REFERENCE: 480124.407

; CURRENT APPLICATION NUMBER: US/09/696,791

; CURRENT FILING DATE: 2000-10-25

; NUMBER OF SEQ ID NOS: 4523

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1137

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Cdk-we-hu ribozyme binding site

US-09-696-791-1137

Query Match 48.4%; Score 9.2; DB 3; Length 19;  
Best Local Similarity 78.6%; Pred. No. 2.2e+05;

Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GGTATCTCCTTCAC 19  
||| ||| ||| |||  
Db 3 GGTAGCTCTTCTC 16

RESULT 38  
US-09-696-791-1138

; Sequence 1138, Application US/09696791

; Patent No. 6770633

; GENERAL INFORMATION:

; APPLICANT: Robbins, Joan M.

; APPLICANT: Tritz, Richard

; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE

; FILE REFERENCE: 480124.407

; CURRENT APPLICATION NUMBER: US/09/696,791

; CURRENT FILING DATE: 2000-10-25

; NUMBER OF SEQ ID NOS: 4523

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1138

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Cdk-we-hu ribozyme binding site

US-09-696-791-1138

Query Match 48.4%; Score 9.2; DB 3; Length 19;  
Best Local Similarity 78.6%; Pred. No. 2.2e+05;

Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GGTATCTCCTTCAC 19  
||| ||| ||| |||  
Db 1 GGTAGCTCTTCTC 14

RESULT 39  
US-09-696-791-1429

; Sequence 1429, Application US/09696791

; Sequence 1429, Application US/09696791

; Patent No. 6770633  
; GENERAL INFORMATION:

; APPLICANT: Robbins, Joan M.

; APPLICANT: Tritz, Richard

; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE

; FILE REFERENCE: 480124.407

; CURRENT APPLICATION NUMBER: US/09/696,791

; CURRENT FILING DATE: 2000-10-25

; NUMBER OF SEQ ID NOS: 4523

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1429

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Cyclin A2 ribozyme binding site

US-09-696-791-1429

Query Match 48.4%; Score 9.2; DB 3; Length 19;  
Best Local Similarity 78.6%; Pred. No. 2.2e+05;

Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CACGGTATCTCCTT 16  
||| ||| ||| |||  
Db 4 CACGTTCTCTCCTT 17

RESULT 40  
US-09-696-791-1430

; Sequence 1430, Application US/09696791

; Patent No. 6770633

; GENERAL INFORMATION:

; APPLICANT: Robbins, Joan M.

; APPLICANT: Tritz, Richard

; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE

; FILE REFERENCE: 480124.407

; CURRENT APPLICATION NUMBER: US/09/696,791

; CURRENT FILING DATE: 2000-10-25

; NUMBER OF SEQ ID NOS: 4523

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1430

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Cyclin A2 ribozyme binding site

US-09-696-791-1430

Query Match 48.4%; Score 9.2; DB 3; Length 19;  
Best Local Similarity 78.6%; Pred. No. 2.2e+05;

Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CACGGTATCTCCTT 16  
||| ||| ||| |||  
Db 3 CACGTTCTCTCCTT 16

Search completed: August 10, 2006, 09:00:57  
Job time : 111.333 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 08:47:46 ; Search time 625.333 Seconds  
(without alignments)  
373.345 Million cell updates/sec

Title: US-10-636-065-29

Perfect score: 19

Sequence: 1 cgcacgctactcttcac 19

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 6941248

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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications NA Main:\*

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16: /BMC\_Celerra\_SIDS3/prodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	14.4	75.8	19	14	US-11-083-784-787223
3	14.4	75.8	19	15	US-11-101-244-787223
4	14	73.7	19	7	US-10-400-382-29
5	14	73.7	19	7	US-10-400-382-107
6	14	73.7	19	10	US-10-975-790-29
7	14	73.7	19	10	US-10-975-790-107
8	13.4	70.5	19	14	US-11-083-784-79689
9	13.4	70.5	19	15	US-11-101-244-79689
10	13	68.4	19	10	US-10-739-904-10
11	13	68.4	19	14	US-11-083-784-1156068
12	13	68.4	19	15	US-11-101-244-1156068
13	12.8	67.4	19	14	US-11-083-784-224158
14	12.8	67.4	19	14	US-11-083-784-761475
15	12.8	67.4	19	15	US-11-101-244-224158
16	12.8	67.4	19	15	US-11-101-244-761475
17	12.6	66.3	19	3	US-09-969-373-2206

18	12.4	65.3	19	14	US-11-083-784-754	Sequence 754, App
19	12.4	65.3	19	14	US-11-083-784-183913	Sequence 183913,
20	12.4	65.3	19	14	US-11-083-784-222011	Sequence 222011,
21	12.4	65.3	19	14	US-11-083-784-475145	Sequence 475145,
22	12.4	65.3	19	14	US-11-083-784-475149	Sequence 475149,
23	12.4	65.3	19	14	US-11-083-784-583673	Sequence 583673,
24	12.4	65.3	19	14	US-11-083-784-798632	Sequence 798632,
25	12.4	65.3	19	14	US-11-083-784-873288	Sequence 873288,
26	12.4	65.3	19	14	US-11-083-784-1087813	Sequence 1087813,
27	12.4	65.3	19	14	US-11-083-784-1087832	Sequence 1087832,
28	12.4	65.3	19	14	US-11-083-784-1180480	Sequence 1180480,
29	12.4	65.3	19	14	US-11-083-784-1191739	Sequence 1191739,
30	12.4	65.3	19	14	US-11-083-784-1191772	Sequence 1191772,
31	12.4	65.3	19	14	US-11-083-784-1306236	Sequence 1306236,
32	12.4	65.3	19	14	US-11-083-784-1585329	Sequence 1585329,
33	12.4	65.3	19	14	US-11-083-784-1585348	Sequence 1585348,
34	12.4	65.3	19	15	US-11-101-244-754	Sequence 754, App
35	12.4	65.3	19	15	US-11-101-244-183913	Sequence 183913,
36	12.4	65.3	19	15	US-11-101-244-222011	Sequence 222011,
37	12.4	65.3	19	15	US-11-101-244-475145	Sequence 475145,
38	12.4	65.3	19	15	US-11-101-244-475149	Sequence 475149,
39	12.4	65.3	19	15	US-11-101-244-583673	Sequence 583673,
40	12.4	65.3	19	15	US-11-101-244-798632	Sequence 798632,
41	12.4	65.3	19	15	US-11-101-244-873288	Sequence 873288,
42	12.4	65.3	19	15	US-11-101-244-1087813	Sequence 1087813,
43	12.4	65.3	19	15	US-11-101-244-1087832	Sequence 1087832,
44	12.4	65.3	19	15	US-11-101-244-1180480	Sequence 1180480,
45	12.4	65.3	19	15	US-11-101-244-1191739	Sequence 1191739,
46	12.4	65.3	19	15	US-11-101-244-1191772	Sequence 1191772,
47	12.4	65.3	19	15	US-11-101-244-1306236	Sequence 1306236,
48	12.4	65.3	19	15	US-11-101-244-1585329	Sequence 1585329,
49	12.4	65.3	19	15	US-11-101-244-1585348	Sequence 1585348,
50	12.2	64.2	19	9	US-10-636-598-33	Sequence 33, Appl
51	12.2	64.2	19	11	US-10-1310-91A-840800	Sequence 840800,
52	12.2	64.2	19	14	US-11-083-784-62682	Sequence 62682, A
53	12.2	64.2	19	14	US-11-083-784-80634	Sequence 80634, A
54	12.2	64.2	19	14	US-11-083-784-193376	Sequence 193376,
55	12.2	64.2	19	14	US-11-083-784-273138	Sequence 273138,
56	12.2	64.2	19	14	US-11-083-784-274885	Sequence 274885,
57	12.2	64.2	19	14	US-11-083-784-343449	Sequence 343449,
58	12.2	64.2	19	14	US-11-083-784-346016	Sequence 346016,
59	12.2	64.2	19	14	US-11-083-784-472120	Sequence 472120,
60	12.2	64.2	19	14	US-11-083-784-472215	Sequence 472215,
61	12.2	64.2	19	14	US-11-083-784-518183	Sequence 518183,
62	12.2	64.2	19	14	US-11-083-784-648223	Sequence 648223,
63	12.2	64.2	19	14	US-11-083-784-972359	Sequence 972359,
64	12.2	64.2	19	14	US-11-083-784-1036216	Sequence 1036216,
65	12.2	64.2	19	14	US-11-083-784-1170322	Sequence 1170322,
66	12.2	64.2	19	14	US-11-083-784-1516953	Sequence 1516953,
67	12.2	64.2	19	15	US-11-101-244-62682	Sequence 62682, A
68	12.2	64.2	19	15	US-11-101-244-80634	Sequence 80634, A
69	12.2	64.2	19	15	US-11-101-244-193376	Sequence 193376,
70	12.2	64.2	19	15	US-11-101-244-273138	Sequence 273138,
71	12.2	64.2	19	15	US-11-101-244-274885	Sequence 274885,
72	12.2	64.2	19	15	US-11-101-244-343449	Sequence 343449,
73	12.2	64.2	19	15	US-11-101-244-346016	Sequence 346016,
74	12.2	64.2	19	15	US-11-101-244-472120	Sequence 472120,
75	12.2	64.2	19	15	US-11-101-244-472215	Sequence 472215,
76	12.2	64.2	19	15	US-11-101-244-518183	Sequence 518183,
77	12.2	64.2	19	15	US-11-101-244-648223	Sequence 648223,
78	12.2	64.2	19	15	US-11-101-244-972359	Sequence 972359,
79	12.2	64.2	19	15	US-11-101-244-1036216	Sequence 1036216,
80	12.2	64.2	19	15	US-11-101-244-1170322	Sequence 1170322,
81	12.2	64.2	19	15	US-11-101-244-1516953	Sequence 1516953,
82	12	63.2	19	14	US-11-083-784-112733	Sequence 112733,
83	12	63.2	19	14	US-11-083-784-112733	Sequence 112733,
84	12	63.2	19	14	US-11-083-784-222012	Sequence 222012,
85	12	63.2	19	14	US-11-083-784-617342	Sequence 617342,
86	12	63.2	19	14	US-11-083-784-75182	Sequence 75182,
87	12	63.2	19	14	US-11-083-784-873317	Sequence 873317,
88	12	63.2	19	14	US-11-083-784-940223	Sequence 940223,
89	12	63.2	19	14	US-11-083-784-1190154	Sequence 1190154,
90	12	63.2	19	14	US-11-083-784-149582	Sequence 149582,
91	12	63.2	19	15	US-11-101-244-112793	Sequence 112793,

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92	12	63.2	617342	19	15	US-11-101-244-617342	Sequence 617342,
93	12	63.2	775182	19	15	US-11-101-244-775182	Sequence 775182,
C 94	12	63.2	873317	19	15	US-11-101-244-873317	Sequence 873317,
95	12	63.2	940223	19	15	US-11-101-244-940223	Sequence 940223,
C 96	12	63.2	1190154	19	15	US-11-101-244-1190154	Sequence 1190154,
C 97	12	63.2	1499582	19	15	US-11-101-244-1499582	Sequence 1499582,
C 98	12	63.2	628444	19	15	US-10-310-914A-628444	Sequence 628444,
C 99	11.8	62.1	1026980	19	11	US-10-310-914A-1026980	Sequence 1026980,
C 100	11.8	62.1	43373	19	14	US-11-083-784-43373	Sequence 43373, A
C 101	11.8	62.1	43424	19	14	US-11-083-784-43424	Sequence 43424, A
C 102	11.8	62.1	227032	19	14	US-11-083-784-227032	Sequence 227032,
C 103	11.8	62.1	267464	19	14	US-11-083-784-267464	Sequence 267464,
C 104	11.8	62.1	267569	19	14	US-11-083-784-267569	Sequence 267569,
C 105	11.8	62.1	267671	19	14	US-11-083-784-267671	Sequence 267671,
C 106	11.8	62.1	267773	19	14	US-11-083-784-267773	Sequence 267773,
C 107	11.8	62.1	267877	19	14	US-11-083-784-267877	Sequence 267877,
C 108	11.8	62.1	417171	19	14	US-11-083-784-417171	Sequence 417171,
C 109	11.8	62.1	507577	19	14	US-11-083-784-507577	Sequence 507577,
C 110	11.8	62.1	518698	19	14	US-11-083-784-518698	Sequence 518698,
C 111	11.8	62.1	532240	19	14	US-11-083-784-532240	Sequence 532240,
C 112	11.8	62.1	532339	19	14	US-11-083-784-532339	Sequence 532339,
C 113	11.8	62.1	535700	19	14	US-11-083-784-535700	Sequence 535700,
C 114	11.8	62.1	535731	19	14	US-11-083-784-535731	Sequence 535731,
C 115	11.8	62.1	535890	19	14	US-11-083-784-535890	Sequence 535890,
C 116	11.8	62.1	535926	19	14	US-11-083-784-535926	Sequence 535926,
C 117	11.8	62.1	609759	19	14	US-11-083-784-609759	Sequence 609759,
C 118	11.8	62.1	728588	19	14	US-11-083-784-728588	Sequence 728588,
C 119	11.8	62.1	728818	19	14	US-11-083-784-728818	Sequence 728818,
C 120	11.8	62.1	929077	19	14	US-11-083-784-929077	Sequence 929077,
C 121	11.8	62.1	929179	19	14	US-11-083-784-929179	Sequence 929179,
C 122	11.8	62.1	978926	19	14	US-11-083-784-978926	Sequence 978926,
C 123	11.8	62.1	978974	19	14	US-11-083-784-978974	Sequence 978974,
C 124	11.8	62.1	979023	19	14	US-11-083-784-979023	Sequence 979023,
C 125	11.8	62.1	979077	19	14	US-11-083-784-979077	Sequence 979077,
C 126	11.8	62.1	1085058	19	14	US-11-083-784-1085058	Sequence 1085058,
C 127	11.8	62.1	1091023	19	14	US-11-083-784-1091023	Sequence 1091023,
C 128	11.8	62.1	1138508	19	14	US-11-083-784-1138508	Sequence 1138508,
C 129	11.8	62.1	1270102	19	14	US-11-083-784-1270102	Sequence 1270102,
C 130	11.8	62.1	1305551	19	14	US-11-083-784-1305551	Sequence 1305551,
C 131	11.8	62.1	1327567	19	14	US-11-083-784-1327567	Sequence 1327567,
C 132	11.8	62.1	1379186	19	14	US-11-083-784-1379186	Sequence 1379186,
C 133	11.8	62.1	1450500	19	14	US-11-083-784-1450500	Sequence 1450500,
C 134	11.8	62.1	1484872	19	14	US-11-083-784-1484872	Sequence 1484872,
C 135	11.8	62.1	1485014	19	14	US-11-083-784-1485014	Sequence 1485014,
C 136	11.8	62.1	1516898	19	14	US-11-083-784-1516898	Sequence 1516898,
C 137	11.8	62.1	43373	19	15	US-11-101-244-43373	Sequence 43373, A
C 138	11.8	62.1	43424	19	15	US-11-101-244-43424	Sequence 43424, A
C 139	11.8	62.1	227032	19	15	US-11-101-244-227032	Sequence 227032,
C 140	11.8	62.1	267464	19	15	US-11-101-244-267464	Sequence 267464,
C 141	11.8	62.1	267569	19	15	US-11-101-244-267569	Sequence 267569,
C 142	11.8	62.1	267671	19	15	US-11-101-244-267671	Sequence 267671,
C 143	11.8	62.1	267773	19	15	US-11-101-244-267773	Sequence 267773,
C 144	11.8	62.1	267877	19	15	US-11-101-244-267877	Sequence 267877,
C 145	11.8	62.1	417171	19	15	US-11-101-244-417171	Sequence 417171,
C 146	11.8	62.1	507577	19	15	US-11-101-244-507577	Sequence 507577,
C 147	11.8	62.1	518698	19	15	US-11-101-244-518698	Sequence 518698,
C 148	11.8	62.1	532240	19	15	US-11-101-244-532240	Sequence 532240,
C 149	11.8	62.1	532339	19	15	US-11-101-244-532339	Sequence 532339,
C 150	11.8	62.1	535700	19	15	US-11-101-244-535700	Sequence 535700,
C 151	11.8	62.1	535731	19	15	US-11-101-244-535731	Sequence 535731,
C 152	11.8	62.1	535890	19	15	US-11-101-244-535890	Sequence 535890,
C 153	11.8	62.1	535926	19	15	US-11-101-244-535926	Sequence 535926,
C 154	11.8	62.1	609759	19	15	US-11-101-244-609759	Sequence 609759,
C 155	11.8	62.1	728588	19	15	US-11-101-244-728588	Sequence 728588,
C 156	11.8	62.1	728818	19	15	US-11-101-244-728818	Sequence 728818,
C 157	11.8	62.1	929077	19	15	US-11-101-244-929077	Sequence 929077,
C 158	11.8	62.1	929179	19	15	US-11-101-244-929179	Sequence 929179,
C 159	11.8	62.1	978926	19	15	US-11-101-244-978926	Sequence 978926,
C 160	11.8	62.1	978974	19	15	US-11-101-244-978974	Sequence 978974,
C 161	11.8	62.1	979023	19	15	US-11-101-244-979023	Sequence 979023,
C 162	11.8	62.1	979077	19	15	US-11-101-244-979077	Sequence 979077,
C 163	11.8	62.1	1085058	19	15	US-11-101-244-1085058	Sequence 1085058,



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239	11.4	60.0	19	14	US-11-083-784-1020269	Sequence 1020269,	C 312	11.2	58.9	19	11	US-10-310-914A-1057116	Sequence 1057116,
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241	11.4	60.0	19	14	US-11-083-784-1041213	Sequence 1041213,	C 314	11.2	58.9	19	11	US-10-310-914A-1301564	Sequence 1301564,
242	11.4	60.0	19	14	US-11-083-784-1108242	Sequence 1108242,	C 315	11.2	58.9	19	14	US-11-083-784-7839	Sequence 7839, Ap
243	11.4	60.0	19	14	US-11-083-784-1108324	Sequence 1108324,	C 316	11.2	58.9	19	14	US-11-083-784-7897	Sequence 7897, Ap
244	11.4	60.0	19	14	US-11-083-784-1179079	Sequence 1179079,	C 317	11.2	58.9	19	14	US-11-083-784-20131	Sequence 20131, A
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246	11.4	60.0	19	14	US-11-083-784-1370161	Sequence 1370161,	C 319	11.2	58.9	19	14	US-11-083-784-51229	Sequence 51229, A
247	11.4	60.0	19	14	US-11-083-784-1415850	Sequence 1415850,	C 320	11.2	58.9	19	14	US-11-083-784-65414	Sequence 65414, A
248	11.4	60.0	19	14	US-11-083-784-1480947	Sequence 1480947,	C 321	11.2	58.9	19	14	US-11-083-784-93455	Sequence 93455, A
249	11.4	60.0	19	14	US-11-083-784-1507475	Sequence 1507475,	C 322	11.2	58.9	19	14	US-11-083-784-96080	Sequence 96080, A
250	11.4	60.0	19	14	US-11-083-784-1516923	Sequence 1516923,	C 323	11.2	58.9	19	14	US-11-083-784-118842	Sequence 118842,
251	11.4	60.0	19	14	US-11-083-784-1526480	Sequence 1526480,	C 324	11.2	58.9	19	14	US-11-083-784-120268	Sequence 120268,
252	11.4	60.0	19	14	US-11-083-784-1531886	Sequence 1531886,	C 325	11.2	58.9	19	14	US-11-083-784-146722	Sequence 146722,
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254	11.4	60.0	19	14	US-11-083-784-1588960	Sequence 1588960,	C 327	11.2	58.9	19	14	US-11-083-784-191644	Sequence 191644,
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257	11.4	60.0	19	15	US-11-101-244-31448	Sequence 31448, A	C 330	11.2	58.9	19	14	US-11-083-784-224244	Sequence 224244,
258	11.4	60.0	19	15	US-11-101-244-31451	Sequence 31451, A	C 331	11.2	58.9	19	14	US-11-083-784-224276	Sequence 224276,
259	11.4	60.0	19	15	US-11-101-244-48400	Sequence 48400, A	C 332	11.2	58.9	19	14	US-11-083-784-236018	Sequence 236018,
260	11.4	60.0	19	15	US-11-101-244-185325	Sequence 185325,	C 333	11.2	58.9	19	14	US-11-083-784-237905	Sequence 237905,
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263	11.4	60.0	19	15	US-11-101-244-185364	Sequence 185364,	C 336	11.2	58.9	19	14	US-11-083-784-389290	Sequence 389290,
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265	11.4	60.0	19	15	US-11-101-244-237456	Sequence 237456,	C 338	11.2	58.9	19	14	US-11-083-784-518161	Sequence 518161,
266	11.4	60.0	19	15	US-11-101-244-249818	Sequence 249818,	C 339	11.2	58.9	19	14	US-11-083-784-537696	Sequence 537696,
267	11.4	60.0	19	15	US-11-101-244-384027	Sequence 384027,	C 340	11.2	58.9	19	14	US-11-083-784-579191	Sequence 579191,
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269	11.4	60.0	19	15	US-11-101-244-440265	Sequence 440265,	C 342	11.2	58.9	19	14	US-11-083-784-587315	Sequence 587315,
270	11.4	60.0	19	15	US-11-101-244-440289	Sequence 440289,	C 343	11.2	58.9	19	14	US-11-083-784-588252	Sequence 588252,
271	11.4	60.0	19	15	US-11-101-244-575038	Sequence 575038,	C 344	11.2	58.9	19	14	US-11-083-784-618851	Sequence 618851,
272	11.4	60.0	19	15	US-11-101-244-575139	Sequence 575139,	C 345	11.2	58.9	19	14	US-11-083-784-654549	Sequence 654549,
273	11.4	60.0	19	15	US-11-101-244-609830	Sequence 609830,	C 346	11.2	58.9	19	14	US-11-083-784-664719	Sequence 664719,
274	11.4	60.0	19	15	US-11-101-244-612205	Sequence 612205,	C 347	11.2	58.9	19	14	US-11-083-784-744816	Sequence 744816,
275	11.4	60.0	19	15	US-11-101-244-656016	Sequence 656016,	C 348	11.2	58.9	19	14	US-11-083-784-744825	Sequence 744825,
276	11.4	60.0	19	15	US-11-101-244-662156	Sequence 662156,	C 349	11.2	58.9	19	14	US-11-083-784-744868	Sequence 744868,
277	11.4	60.0	19	15	US-11-101-244-662255	Sequence 662255,	C 350	11.2	58.9	19	14	US-11-083-784-772827	Sequence 772827,
278	11.4	60.0	19	15	US-11-101-244-702380	Sequence 702380,	C 351	11.2	58.9	19	14	US-11-083-784-772887	Sequence 772887,
279	11.4	60.0	19	15	US-11-101-244-708914	Sequence 708914,	C 352	11.2	58.9	19	14	US-11-083-784-784385	Sequence 784385,
280	11.4	60.0	19	15	US-11-101-244-728500	Sequence 728500,	C 353	11.2	58.9	19	14	US-11-083-784-780199	Sequence 780199,
281	11.4	60.0	19	15	US-11-101-244-854864	Sequence 854864,	C 354	11.2	58.9	19	14	US-11-083-784-808982	Sequence 808982,
282	11.4	60.0	19	15	US-11-101-244-944650	Sequence 944650,	C 355	11.2	58.9	19	14	US-11-083-784-823362	Sequence 823362,
283	11.4	60.0	19	15	US-11-101-244-944734	Sequence 944734,	C 356	11.2	58.9	19	14	US-11-083-784-856423	Sequence 856423,
284	11.4	60.0	19	15	US-11-101-244-944849	Sequence 944849,	C 357	11.2	58.9	19	14	US-11-083-784-873164	Sequence 873164,
285	11.4	60.0	19	15	US-11-101-244-944950	Sequence 944950,	C 358	11.2	58.9	19	14	US-11-083-784-880982	Sequence 880982,
286	11.4	60.0	19	15	US-11-101-244-945051	Sequence 945051,	C 359	11.2	58.9	19	14	US-11-083-784-919024	Sequence 919024,
287	11.4	60.0	19	15	US-11-101-244-967894	Sequence 967894,	C 360	11.2	58.9	19	14	US-11-083-784-974315	Sequence 974315,
288	11.4	60.0	19	15	US-11-101-244-1020235	Sequence 1020235,	C 361	11.2	58.9	19	14	US-11-083-784-985475	Sequence 985475,
289	11.4	60.0	19	15	US-11-101-244-1020262	Sequence 1020262,	C 362	11.2	58.9	19	14	US-11-083-784-1036215	Sequence 1036215,
290	11.4	60.0	19	15	US-11-101-244-1020268	Sequence 1020268,	C 363	11.2	58.9	19	14	US-11-083-784-1043139	Sequence 1043139,
291	11.4	60.0	19	15	US-11-101-244-1020269	Sequence 1020269,	C 364	11.2	58.9	19	14	US-11-083-784-1073039	Sequence 1073039,
292	11.4	60.0	19	15	US-11-101-244-1020279	Sequence 1020279,	C 365	11.2	58.9	19	14	US-11-083-784-1073254	Sequence 1073254,
293	11.4	60.0	19	15	US-11-101-244-1041213	Sequence 1041213,	C 366	11.2	58.9	19	14	US-11-083-784-1098251	Sequence 1098251,
294	11.4	60.0	19	15	US-11-101-244-1108242	Sequence 1108242,	C 367	11.2	58.9	19	14	US-11-083-784-1112807	Sequence 1112807,
295	11.4	60.0	19	15	US-11-101-244-1108324	Sequence 1108324,	C 368	11.2	58.9	19	14	US-11-083-784-1112817	Sequence 1112817,
296	11.4	60.0	19	15	US-11-101-244-1179079	Sequence 1179079,	C 369	11.2	58.9	19	14	US-11-083-784-1113282	Sequence 1113282,
297	11.4	60.0	19	15	US-11-101-244-1214084	Sequence 1214084,	C 370	11.2	58.9	19	14	US-11-083-784-1121360	Sequence 1121360,
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299	11.4	60.0	19	15	US-11-101-244-1415850	Sequence 1415850,	C 372	11.2	58.9	19	14	US-11-083-784-1171743	Sequence 1171743,
300	11.4	60.0	19	15	US-11-101-244-1480947	Sequence 1480947,	C 373	11.2	58.9	19	14	US-11-083-784-1209251	Sequence 1209251,
301	11.4	60.0	19	15	US-11-101-244-1507475	Sequence 1507475,	C 374	11.2	58.9	19	14	US-11-083-784-1209337	Sequence 1209337,
302	11.4	60.0	19	15	US-11-101-244-1516923	Sequence 1516923,	C 375	11.2	58.9	19	14	US-11-083-784-1281486	Sequence 1281486,
303	11.4	60.0	19	15	US-11-101-244-1531886	Sequence 1531886,	C 376	11.2	58.9	19	14	US-11-083-784-12931821	Sequence 12931821,
304	11.4	60.0	19	15	US-11-101-244-1586384	Sequence 1586384,	C 377	11.2	58.9	19	14	US-11-083-784-1293500	Sequence 1293500,
305	11.4	60.0	19	15	US-11-101-244-1588960	Sequence 1588960,	C 378	11.2	58.9	19	14	US-11-083-784-1324954	Sequence 1324954,
306	11.4	60.0	19	15	US-11-101-244-1591240	Sequence 1591240,	C 379	11.2	58.9	19	14	US-11-083-784-142570	Sequence 142570,
307	11.4	60.0	19	15	US-10-310-914A-226941,	Sequence 226941,	C 380	11.2	58.9	19	14	US-11-083-784-1449798	Sequence 1449798,
308	11.2	58.9	19	11	US-10-310-914A-366185	Sequence 366185,	C 381	11.2	58.9	19	14	US-11-083-784-1499798	Sequence 1499798,
309	11.2	58.9	19	11	US-10-310-914A-366185	Sequence 366185,	C 382	11.2	58.9	19	14	US-11-083-784-1499808	Sequence 1499808,

383	11.2	58.9	19	14	US-11-083-784-1481525	Sequence 1481525,
384	11.2	58.9	19	14	US-11-083-784-1558682	Sequence 1558682,
385	11.2	58.9	19	14	US-11-083-784-1567299	Sequence 1567299,
386	11.2	58.9	19	14	US-11-083-784-1589489	Sequence 1589489,
387	11.2	58.9	19	14	US-11-083-784-1589494	Sequence 1589494,
388	11.2	58.9	19	14	US-11-101-244-7839	Sequence 7839, Ap
389	11.2	58.9	19	15	US-11-101-244-7897	Sequence 7897, Ap
390	11.2	58.9	19	15	US-11-101-244-20131	Sequence 20131, A
391	11.2	58.9	19	15	US-11-101-244-30759	Sequence 30759, A
392	11.2	58.9	19	15	US-11-101-244-51229	Sequence 51229, A
393	11.2	58.9	19	15	US-11-101-244-65414	Sequence 65414, A
394	11.2	58.9	19	15	US-11-101-244-93455	Sequence 93455, A
395	11.2	58.9	19	15	US-11-101-244-96080	Sequence 96080, A
396	11.2	58.9	19	15	US-11-101-244-118842	Sequence 118842,
397	11.2	58.9	19	15	US-11-101-244-120268	Sequence 120268,
398	11.2	58.9	19	15	US-11-101-244-146722	Sequence 146722,
399	11.2	58.9	19	15	US-11-101-244-156911	Sequence 156911,
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401	11.2	58.9	19	15	US-11-101-244-191666	Sequence 191666,
402	11.2	58.9	19	15	US-11-101-244-193397	Sequence 193397,
403	11.2	58.9	19	15	US-11-101-244-224244	Sequence 224244,
404	11.2	58.9	19	15	US-11-101-244-224276	Sequence 224276,
405	11.2	58.9	19	15	US-11-101-244-236018	Sequence 236018,
406	11.2	58.9	19	15	US-11-101-244-236027	Sequence 236027,
407	11.2	58.9	19	15	US-11-101-244-277905	Sequence 277905,
408	11.2	58.9	19	15	US-11-101-244-325875	Sequence 325875,
409	11.2	58.9	19	15	US-11-101-244-346400	Sequence 346400,
410	11.2	58.9	19	15	US-11-101-244-389329	Sequence 389329,
411	11.2	58.9	19	15	US-11-101-244-505329	Sequence 505329,
412	11.2	58.9	19	15	US-11-101-244-518161	Sequence 518161,
413	11.2	58.9	19	15	US-11-101-244-537656	Sequence 537656,
414	11.2	58.9	19	15	US-11-101-244-579191	Sequence 579191,
415	11.2	58.9	19	15	US-11-101-244-587302	Sequence 587302,
416	11.2	58.9	19	15	US-11-101-244-587315	Sequence 587315,
417	11.2	58.9	19	15	US-11-101-244-588252	Sequence 588252,
418	11.2	58.9	19	15	US-11-101-244-618851	Sequence 618851,
419	11.2	58.9	19	15	US-11-101-244-664549	Sequence 664549,
420	11.2	58.9	19	15	US-11-101-244-664719	Sequence 664719,
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423	11.2	58.9	19	15	US-11-101-244-744868	Sequence 744868,
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430	11.2	58.9	19	15	US-11-101-244-873164	Sequence 873164,
431	11.2	58.9	19	15	US-11-101-244-890982	Sequence 890982,
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435	11.2	58.9	19	15	US-11-101-244-1036215	Sequence 1036215,
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441	11.2	58.9	19	15	US-11-101-244-1112807	Sequence 1112807,
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445	11.2	58.9	19	15	US-11-101-244-1171715	Sequence 1171715,
446	11.2	58.9	19	15	US-11-101-244-1171743	Sequence 1171743,
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453	11.2	58.9	19	15	US-11-101-244-1342570	Sequence 1342570,
454	11.2	58.9	19	15	US-11-101-244-1449798	Sequence 1449798,
455	11.2	58.9	19	15	US-11-101-244-1449808	Sequence 1449808,
456	11.2	58.9	19	15	US-11-101-244-1481525	Sequence 1481525,
457	11.2	58.9	19	15	US-11-101-244-1558682	Sequence 1558682,
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460	11.2	58.9	19	15	US-11-101-244-1589494	Sequence 1589494,
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462	11.2	58.9	19	10	US-10-671-883-35	Sequence 35, Ap1
463	11.2	58.9	19	10	US-10-671-883-43	Sequence 43, Ap1
464	11.2	58.9	19	10	US-10-864-044-39	Sequence 39, Ap1
465	11.2	58.9	19	10	US-10-864-044-139	Sequence 139, App
466	11.2	58.9	19	11	US-10-310-914A-117520	Sequence 1137520,
467	11.2	58.9	19	11	US-10-310-914A-1333042	Sequence 1323042,
468	11.2	58.9	19	11	US-10-310-914A-1333076	Sequence 1323076,
469	11.2	58.9	19	14	US-11-083-784-753	Sequence 753, App
470	11.2	58.9	19	14	US-11-083-784-40450	Sequence 40450, A
471	11.2	58.9	19	14	US-11-083-784-76412	Sequence 76412, A
472	11.2	58.9	19	14	US-11-083-784-93476	Sequence 93476, A
473	11.2	58.9	19	14	US-11-083-784-112575	Sequence 112575,
474	11.2	58.9	19	14	US-11-083-784-112811	Sequence 112811,
475	11.2	58.9	19	14	US-11-083-784-165071	Sequence 165071,
476	11.2	58.9	19	14	US-11-083-784-165170	Sequence 165170,
477	11.2	58.9	19	14	US-11-083-784-165273	Sequence 165273,
478	11.2	58.9	19	14	US-11-083-784-165373	Sequence 165373,
479	11.2	58.9	19	14	US-11-083-784-165483	Sequence 165483,
480	11.2	58.9	19	14	US-11-083-784-185350	Sequence 185350,
481	11.2	58.9	19	14	US-11-083-784-222010	Sequence 222010,
482	11.2	58.9	19	14	US-11-083-784-415574	Sequence 415574,
483	11.2	58.9	19	14	US-11-083-784-415594	Sequence 415594,
484	11.2	58.9	19	14	US-11-083-784-415625	Sequence 415625,
485	11.2	58.9	19	14	US-11-083-784-442137	Sequence 442137,
486	11.2	58.9	19	14	US-11-083-784-447063	Sequence 447063,
487	11.2	58.9	19	14	US-11-083-784-473387	Sequence 473387,
488	11.2	58.9	19	14	US-11-083-784-509990	Sequence 509990,
489	11.2	58.9	19	14	US-11-083-784-518167	Sequence 518167,
490	11.2	58.9	19	14	US-11-083-784-518944	Sequence 518944,
491	11.2	58.9	19	14	US-11-083-784-559609	Sequence 559609,
492	11.2	58.9	19	14	US-11-083-784-633006	Sequence 633006,
493	11.2	58.9	19	14	US-11-083-784-642216	Sequence 642216,
494	11.2	58.9	19	14	US-11-083-784-642267	Sequence 642267,
495	11.2	58.9	19	14	US-11-083-784-649640	Sequence 649640,
496	11.2	58.9	19	14	US-11-083-784-649671	Sequence 649671,
497	11.2	58.9	19	14	US-11-083-784-666334	Sequence 666334,
498	11.2	58.9	19	14	US-11-083-784-666398	Sequence 666398,
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504	11.2	58.9	19	14	US-11-083-784-877409	Sequence 877409,
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523	11.2	58.9	19	14	US-11-083-784-1344077	Sequence 1344077,
524	11.2	58.9	19	14	US-11-083-784-1379512	Sequence 1379512,
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527	11.2	58.9	19	14	US-11-083-784-1391776	Sequence 1391776,
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C 530	11	57.9	19	14	US-11-083-784-1394946	Sequence 1394946,	C 603	11	57.9	19	15	US-11-110-011-23	Sequence 23, App1
C 531	11	57.9	19	14	US-11-083-784-1415916	Sequence 1415916,	C 604	10.8	56.8	19	7	US-10-251-117-626	Sequence 626, App
C 532	11	57.9	19	14	US-11-083-784-1487768	Sequence 1487768,	C 605	10.8	56.8	19	7	US-10-251-117-933	Sequence 933, App
C 533	11	57.9	19	14	US-11-083-784-1538882	Sequence 1538882,	C 606	10.8	56.8	19	10	US-10-923-354-572	Sequence 572, App
C 534	11	57.9	19	14	US-11-083-784-1545060	Sequence 1545060,	C 607	10.8	56.8	19	10	US-10-923-354-879	Sequence 879, App
C 535	11	57.9	19	14	US-11-083-784-1569410	Sequence 1569410,	C 608	10.8	56.8	19	11	US-10-310-914A-44955	Sequence 44955, A
C 536	11	57.9	19	15	US-11-101-244-753	Sequence 753, App	C 609	10.8	56.8	19	11	US-10-310-914A-56001	Sequence 56001, A
C 537	11	57.9	19	15	US-11-101-244-40450	Sequence 40450, A	C 610	10.8	56.8	19	11	US-10-310-914A-62832	Sequence 62832,
C 538	11	57.9	19	15	US-11-101-244-76412	Sequence 76412, A	C 611	10.8	56.8	19	11	US-10-310-914A-1106388	Sequence 1106388,
C 539	11	57.9	19	15	US-11-101-244-93476	Sequence 93476, A	C 612	10.8	56.8	19	11	US-10-310-914A-1106627	Sequence 1106627,
C 540	11	57.9	19	15	US-11-101-244-112575	Sequence 112575,	C 613	10.8	56.8	19	11	US-10-310-914A-1159114	Sequence 1159114,
C 541	11	57.9	19	15	US-11-101-244-112811	Sequence 112811,	C 614	10.8	56.8	19	14	US-11-083-784-880	Sequence 880, App
C 542	11	57.9	19	15	US-11-101-244-165071	Sequence 165071,	C 615	10.8	56.8	19	14	US-11-083-784-15392	Sequence 15392, App
C 543	11	57.9	19	15	US-11-101-244-165170	Sequence 165170,	C 616	10.8	56.8	19	14	US-11-083-784-17557	Sequence 17457, A
C 544	11	57.9	19	15	US-11-101-244-165273	Sequence 165273,	C 617	10.8	56.8	19	14	US-11-083-784-17554	Sequence 17554, A
C 545	11	57.9	19	15	US-11-101-244-165373	Sequence 165373,	C 618	10.8	56.8	19	14	US-11-083-784-17656	Sequence 17656, A
C 546	11	57.9	19	15	US-11-101-244-165483	Sequence 165483,	C 619	10.8	56.8	19	14	US-11-083-784-17755	Sequence 17755, A
C 547	11	57.9	19	15	US-11-101-244-185350	Sequence 185350,	C 620	10.8	56.8	19	14	US-11-083-784-17855	Sequence 17855, A
C 548	11	57.9	19	15	US-11-101-244-223010	Sequence 223010,	C 621	10.8	56.8	19	14	US-11-083-784-17955	Sequence 17955, A
C 549	11	57.9	19	15	US-11-101-244-415574	Sequence 415574,	C 622	10.8	56.8	19	14	US-11-083-784-17955	Sequence 17955, A
C 550	11	57.9	19	15	US-11-101-244-415594	Sequence 415594,	C 623	10.8	56.8	19	14	US-11-083-784-18044	Sequence 18044, A
C 551	11	57.9	19	15	US-11-101-244-415625	Sequence 415625,	C 624	10.8	56.8	19	14	US-11-083-784-63911	Sequence 63911, A
C 552	11	57.9	19	15	US-11-101-244-442137	Sequence 442137,	C 625	10.8	56.8	19	14	US-11-083-784-152817	Sequence 152817,
C 553	11	57.9	19	15	US-11-101-244-442137	Sequence 442137,	C 626	10.8	56.8	19	14	US-11-083-784-152817	Sequence 152817,
C 554	11	57.9	19	15	US-11-101-244-473387	Sequence 473387,	C 627	10.8	56.8	19	14	US-11-083-784-152427	Sequence 152427,
C 555	11	57.9	19	15	US-11-101-244-509990	Sequence 509990,	C 628	10.8	56.8	19	14	US-11-083-784-157546	Sequence 157546,
C 556	11	57.9	19	15	US-11-101-244-518167	Sequence 518167,	C 629	10.8	56.8	19	14	US-11-083-784-16525	Sequence 16525,
C 557	11	57.9	19	15	US-11-101-244-518944	Sequence 518944,	C 630	10.8	56.8	19	14	US-11-083-784-152794	Sequence 152794,
C 558	11	57.9	19	15	US-11-101-244-559809	Sequence 559809,	C 631	10.8	56.8	19	14	US-11-083-784-152817	Sequence 152817,
C 559	11	57.9	19	15	US-11-101-244-633006	Sequence 633006,	C 632	10.8	56.8	19	14	US-11-083-784-162427	Sequence 162427,
C 560	11	57.9	19	15	US-11-101-244-643216	Sequence 643216,	C 633	10.8	56.8	19	14	US-11-083-784-162427	Sequence 162427,
C 561	11	57.9	19	15	US-11-101-244-643267	Sequence 643267,	C 634	10.8	56.8	19	14	US-11-083-784-16525	Sequence 16525,
C 562	11	57.9	19	15	US-11-101-244-643640	Sequence 643640,	C 635	10.8	56.8	19	14	US-11-083-784-165616	Sequence 165616,
C 563	11	57.9	19	15	US-11-101-244-645671	Sequence 645671,	C 636	10.8	56.8	19	14	US-11-083-784-202557	Sequence 202557,
C 564	11	57.9	19	15	US-11-101-244-666334	Sequence 666334,	C 637	10.8	56.8	19	14	US-11-083-784-224249	Sequence 224249,
C 565	11	57.9	19	15	US-11-101-244-666398	Sequence 666398,	C 638	10.8	56.8	19	14	US-11-083-784-240402	Sequence 240402,
C 566	11	57.9	19	15	US-11-101-244-666398	Sequence 666398,	C 639	10.8	56.8	19	14	US-11-083-784-240641	Sequence 240641,
C 567	11	57.9	19	15	US-11-101-244-669428	Sequence 669428,	C 640	10.8	56.8	19	14	US-11-083-784-241175	Sequence 241175,
C 568	11	57.9	19	15	US-11-101-244-739979	Sequence 739979,	C 641	10.8	56.8	19	14	US-11-083-784-267679	Sequence 267679,
C 569	11	57.9	19	15	US-11-101-244-813149	Sequence 813149,	C 642	10.8	56.8	19	14	US-11-083-784-267679	Sequence 267679,
C 570	11	57.9	19	15	US-11-101-244-813149	Sequence 813149,	C 643	10.8	56.8	19	14	US-11-083-784-267679	Sequence 267679,
C 571	11	57.9	19	15	US-11-101-244-877308	Sequence 877308,	C 644	10.8	56.8	19	14	US-11-083-784-267679	Sequence 267679,
C 572	11	57.9	19	15	US-11-101-244-877409	Sequence 877409,	C 645	10.8	56.8	19	14	US-11-083-784-267679	Sequence 267679,
C 573	11	57.9	19	15	US-11-101-244-878601	Sequence 878601,	C 646	10.8	56.8	19	14	US-11-083-784-267679	Sequence 267679,
C 574	11	57.9	19	15	US-11-101-244-977457	Sequence 977457,	C 647	10.8	56.8	19	14	US-11-083-784-267679	Sequence 267679,
C 575	11	57.9	19	15	US-11-101-244-977466	Sequence 977466,	C 648	10.8	56.8	19	14	US-11-083-784-267679	Sequence 267679,
C 576	11	57.9	19	15	US-11-101-244-1028639	Sequence 1028639,	C 649	10.8	56.8	19	14	US-11-083-784-267679	Sequence 267679,
C 577	11	57.9	19	15	US-11-101-244-1033199	Sequence 1033199,	C 650	10.8	56.8	19	14	US-11-083-784-267679	Sequence 267679,
C 578	11	57.9	19	15	US-11-101-244-1033207	Sequence 1033207,	C 651	10.8	56.8	19	14	US-11-083-784-324131	Sequence 324131,
C 579	11	57.9	19	15	US-11-101-244-1033214	Sequence 1033214,	C 652	10.8	56.8	19	14	US-11-083-784-324232	Sequence 324232,
C 580	11	57.9	19	15	US-11-101-244-1037013	Sequence 1037013,	C 653	10.8	56.8	19	14	US-11-083-784-325880	Sequence 325880,
C 581	11	57.9	19	15	US-11-101-244-1041093	Sequence 1041093,	C 654	10.8	56.8	19	14	US-11-083-784-325925	Sequence 325925,
C 582	11	57.9	19	15	US-11-101-244-1156298	Sequence 1156298,	C 655	10.8	56.8	19	14	US-11-083-784-330918	Sequence 330918,
C 583	11	57.9	19	15	US-11-101-244-1156298	Sequence 1156298,	C 656	10.8	56.8	19	14	US-11-083-784-336510	Sequence 336510,
C 584	11	57.9	19	15	US-11-101-244-1164064	Sequence 1164064,	C 657	10.8	56.8	19	14	US-11-083-784-336710	Sequence 336710,
C 585	11	57.9	19	15	US-11-101-244-1206330	Sequence 1206330,	C 658	10.8	56.8	19	14	US-11-083-784-336710	Sequence 336710,
C 586	11	57.9	19	15	US-11-101-244-1206338	Sequence 1206338,	C 659	10.8	56.8	19	14	US-11-083-784-339066	Sequence 339066,
C 587	11	57.9	19	15	US-11-101-244-1293077	Sequence 1293077,	C 660	10.8	56.8	19	14	US-11-083-784-360672	Sequence 360672,
C 588	11	57.9	19	15	US-11-101-244-1305606	Sequence 1305606,	C 661	10.8	56.8	19	14	US-11-083-784-360672	Sequence 360672,
C 589	11	57.9	19	15	US-11-101-244-1305606	Sequence 1305606,	C 662	10.8	56.8	19	14	US-11-083-784-363791	Sequence 363791,
C 590	11	57.9	19	15	US-11-101-244-1326818	Sequence 1326818,	C 663	10.8	56.8	19	14	US-11-083-784-383845	Sequence 383845,
C 591	11	57.9	19	15	US-11-101-244-1344077	Sequence 1344077,	C 664	10.8	56.8	19	14	US-11-083-784-389260	Sequence 389260,
C 592	11	57.9	19	15	US-11-101-244-1379512	Sequence 1379512,	C 665	10.8	56.8	19	14	US-11-083-784-390580	Sequence 390580,
C 593	11	57.9	19	15	US-11-101-244-1388369	Sequence 1388369,	C 666	10.8	56.8	19	14	US-11-083-784-390712	Sequence 390712,
C 594	11	57.9	19	15	US-11-101-244-1391731	Sequence 1391731,	C 667	10.8	56.8	19	14	US-11-083-784-430712	Sequence 430712,
C 595	11	57.9	19	15	US-11-101-244-1391807	Sequence 1391807,	C 668	10.8	56.8	19	14	US-11-083-784-434661	Sequence 434661,
C 596	11	57.9	19	15	US-11-101-244-1394923	Sequence 1394923,	C 669	10.8	56.8	19	14	US-11-083-784-434672	Sequence 434672,
C 597	11	57.9	19	15	US-11-101-244-1394923	Sequence 1394923,	C 670	10.8	56.8	19	14	US-11-083-784-444689	Sequence 444689,
C 598	11	57.9	19	15	US-11-101-244-1415916	Sequence 1415916,	C 671	10.8	56.8	19	14	US-11-083-784-469666	Sequence 469666,
C 599	11	57.9	19	15	US-11-101-244-1487768	Sequence 1487768,	C 672	10.8	56.8	19	14	US-11-083-784-469765	Sequence 469765,
C 600	11	57.9	19	15	US-11-101-244-1538882	Sequence 1538882,	C 673	10.8	56.8	19	14	US-11-083-784-469819	Sequence 469819,
C 601	11	57.9	19	15	US-11-101-244-1545060	Sequence 1545060,	C 674	10.8	56.8	19	14	US-11-083-784-486076	Sequence 486076,

C 675	-10.8	56.8	19	14	US-11-083-784-486104	Sequence 486104,	C 748	10.8	56.8	19	14	US-11-083-784-1277890	Sequence 1277890,
C 676	-10.8	56.8	19	14	US-11-083-784-486136	Sequence 486136,	C 749	10.8	56.8	19	14	US-11-083-784-1277922	Sequence 1277922,
C 677	-10.8	56.8	19	14	US-11-083-784-501009	Sequence 501009,	C 750	10.8	56.8	19	14	US-11-083-784-1281531	Sequence 1281531,
C 678	-10.8	56.8	19	14	US-11-083-784-505436	Sequence 505436,	C 751	10.8	56.8	19	14	US-11-083-784-1305609	Sequence 1305609,
C 679	-10.8	56.8	19	14	US-11-083-784-513499	Sequence 513499,	C 752	10.8	56.8	19	14	US-11-083-784-1330468	Sequence 1330468,
C 680	-10.8	56.8	19	14	US-11-083-784-513502	Sequence 513502,	C 753	10.8	56.8	19	14	US-11-083-784-1330474	Sequence 1330474,
C 681	-10.8	56.8	19	14	US-11-083-784-553705	Sequence 553705,	C 754	10.8	56.8	19	14	US-11-083-784-1351416	Sequence 1351416,
C 682	-10.8	56.8	19	14	US-11-083-784-554055	Sequence 554055,	C 755	10.8	56.8	19	14	US-11-083-784-1351420	Sequence 1351420,
C 683	-10.8	56.8	19	14	US-11-083-784-568816	Sequence 568816,	C 756	10.8	56.8	19	14	US-11-083-784-1351433	Sequence 1351433,
C 684	-10.8	56.8	19	14	US-11-083-784-568927	Sequence 568927,	C 757	10.8	56.8	19	14	US-11-083-784-1395315	Sequence 1395315,
C 685	-10.8	56.8	19	14	US-11-083-784-572332	Sequence 572332,	C 758	10.8	56.8	19	14	US-11-083-784-1395853	Sequence 1395853,
C 686	-10.8	56.8	19	14	US-11-083-784-572607	Sequence 572607,	C 759	10.8	56.8	19	14	US-11-083-784-1425265	Sequence 1425265,
C 687	-10.8	56.8	19	14	US-11-083-784-572691	Sequence 572691,	C 760	10.8	56.8	19	14	US-11-083-784-1431142	Sequence 1431142,
C 688	-10.8	56.8	19	14	US-11-083-784-580416	Sequence 580416,	C 761	10.8	56.8	19	14	US-11-083-784-1431153	Sequence 1431153,
C 689	-10.8	56.8	19	14	US-11-083-784-593993	Sequence 593993,	C 762	10.8	56.8	19	14	US-11-083-784-1443616	Sequence 1443616,
C 690	-10.8	56.8	19	14	US-11-083-784-594022	Sequence 594022,	C 763	10.8	56.8	19	14	US-11-083-784-1445855	Sequence 1445855,
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C 693	-10.8	56.8	19	14	US-11-083-784-599745	Sequence 599745,	C 766	10.8	56.8	19	14	US-11-083-784-1460811	Sequence 1460811,
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C 695	-10.8	56.8	19	14	US-11-083-784-633180	Sequence 633180,	C 768	10.8	56.8	19	14	US-11-083-784-1474448	Sequence 1474448,
C 696	-10.8	56.8	19	14	US-11-083-784-646600	Sequence 646600,	C 769	10.8	56.8	19	14	US-11-083-784-1484903	Sequence 1484903,
C 697	-10.8	56.8	19	14	US-11-083-784-648239	Sequence 648239,	C 770	10.8	56.8	19	14	US-11-083-784-1516651	Sequence 1516651,
C 698	-10.8	56.8	19	14	US-11-083-784-658095	Sequence 658095,	C 771	10.8	56.8	19	14	US-11-083-784-1517262	Sequence 1517262,
C 699	-10.8	56.8	19	14	US-11-083-784-658195	Sequence 658195,	C 772	10.8	56.8	19	14	US-11-083-784-1562109	Sequence 1562109,
C 700	-10.8	56.8	19	14	US-11-083-784-6587518	Sequence 6587518,	C 773	10.8	56.8	19	14	US-11-083-784-1589574	Sequence 1589574,
C 701	-10.8	56.8	19	14	US-11-083-784-716277	Sequence 716277,	C 774	10.8	56.8	19	15	US-11-101-244-880	Sequence 880, App
C 702	-10.8	56.8	19	14	US-11-083-784-716304	Sequence 716304,	C 775	10.8	56.8	19	15	US-11-101-244-1892	Sequence 7892, App
C 703	-10.8	56.8	19	14	US-11-083-784-731789	Sequence 731789,	C 776	10.8	56.8	19	15	US-11-101-244-15332	Sequence 15392, A
C 704	-10.8	56.8	19	14	US-11-083-784-745656	Sequence 745656,	C 777	10.8	56.8	19	15	US-11-101-244-17457	Sequence 17457, A
C 705	-10.8	56.8	19	14	US-11-083-784-781918	Sequence 781918,	C 778	10.8	56.8	19	15	US-11-101-244-17554	Sequence 17554, A
C 706	-10.8	56.8	19	14	US-11-083-784-786630	Sequence 786630,	C 779	10.8	56.8	19	15	US-11-101-244-17666	Sequence 17656, A
C 707	-10.8	56.8	19	14	US-11-083-784-814657	Sequence 814657,	C 780	10.8	56.8	19	15	US-11-101-244-17755	Sequence 17755, A
C 708	-10.8	56.8	19	14	US-11-083-784-839928	Sequence 839928,	C 781	10.8	56.8	19	15	US-11-101-244-17856	Sequence 17856, A
C 709	-10.8	56.8	19	14	US-11-083-784-8733932	Sequence 8733932,	C 782	10.8	56.8	19	15	US-11-101-244-17955	Sequence 17955, A
C 710	-10.8	56.8	19	14	US-11-083-784-874469	Sequence 874469,	C 783	10.8	56.8	19	15	US-11-101-244-63811	Sequence 63811, A
C 711	-10.8	56.8	19	14	US-11-083-784-895717	Sequence 895717,	C 784	10.8	56.8	19	15	US-11-101-244-63911	Sequence 63911, A
C 712	-10.8	56.8	19	14	US-11-083-784-915123	Sequence 915123,	C 785	10.8	56.8	19	15	US-11-101-244-64010	Sequence 64010, A
C 713	-10.8	56.8	19	14	US-11-083-784-921916	Sequence 921916,	C 786	10.8	56.8	19	15	US-11-101-244-102948	Sequence 102948,
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C 715	-10.8	56.8	19	14	US-11-083-784-935774	Sequence 935774,	C 788	10.8	56.8	19	15	US-11-101-244-146721	Sequence 146721,
C 716	-10.8	56.8	19	14	US-11-083-784-935832	Sequence 935832,	C 789	10.8	56.8	19	15	US-11-101-244-152794	Sequence 152794,
C 717	-10.8	56.8	19	14	US-11-083-784-9358743	Sequence 9358743,	C 790	10.8	56.8	19	15	US-11-101-244-152917	Sequence 152917,
C 718	-10.8	56.8	19	14	US-11-083-784-949400	Sequence 949400,	C 791	10.8	56.8	19	15	US-11-101-244-152917	Sequence 152917,
C 719	-10.8	56.8	19	14	US-11-083-784-949437	Sequence 949437,	C 792	10.8	56.8	19	15	US-11-101-244-162427	Sequence 162427,
C 720	-10.8	56.8	19	14	US-11-083-784-963013	Sequence 963013,	C 793	10.8	56.8	19	15	US-11-101-244-167546	Sequence 167546,
C 721	-10.8	56.8	19	14	US-11-083-784-963036	Sequence 963036,	C 794	10.8	56.8	19	15	US-11-101-244-196629	Sequence 196629,
C 722	-10.8	56.8	19	14	US-11-083-784-986096	Sequence 986096,	C 795	10.8	56.8	19	15	US-11-101-244-196616	Sequence 196616,
C 723	-10.8	56.8	19	14	US-11-083-784-992457	Sequence 992457,	C 796	10.8	56.8	19	15	US-11-101-244-202557	Sequence 202557,
C 724	-10.8	56.8	19	14	US-11-083-784-1003600	Sequence 1003600,	C 797	10.8	56.8	19	15	US-11-101-244-224249	Sequence 224249,
C 725	-10.8	56.8	19	14	US-11-083-784-1003626	Sequence 1003626,	C 798	10.8	56.8	19	15	US-11-101-244-240402	Sequence 240402,
C 726	-10.8	56.8	19	14	US-11-083-784-1003658	Sequence 1003658,	C 799	10.8	56.8	19	15	US-11-101-244-240641	Sequence 240641,
C 727	-10.8	56.8	19	14	US-11-083-784-1036686	Sequence 1036686,	C 800	10.8	56.8	19	15	US-11-101-244-241175	Sequence 241175,
C 728	-10.8	56.8	19	14	US-11-083-784-1041287	Sequence 1041287,	C 801	10.8	56.8	19	15	US-11-101-244-266799	Sequence 266799,
C 729	-10.8	56.8	19	14	US-11-083-784-1043478	Sequence 1043478,	C 802	10.8	56.8	19	15	US-11-101-244-266822	Sequence 266822,
C 730	-10.8	56.8	19	14	US-11-083-784-1049272	Sequence 1049272,	C 803	10.8	56.8	19	15	US-11-101-244-267407	Sequence 267407,
C 731	-10.8	56.8	19	14	US-11-083-784-1051135	Sequence 1051135,	C 804	10.8	56.8	19	15	US-11-101-244-267507	Sequence 267507,
C 732	-10.8	56.8	19	14	US-11-083-784-1051181	Sequence 1051181,	C 805	10.8	56.8	19	15	US-11-101-244-267607	Sequence 267607,
C 733	-10.8	56.8	19	14	US-11-083-784-1074083	Sequence 1074083,	C 806	10.8	56.8	19	15	US-11-101-244-267707	Sequence 267707,
C 734	-10.8	56.8	19	14	US-11-083-784-1084994	Sequence 1084994,	C 807	10.8	56.8	19	15	US-11-101-244-273808	Sequence 273808,
C 735	-10.8	56.8	19	14	US-11-083-784-1085100	Sequence 1085100,	C 808	10.8	56.8	19	15	US-11-101-244-273808	Sequence 273808,
C 736	-10.8	56.8	19	14	US-11-083-784-1090966	Sequence 1090966,	C 809	10.8	56.8	19	15	US-11-101-244-280504	Sequence 280504,
C 737	-10.8	56.8	19	14	US-11-083-784-1113172	Sequence 1113172,	C 810	10.8	56.8	19	15	US-11-101-244-294659	Sequence 294659,
C 738	-10.8	56.8	19	14	US-11-083-784-1113250	Sequence 1113250,	C 811	10.8	56.8	19	15	US-11-101-244-324131	Sequence 324131,
C 739	-10.8	56.8	19	14	US-11-083-784-1128521	Sequence 1128521,	C 812	10.8	56.8	19	15	US-11-101-244-324232	Sequence 324232,
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C 823	10.8	56.8	19	15	US-11-101-244-389260	Sequence 389260,
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C 924	10.8	56.8	19	15	US-11-101-244-1516531	Sequence 1516531,
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C 943	10.6	55.8	19	10	US-10-922-672-938	Sequence 938, App
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## ALIGNMENTS

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RESULT 1
US-10-636-065-29
; Sequence 29, Application US/10636065
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636,065
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: based on Homo sapiens
US-10-636-065-29
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Best Local Similarity 100.0%; Pred. No. 9.2;
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; Sequence 787223, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 787223
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-787223
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RESULT 3
US-11-101-244-787223/C
; Sequence 787223, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 787223
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-787223
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Best Local Similarity 93.8%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 3 CACGGATCTCTCTTCA 18
Db 3 CACGGATCTCTCTTCA 18
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Db 16 CACGGAATCTCTTCA 1

RESULT 4

US-10-400-382-29

Sequence 29, Application US/10400382

Publication No. US20030190659A1

GENERAL INFORMATION:

APPLICANT: Lacasse, Eric

APPLICANT: McManus, Daniel

APPLICANT: Durkin, Jonathan P.

TITLE OF INVENTION: Antisense iAP Nucleobase Oligomers and

FILE REFERENCE: 07891/025004

CURRENT APPLICATION NUMBER: US/10/400,382

PRIOR FILING DATE: 2003-03-27

PRIOR APPLICATION NUMBER: US 60/367,853

NUMBER OF SEQ ID NOS: 460

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 29

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: based on Homo sapiens.

OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,

OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog

NAME/KEY: misc feature

LOCATION: 8, 10, 12, 15, 16

OTHER INFORMATION: n = T or U

US-10-400-382-29

Query Match 73.7%; Score 14; DB 7; Length 19;

Best Local Similarity 73.7%; Pred. No. 3.9e+03;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCTTCAC 19

Db 1 CGCAGGNNANCCNNCAC 19

RESULT 5

US-10-400-382-107

Sequence 107, Application US/10400382

Publication No. US20030190659A1

GENERAL INFORMATION:

APPLICANT: Lacasse, Eric

APPLICANT: McManus, Daniel

APPLICANT: Durkin, Jonathan P.

TITLE OF INVENTION: Antisense iAP Nucleobase Oligomers and

FILE REFERENCE: 07891/025004

CURRENT APPLICATION NUMBER: US/10/400,382

PRIOR FILING DATE: 2003-03-27

PRIOR APPLICATION NUMBER: US 60/367,853

NUMBER OF SEQ ID NOS: 460

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 107

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: based on Homo sapiens.

OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,

OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog

NAME/KEY: misc feature

LOCATION: 8, 10, 12, 15, 16

OTHER INFORMATION: n = T or U

US-10-400-382-107

Query Match 73.7%; Score 14; DB 7; Length 19;

Best Local Similarity 73.7%; Pred. No. 3.9e+03;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCTTCAC 19

Db 1 CGCAGGNNANCCNNCAC 19

RESULT 6

US-10-975-790-29

Sequence 29, Application US/10975790

Publication No. US20050119217A1

GENERAL INFORMATION:

APPLICANT: Lacasse, Eric

APPLICANT: McManus, Daniel

APPLICANT: Durkin, Jonathan P.

TITLE OF INVENTION: METHODS AND REAGENTS FOR THE TREATMENT

FILE REFERENCE: 07891/039002

CURRENT APPLICATION NUMBER: US/10/975,790

PRIOR FILING DATE: 2004-10-28

PRIOR APPLICATION NUMBER: 60/516,263

NUMBER OF SEQ ID NOS: 490

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 29

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: based on Homo sapiens.

OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,

OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog

NAME/KEY: misc feature

LOCATION: 8, 10, 12, 15, 16

OTHER INFORMATION: n = T or U

US-10-975-790-29

Query Match 73.7%; Score 14; DB 10; Length 19;

Best Local Similarity 73.7%; Pred. No. 3.9e+03;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGCAGGTATCTCTTCAC 19

Db 1 CGCAGGNNANCCNNCAC 19

RESULT 7

US-10-975-790-107

Sequence 107, Application US/10975790

Publication No. US20050119217A1

GENERAL INFORMATION:

APPLICANT: Lacasse, Eric

APPLICANT: McManus, Daniel

APPLICANT: Durkin, Jonathan P.

TITLE OF INVENTION: METHODS AND REAGENTS FOR THE TREATMENT

FILE REFERENCE: 07891/039002

CURRENT APPLICATION NUMBER: US/10/975,790

PRIOR FILING DATE: 2004-10-28

PRIOR APPLICATION NUMBER: 60/516,263

NUMBER OF SEQ ID NOS: 490

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 107

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: based on Homo sapiens.

```
; OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,  
; OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 8, 10, 12, 15, 16  
; OTHER INFORMATION: n = T or U  
; US-10-975-790-107
```

```
Query Match          73.7%; Score 14; DB 10; Length 19;  
Best Local Similarity 73.7%; Pred. No. 3.2e+03;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      1 CGCAGCGATCTCTTCAC 19  
Db      1 CGCAGCGANNCNNCCAC 19
```

```
RESULT 8  
US-11-083-784-798689/c
```

```
; Sequence 798689, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 798689  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
; US-11-083-784-798689
```

```
Query Match          70.5%; Score 13.4; DB 14; Length 19;  
Best Local Similarity 93.3%; Pred. No. 8.2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 CGGTATCTCTTCAC 19  
Db      18 CAGTATCTCTTCAC 4
```

```
RESULT 9  
US-11-101-244-798689/c
```

```
; Sequence 798689, Application US/1101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137
```

```
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 798689  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
; US-11-101-244-798689
```

```
Query Match          70.5%; Score 13.4; DB 15; Length 19;  
Best Local Similarity 93.3%; Pred. No. 8.2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 CGGTATCTCTTCAC 19  
Db      18 CAGTATCTCTTCAC 4
```

```
RESULT 10  
US-10-739-904-10/c
```

```
; Sequence 10, Application US/10739904  
; Publication No. US20050181373A1  
; GENERAL INFORMATION:
```

```
; APPLICANT: SMITH, Timothy P.  
; APPLICANT: CASAS, Eduardo  
; TITLE OF INVENTION: Single Nucleotide Polymorphism Markers in the Bovine  
; FILE REFERENCE: 0103.03 Timothy P. Smith et al.  
; CURRENT APPLICATION NUMBER: US/10/739,904  
; CURRENT FILING DATE: 2003-12-18  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; US-10-739-904-10
```

```
Query Match          68.4%; Score 13; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 CACGTATCTCTCT 15  
Db      17 CACGTATCTCTCT 5
```

```
RESULT 11  
US-11-083-784-1156068/c
```

```
; Sequence 1156068, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1156068  
; LENGTH: 19  
; TYPE: RNA
```



```
; ORGANISM: Homo sapiens
US-11-083-784-1156068

Query Match
Best Local Similarity 68.4%; Score 13; DB 14; Length 19;
Matches 13; Conservative 100.0%; Pred. No. 1.3e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTATCTCTCTCA 18
Db 13 GGTATCTCTCTCA 1

RESULT 12
US-11-101-244-1156068/C
; Sequence 1156068, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1156068
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1156068

Query Match
Best Local Similarity 68.4%; Score 13; DB 15; Length 19;
Matches 13; Conservative 100.0%; Pred. No. 1.3e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTATCTCTCTCA 18
Db 13 GGTATCTCTCTCA 1

RESULT 13
US-11-083-784-224158/C
; Sequence 224158, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 224158
; LENGTH: 19
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-224158

Query Match
Best Local Similarity 67.4%; Score 12.8; DB 14; Length 19;
Matches 14; Conservative 87.5%; Pred. No. 1.7e+04; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCACGGTATCTCTTC 17
Db 17 GCACGGTATCTCTTC 2

RESULT 14
US-11-083-784-761475/C
; Sequence 761475, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 761475
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-761475

Query Match
Best Local Similarity 67.4%; Score 12.8; DB 14; Length 19;
Matches 14; Conservative 87.5%; Pred. No. 1.7e+04; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCACGGTATCTCTTC 17
Db 17 GCACGGTATCTCTTC 2

RESULT 15
US-11-101-244-224158/C
; Sequence 224158, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 224158
```

LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-224158

Query Match 67.4%; Score 12.8; DB 15; Length 19;  
Best Local Similarity 87.5%; Pred. No. 1.7e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGGATATCTCCTTC 17  
Db 17 GCACAGTATCTCCTTC 2

RESULT 16  
US-11-101-244-761475/c  
Sequence 761475, Application US/11101244  
Publication No. US2005024679A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 761475  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-761475

Query Match 67.4%; Score 12.8; DB 15; Length 19;  
Best Local Similarity 87.5%; Pred. No. 1.7e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCACGGATATCTCCTTC 17  
Db 17 GCACAGTATCTCCTTC 2

RESULT 17  
US-09-969-373-2206  
Sequence 2206, Application US/09969373  
Patent No. US20020133852A1  
GENERAL INFORMATION:  
APPLICANT: Eifert, Roger J.  
APPLICANT: Hauge, Brian M.  
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
FILE REFERENCE: 38-10(52679)A  
CURRENT APPLICATION NUMBER: US/09/969,373  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US 09/754,853  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: US 09/760,427  
PRIOR FILING DATE: 2001-01-13  
PRIOR APPLICATION NUMBER: US 09/855,768  
PRIOR FILING DATE: 2001-05-15  
NUMBER OF SEQ ID NOS: 4593  
SEQ ID NO 2206  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Glycine max  
US-09-969-373-2206

Query Match 66.3%; Score 12.6; DB 3; Length 19;  
Best Local Similarity 78.9%; Pred. No. 2.2e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCTTCAC 19  
Db 1 CCACGTCTCTCTTCCTTC 19

RESULT 18  
US-11-083-784-754/c  
Sequence 754, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 754  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-754

Query Match 65.3%; Score 12.4; DB 14; Length 19;  
Best Local Similarity 92.9%; Pred. No. 2.7e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CACGGTATCTCCTT 16  
Db 16 CACGGTATCTCCTT 3

RESULT 19  
US-11-083-784-183913  
Sequence 183913, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 183913  
LENGTH: 19

```

; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-183913

Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 64.3%; Pred. No. 2.7e+04;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy      6 GGATCTCTCTCCAC 19
Db      1 GGAATCCTCCUCCAC 14

RESULT 20
US-11-083-784-222011/c
; Sequence 222011, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Inc.
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 222011
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-222011

Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      3 CACGATCTCTCTT 16
Db      16 CACGATCTCTCTT 3

RESULT 21
US-11-083-784-475145/c
; Sequence 475145, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
```

```

; SOFTWARE: Proprietary
; SEQ ID NO 475145
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-475145

Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CGCAGGATCTCTCC 14
Db      14 CGCAGGATCTCTCC 1

RESULT 22
US-11-083-784-475149/c
; Sequence 475149, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 475149
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-475149

Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CGCAGGATCTCTCC 14
Db      16 CGCAGGATCTCTCC 3

RESULT 23
US-11-083-784-583673/c
; Sequence 583673, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
```

```
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 583673
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-583673
```

```
Query Match
Best Local Similarity 65.3%; Score 12.4; DB 14; Length 19;
Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 CGGTATCTCTTCA 18
DB 14 CAGTATCTCTTCA 1
```

## RESULT 24

```
US-11-083-784-798632/c
; Sequence 798632, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 798632
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-798632
```

```
Query Match
Best Local Similarity 65.3%; Score 12.4; DB 14; Length 19;
Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 CGGTATCTCTTCA 18
DB 14 CAGTATCTCTTCA 1
```

## RESULT 25

```
US-11-083-784-873288/c
; Sequence 873288, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
```

```
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 873288
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-873288
```

```
Query Match
Best Local Similarity 65.3%; Score 12.4; DB 14; Length 19;
Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 CGGTATCTCTTCA 18
DB 14 CAGTATCTCTTCA 1
```

## RESULT 26

```
US-11-083-784-1087813/c
; Sequence 1087813, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1087813
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1087813
```

```
Query Match
Best Local Similarity 65.3%; Score 12.4; DB 14; Length 19;
Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 ACGTATCTCTTTC 17
DB 18 ACGTATCTCTTTC 5
```

## RESULT 27

```
US-11-083-784-1087832/c
; Sequence 1087832, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

Fri Aug 11 11:55:57 2006

```

; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1087832
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1087832

```

```

Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      4 ACGGATCTCTCCTTC 17
Db      15 ACGGATCTCTCCTTC 2

```

```

RESULT 28
US-11-083-784-1180480/c
; Sequence 1180480, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1180480
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1180480

```

```

Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      3 CACGGATCTCTCCTTC 16
Db      16 CACGGATCTCTCCTTC 3

```

```

RESULT 29
US-11-083-784-1191739/c
; Sequence 1191739, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1191739
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1191739

```

```

Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      4 ACGGATCTCTCCTTC 17
Db      18 ACGGATCTCTCCTTC 5

```

```

RESULT 30
US-11-083-784-1191772/c
; Sequence 1191772, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1191772
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1191772

```

```

Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      4 ACGGATCTCTCCTTC 17
Db      15 ACGGATCTCTCCTTC 2

```

```

RESULT 31
US-11-083-784-1306236
; Sequence 1306236, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia

```

```
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO: 1306236
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1306236
```

```
Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 57.1%; Pred. No. 2.7e+04;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 CACGGTATCTCCTT 16
      ||| | | | | | | | | |
Db      1 CACGUAUUCUCCU 14
```

```
RESULT 32
US-11-083-784-1585329/c
/ Sequence 1585329, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO: 1585329
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1585329
```

```
Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 ACGGTATCTCCTTC 17
      ||| | | | | | | | | |
Db      18 ACAGTATCTCCTTC 5
```

```
RESULT 33
US-11-083-784-1585348/c
/ Sequence 1585348, Application US/11083784
/ Publication No. US20050245475A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO: 1585348
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1585348
```

```
Query Match      65.3%; Score 12.4; DB 14; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 ACGGTATCTCCTTC 17
      ||| | | | | | | | | |
Db      15 ACAGTATCTCCTTC 2
```

```
RESULT 34
US-11-101-244-754/c
/ Sequence 754, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO: 754
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-754
```

```
Query Match      65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 CACGGTATCTCCTT 16
      ||| | | | | | | | | |
Db      16 CACGGTATCTCCTT 3
```

```
RESULT 35
US-11-101-244-183913
/ Sequence 183913, Application US/11101244
```

Fri Aug 11 11:55:57 2006

```

; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 183913
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-183913

```

```

Query Match      65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 64.3%; Pred. No. 2.7e+04;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY      6 GGTATCTCTCTTCC 19
Db      1 GGAUUCUCUCUCCAC 14

```

```

RESULT 36
US-11-101-244-222011/c
; Sequence 222011, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 222011
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-222011

```

```

Query Match      65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      3 CACGGTATCTCTT 16
Db      16 CACGGTATCTCTT 3

```

```

RESULT 37
US-11-101-244-475145/c
; Sequence 475145, Application US/11101244
; Publication No. US20050246794A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 475145
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-475145

```

```

Query Match      65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 CGCACGGTATCTCC 14
Db      14 CGCACGGTATCTCC 1

```

```

RESULT 38
US-11-101-244-475149/c
; Sequence 475149, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 475149
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-475149

```

```

Query Match      65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 CGCACGGTATCTCC 14
Db      16 CGCACGGTATCTCC 3

```

```

RESULT 39
US-11-101-244-583673/c
; Sequence 583673, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 583673
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-583673

```

```

Query Match          65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      5 CGGTATCTCCTTCA 18
      | |||||
Db      14 CAGTATCTCCTTCA 1

```

```

RESULT 40
US-11-101-244-798632/c
; Sequence 798632, Application US/11/101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 798632
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-798632

```

```

Query Match          65.3%; Score 12.4; DB 15; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      5 CGGTATCTCCTTCA 18
      | |||||
Db      14 CAGTATCTCCTTCA 1

```

Search completed: August 10, 2006, 09:22:26  
 Job time : 641.333 secs



GenCore version 5.1.9  
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OM nucleic - nucleic search, using bw model

Run on: August 10, 2006, 08:51:05 ; Search time 88.3333 Seconds  
(without alignments)  
341.586 Million cell updates/sec

Title: US-10-636-065-29  
Perfect score: 19  
Sequence: 1 cgcacgctatctcttcac 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 27232

Minimum DB seq length: 19  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

Published Applications NA New:\*  
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2: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	57.9	19	US-10-921-554-39	Sequence 39, App1
2	11	57.9	19	US-10-921-554-139	Sequence 139, App
3	10.6	55.8	19	US-11-293-697-5004	Sequence 5004, App
4	10	52.6	19	US-11-217-936-416	Sequence 416, App
5	10	52.6	19	US-11-217-936-526	Sequence 526, App
6	10	52.6	19	US-11-217-936-1455	Sequence 1455, App
7	10	52.6	19	US-11-217-936-1924	Sequence 1924, App
8	9.8	51.6	19	US-10-921-554-94	Sequence 94, App1
9	9.8	51.6	19	US-10-921-554-194	Sequence 194, App
10	9.8	51.6	19	US-11-344-702-269	Sequence 269, App
11	9.8	51.6	19	US-11-344-702-270	Sequence 270, App
12	9.8	51.6	19	US-11-344-702-271	Sequence 271, App
13	9.8	51.6	19	US-11-345-361-269	Sequence 269, App
14	9.8	51.6	19	US-11-345-361-270	Sequence 270, App
15	9.8	51.6	19	US-11-345-361-271	Sequence 271, App
16	9.8	51.6	19	US-11-217-936-98	Sequence 98, App1
17	9.8	51.6	19	US-11-217-936-213	Sequence 213, App
18	9.8	51.6	19	US-11-217-936-2810	Sequence 2810, App
19	9.8	51.6	19	US-11-217-936-3037	Sequence 3037, App
20	9.6	50.5	19	US-10-424-339-335	Sequence 335, App
21	9.6	50.5	19	US-10-424-339-440	Sequence 440, App
22	9.6	50.5	19	US-11-102-097-517	Sequence 517, App
23	9.4	49.5	19	US-11-256-694-308	Sequence 308, App

24	9.4	49.5	19	US-11-256-694-319	Sequence 319, App
25	9.4	49.5	19	US-11-256-694-332	Sequence 332, App
26	9.4	49.5	19	US-11-256-694-333	Sequence 333, App
27	9.4	49.5	19	US-11-256-694-340	Sequence 340, App
28	9.4	49.5	19	US-11-256-694-351	Sequence 351, App
29	9.4	49.5	19	US-11-256-694-362	Sequence 362, App
30	9.4	49.5	19	US-11-256-694-373	Sequence 373, App
31	9.4	49.5	19	US-11-256-694-384	Sequence 384, App
32	9.4	49.5	19	US-11-256-694-395	Sequence 395, App
33	9.4	49.5	19	US-11-256-694-406	Sequence 406, App
34	9.4	49.5	19	US-11-217-936-4182	Sequence 4182, App
35	9.4	49.5	19	US-11-217-936-4183	Sequence 4183, App
36	9.2	48.4	19	US-11-217-936-2328	Sequence 2328, App
37	9.2	48.4	19	US-11-217-936-2346	Sequence 2346, App
38	9.2	48.4	19	US-10-825-485-591	Sequence 591, App
39	9.2	48.4	19	US-11-251-465-467	Sequence 467, App
40	9.2	48.4	19	US-11-217-936-1014	Sequence 1014, App
41	9.2	48.4	19	US-11-217-936-1483	Sequence 1483, App
42	9.2	48.4	19	US-11-217-936-2328	Sequence 2328, App
43	9.2	48.4	19	US-11-217-936-2346	Sequence 2346, App
44	9.2	48.4	19	US-11-217-936-2623	Sequence 2623, App
45	9.2	48.4	19	US-11-217-936-2641	Sequence 2641, App
46	9.2	48.4	19	US-11-217-936-4182	Sequence 4182, App
47	9.2	48.4	19	US-11-217-936-4440	Sequence 4440, App
48	9.2	48.4	19	US-11-102-097-1846	Sequence 1846, App
49	9.2	48.4	19	US-11-102-097-1847	Sequence 1847, App
50	9	47.4	19	US-10-987-453-152	Sequence 152, App
51	9	47.4	19	US-10-424-339-818	Sequence 818, App
52	9	47.4	19	US-10-424-339-846	Sequence 846, App
53	9	47.4	19	US-10-424-339-1027	Sequence 1027, App
54	9	47.4	19	US-10-424-339-1055	Sequence 1055, App
55	9	47.4	19	US-11-344-702-223	Sequence 223, App
56	9	47.4	19	US-11-345-361-223	Sequence 223, App
57	9	47.4	19	US-11-217-936-425	Sequence 425, App
58	9	47.4	19	US-11-217-936-535	Sequence 535, App
59	9	47.4	19	US-11-217-936-1440	Sequence 1440, App
60	9	47.4	19	US-11-217-936-1909	Sequence 1909, App
61	9	47.4	19	US-11-217-936-4728	Sequence 4728, App
62	9	47.4	19	US-11-102-097-1554	Sequence 1554, App
63	9	47.4	19	US-11-102-097-1555	Sequence 1555, App
64	9	47.4	19	US-11-102-097-1556	Sequence 1556, App
65	9	47.4	19	US-11-102-097-1557	Sequence 1557, App
66	9	47.4	19	US-11-102-097-2727	Sequence 2727, App
67	9	47.4	19	US-11-102-097-2890	Sequence 2890, App
68	8.8	46.3	19	US-10-501-814-10	Sequence 10, App1
69	8.8	46.3	19	US-10-501-834-101	Sequence 101, App
70	8.8	46.3	19	US-10-515-598-10	Sequence 10, App1
71	8.8	46.3	19	US-10-524-399-3	Sequence 3, App1
72	8.8	46.3	19	US-10-424-339-103	Sequence 103, App
73	8.8	46.3	19	US-10-424-339-266	Sequence 266, App
74	8.8	46.3	19	US-10-424-339-1356	Sequence 1356, App
75	8.8	46.3	19	US-10-424-339-1537	Sequence 1537, App
76	8.8	46.3	19	US-10-525-726-13	Sequence 13, App1
77	8.8	46.3	19	US-10-921-554-47	Sequence 47, App1
78	8.8	46.3	19	US-10-921-554-147	Sequence 147, App
79	8.8	46.3	19	US-10-512-466-10	Sequence 10, App1
80	8.8	46.3	19	US-10-825-485-64	Sequence 64, App1
81	8.8	46.3	19	US-10-825-485-371	Sequence 371, App
82	8.8	46.3	19	US-11-344-702-393	Sequence 393, App
83	8.8	46.3	19	US-11-344-702-394	Sequence 394, App
84	8.8	46.3	19	US-11-345-361-393	Sequence 393, App
85	8.8	46.3	19	US-11-345-361-394	Sequence 394, App
86	8.8	46.3	19	US-11-251-465-179	Sequence 179, App
87	8.8	46.3	19	US-11-251-465-421	Sequence 421, App
88	8.8	46.3	19	US-11-251-465-547	Sequence 547, App
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90	8.8	46.3	19	US-11-217-936-13	Sequence 13, App1
91	8.8	46.3	19	US-11-217-936-128	Sequence 128, App
92	8.8	46.3	19	US-11-217-936-1099	Sequence 1099, App
93	8.8	46.3	19	US-11-217-936-1568	Sequence 1568, App
94	8.8	46.3	19	US-11-217-936-3353	Sequence 3353, App
95	8.8	46.3	19	US-11-217-936-3526	Sequence 3526, App
96	8.8	46.3	19	US-11-217-936-3829	Sequence 3829, App

C 97	8.8	46.3	19	9	US-11-217-936-3925	Sequence 3925, Ap	C 170	8.2	43.2	19	9	US-11-102-097-516	Sequence 516, App
C 98	8.6	45.3	19	6	US-10-825-485-72	Sequence 72, Appl	C 171	8.2	43.2	19	9	US-11-102-097-959	Sequence 959, App
C 99	8.6	45.3	19	6	US-10-825-485-83	Sequence 83, Appl	C 172	8.2	43.2	19	9	US-11-102-097-959	Sequence 959, App
100	8.6	45.3	19	6	US-10-825-485-379	Sequence 379, App	C 173	8.2	43.2	19	9	US-11-102-097-1000	Sequence 1000, Ap
101	8.6	45.3	19	6	US-10-825-485-390	Sequence 390, App	C 174	8.2	43.2	19	9	US-11-375-650-11	Sequence 11, Appl
102	8.6	45.3	19	6	US-10-479-225A-270	Sequence 270, App	C 175	8.2	43.2	19	6	US-10-424-339-860	Sequence 860, App
C 103	8.6	45.3	19	6	US-10-479-225A-273	Sequence 273, App	C 176	8	42.1	19	6	US-10-424-339-1338	Sequence 1338, Ap
C 104	8.6	45.3	19	8	US-11-283-550-3	Sequence 3, Appl1	C 177	8	42.1	19	6	US-10-424-339-1338	Sequence 1338, Ap
C 105	8.6	45.3	19	9	US-11-217-936-2924	Sequence 2924, Ap	C 178	8	42.1	19	6	US-10-424-339-1519	Sequence 1519, Ap
C 106	8.6	45.3	19	9	US-11-217-936-3151	Sequence 3151, Ap	C 179	8	42.1	19	6	US-10-536-804-23	Sequence 23, Appl
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C 108	8.6	45.3	19	9	US-11-217-936-4813	Sequence 4813, Ap	C 181	8	42.1	19	6	US-10-881-580-8	Sequence 8, Appl1
C 109	8.4	44.2	19	6	US-10-517-441-1243	Sequence 1243, Ap	C 182	8	42.1	19	6	US-10-881-580-136	Sequence 136, Appl
C 110	8.4	44.2	19	6	US-10-424-339-390	Sequence 390, App	C 183	8	42.1	19	6	US-10-825-485-305	Sequence 305, App
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C 112	8.4	44.2	19	6	US-10-424-339-495	Sequence 495, App	C 185	8	42.1	19	7	US-11-344-702-111	Sequence 111, App
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C 114	8.4	44.2	19	6	US-10-424-339-882	Sequence 882, App	C 187	8	42.1	19	7	US-11-344-702-159	Sequence 159, App
C 115	8.4	44.2	19	6	US-10-424-339-1091	Sequence 1091, Ap	C 188	8	42.1	19	7	US-11-344-702-451	Sequence 451, App
C 116	8.4	44.2	19	6	US-10-424-339-1374	Sequence 1374, Ap	C 189	8	42.1	19	7	US-11-344-702-584	Sequence 584, App
C 117	8.4	44.2	19	6	US-10-534-780-1555	Sequence 1555, Ap	C 190	8	42.1	19	7	US-11-344-702-618	Sequence 618, App
C 118	8.4	44.2	19	6	US-10-534-780-26	Sequence 26, Appl	C 191	8	42.1	19	7	US-11-345-361-111	Sequence 111, App
C 119	8.4	44.2	19	7	US-11-344-702-336	Sequence 336, App	C 192	8	42.1	19	7	US-11-345-361-175	Sequence 175, App
C 120	8.4	44.2	19	7	US-11-344-702-689	Sequence 689, App	C 193	8	42.1	19	7	US-11-345-361-199	Sequence 199, App
C 121	8.4	44.2	19	7	US-11-345-361-336	Sequence 336, App	C 194	8	42.1	19	7	US-11-345-361-451	Sequence 451, App
C 122	8.4	44.2	19	7	US-11-445-361-689	Sequence 689, App	C 195	8	42.1	19	7	US-11-345-361-584	Sequence 584, App
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C 124	8.4	44.2	19	8	US-11-251-465-191	Sequence 191, App	C 197	8	42.1	19	8	US-11-245-473-4	Sequence 4, Appl1
C 125	8.4	44.2	19	8	US-11-051-164-6	Sequence 6, Appl1	C 198	8	42.1	19	8	US-11-251-465-155	Sequence 155, App
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C 127	8.4	44.2	19	8	US-11-018-443-17	Sequence 17, Appl	C 200	8	42.1	19	8	US-11-283-484A-23	Sequence 23, Appl1
C 128	8.4	44.2	19	9	US-11-217-936-541	Sequence 541, App	C 201	8	42.1	19	9	US-11-217-936-1415	Sequence 1415, Ap
C 129	8.4	44.2	19	9	US-11-217-936-5541	Sequence 5541, App	C 202	8	42.1	19	9	US-11-217-936-1884	Sequence 1884, Ap
C 130	8.4	44.2	19	9	US-11-217-936-2132	Sequence 2132, Ap	C 203	8	42.1	19	9	US-11-217-936-3351	Sequence 3351, Ap
C 131	8.4	44.2	19	9	US-11-217-936-2232	Sequence 2232, Ap	C 204	8	42.1	19	9	US-11-217-936-3524	Sequence 3524, Ap
C 132	8.4	44.2	19	9	US-11-217-936-2237	Sequence 2237, Ap	C 205	8	42.1	19	9	US-11-217-936-4143	Sequence 4143, Ap
C 133	8.4	44.2	19	9	US-11-217-936-2427	Sequence 2427, Ap	C 206	8	42.1	19	9	US-11-217-936-4145	Sequence 4145, Ap
C 134	8.4	44.2	19	9	US-11-217-936-2527	Sequence 2527, Ap	C 207	8	42.1	19	9	US-11-217-936-4401	Sequence 4401, Ap
C 135	8.4	44.2	19	9	US-11-217-936-2592	Sequence 2592, Ap	C 208	8	42.1	19	9	US-11-217-936-4403	Sequence 4403, Ap
C 136	8.4	44.2	19	9	US-11-320-422-35	Sequence 35, Appl1	C 209	8	42.1	19	9	US-11-102-097-1716	Sequence 1716, Ap
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C 139	8.4	44.2	19	9	US-11-102-097-1233	Sequence 1233, Ap	C 212	8	42.1	19	9	US-11-102-097-1719	Sequence 1719, Ap
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C 142	8.2	43.2	19	6	US-10-562-412-14	Sequence 14, Appl	C 215	8	42.1	19	9	US-11-102-097-2432	Sequence 2432, Ap
C 143	8.2	43.2	19	6	US-10-479-225A-160	Sequence 160, App	C 216	7.8	41.1	19	6	US-10-424-339-55	Sequence 55, Appl1
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C 149	8.2	43.2	19	6	US-10-479-225A-259	Sequence 259, App	C 222	7.8	41.1	19	6	US-10-424-339-1401	Sequence 1401, Ap
C 150	8.2	43.2	19	6	US-10-479-225A-272	Sequence 272, App	C 223	7.8	41.1	19	6	US-10-424-339-1582	Sequence 1582, Ap
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C 153	8.2	43.2	19	6	US-10-479-225A-330	Sequence 330, App	C 226	7.8	41.1	19	6	US-10-921-554-71	Sequence 71, Appl1
C 154	8.2	43.2	19	6	US-10-479-225A-331	Sequence 331, App	C 227	7.8	41.1	19	6	US-10-921-554-171	Sequence 171, App
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C 165	8.2	43.2	19	9	US-11-217-936-2091	Sequence 2091, Ap	C 238	7.8	41.1	19	7	US-11-344-702-559	Sequence 559, App
C 166	8.2	43.2	19	9	US-11-217-936-2386	Sequence 2386, Ap	C 239	7.8	41.1	19	7	US-11-344-702-560	Sequence 560, App
C 167	8.2	43.2	19	9	US-11-217-936-4740	Sequence 4740, Ap	C 240	7.8	41.1	19	7	US-11-344-702-561	Sequence 561, App
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C 169	8.2	43.2	19	9	US-11-329-900-20	Sequence 20, Appl1	C 242	7.8	41.1	19	7	US-11-344-702-638	Sequence 638, App

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C 244	7.8	41.1	19	7	US-11-344-702-640	Sequence 640, App	317	7.6	40.0	19	6	US-10-825-485-51	Sequence 51, App1
C 245	7.8	41.1	19	7	US-11-344-702-641	Sequence 641, App	318	7.6	40.0	19	6	US-10-825-485-236	Sequence 236, App
246	7.8	41.1	19	7	US-11-344-702-680	Sequence 680, App	C 319	7.6	40.0	19	6	US-10-825-485-358	Sequence 358, App
247	7.8	41.1	19	7	US-11-345-361-108	Sequence 108, App	C 320	7.6	40.0	19	6	US-10-825-485-543	Sequence 543, App
248	7.8	41.1	19	7	US-11-345-361-524	Sequence 524, App	C 321	7.6	40.0	19	6	US-10-514-558-34	Sequence 34, App1
249	7.8	41.1	19	7	US-11-345-361-525	Sequence 525, App	C 322	7.6	40.0	19	7	US-11-344-702-154	Sequence 154, App
250	7.8	41.1	19	7	US-11-345-361-526	Sequence 526, App	C 323	7.6	40.0	19	7	US-11-344-702-306	Sequence 306, App
251	7.8	41.1	19	7	US-11-345-361-558	Sequence 558, App	C 324	7.6	40.0	19	7	US-11-344-702-602	Sequence 602, App
252	7.8	41.1	19	7	US-11-345-361-559	Sequence 559, App	C 325	7.6	40.0	19	7	US-11-344-702-603	Sequence 603, App
253	7.8	41.1	19	7	US-11-345-361-560	Sequence 560, App	C 326	7.6	40.0	19	7	US-11-345-361-154	Sequence 154, App
254	7.8	41.1	19	7	US-11-345-361-561	Sequence 561, App	C 327	7.6	40.0	19	7	US-11-345-361-306	Sequence 306, App
C 255	7.8	41.1	19	7	US-11-345-361-562	Sequence 562, App	C 328	7.6	40.0	19	7	US-11-345-361-602	Sequence 602, App
C 256	7.8	41.1	19	7	US-11-345-361-638	Sequence 638, App	C 329	7.6	40.0	19	7	US-11-345-361-603	Sequence 603, App
C 257	7.8	41.1	19	7	US-11-345-361-639	Sequence 639, App	C 330	7.6	40.0	19	8	US-11-283-522-29	Sequence 29, App1
C 258	7.8	41.1	19	7	US-11-345-361-640	Sequence 640, App	C 331	7.6	40.0	19	8	US-11-281-229-33	Sequence 33, App1
C 259	7.8	41.1	19	7	US-11-345-361-641	Sequence 641, App	C 332	7.6	40.0	19	9	US-11-217-936-19	Sequence 19, App1
C 260	7.8	41.1	19	7	US-11-345-361-680	Sequence 680, App	C 333	7.6	40.0	19	9	US-11-217-936-134	Sequence 134, App1
261	7.8	41.1	19	8	US-11-251-465-168	Sequence 168, App	C 334	7.6	40.0	19	9	US-11-217-936-1191	Sequence 1191, App
262	7.8	41.1	19	8	US-11-251-465-166	Sequence 166, App	C 335	7.6	40.0	19	9	US-11-217-936-1222	Sequence 1222, App
263	7.8	41.1	19	8	US-11-251-465-443	Sequence 443, App	C 336	7.6	40.0	19	9	US-11-217-936-1660	Sequence 1660, App
C 264	7.8	41.1	19	8	US-11-251-465-671	Sequence 671, App	C 337	7.6	40.0	19	9	US-11-217-936-1691	Sequence 1691, App
C 265	7.8	41.1	19	8	US-11-233-507-94	Sequence 671, App	C 338	7.6	40.0	19	9	US-11-217-936-2086	Sequence 2086, App
C 266	7.8	41.1	19	8	US-11-018-443-25	Sequence 25, App1	C 339	7.6	40.0	19	9	US-11-217-936-2323	Sequence 2323, App
C 267	7.8	41.1	19	9	US-11-217-936-433	Sequence 433, App	C 340	7.6	40.0	19	9	US-11-217-936-2381	Sequence 2381, App
C 268	7.8	41.1	19	9	US-11-217-936-543	Sequence 543, App	C 341	7.6	40.0	19	9	US-11-217-936-2779	Sequence 2779, App
C 269	7.8	41.1	19	9	US-11-217-936-1043	Sequence 1043, App	C 342	7.6	40.0	19	9	US-11-217-936-2885	Sequence 2885, App
C 270	7.8	41.1	19	9	US-11-217-936-1066	Sequence 1066, App	C 343	7.6	40.0	19	9	US-11-217-936-2885	Sequence 2885, App
C 271	7.8	41.1	19	9	US-11-217-936-1180	Sequence 1180, App	C 344	7.6	40.0	19	9	US-11-217-936-2961	Sequence 2961, App
C 272	7.8	41.1	19	9	US-11-217-936-1284	Sequence 1284, App	C 345	7.6	40.0	19	9	US-11-217-936-3006	Sequence 3006, App
273	7.8	41.1	19	9	US-11-217-936-1512	Sequence 1512, App	C 346	7.6	40.0	19	9	US-11-217-936-3112	Sequence 3112, App
274	7.8	41.1	19	9	US-11-217-936-1513	Sequence 1513, App	C 347	7.6	40.0	19	9	US-11-217-936-3188	Sequence 3188, App
275	7.8	41.1	19	9	US-11-217-936-1649	Sequence 1649, App	C 348	7.6	40.0	19	9	US-11-217-936-3449	Sequence 3449, App
C 276	7.8	41.1	19	9	US-11-217-936-1753	Sequence 1753, App	C 349	7.6	40.0	19	9	US-11-217-936-3475	Sequence 3475, App
C 277	7.8	41.1	19	9	US-11-217-936-2203	Sequence 2203, App	C 350	7.6	40.0	19	9	US-11-217-936-3622	Sequence 3622, App
C 278	7.8	41.1	19	9	US-11-217-936-2498	Sequence 2498, App	C 351	7.6	40.0	19	9	US-11-217-936-3626	Sequence 3626, App
C 279	7.8	41.1	19	9	US-11-217-936-3490	Sequence 3490, App	C 352	7.6	40.0	19	9	US-11-217-936-3816	Sequence 3816, App
C 280	7.8	41.1	19	9	US-11-217-936-3663	Sequence 3663, App	C 353	7.6	40.0	19	9	US-11-217-936-3922	Sequence 3922, App
C 281	7.8	41.1	19	9	US-11-217-936-4183	Sequence 4183, App	C 354	7.6	40.0	19	9	US-11-296-920-30	Sequence 30, App1
C 282	7.8	41.1	19	9	US-11-217-936-4441	Sequence 4441, App	C 355	7.6	40.0	19	9	US-11-299-260-30	Sequence 30, App1
C 283	7.8	41.1	19	9	US-11-217-936-4714	Sequence 4714, App	C 356	7.6	40.0	19	9	US-11-102-097-379	Sequence 379, App
284	7.8	41.1	19	9	US-11-217-936-4811	Sequence 4811, App	C 357	7.6	40.0	19	9	US-11-102-097-380	Sequence 380, App
C 285	7.8	41.1	19	9	US-11-233-495-24	Sequence 24, App1	C 358	7.6	40.0	19	9	US-11-102-097-399	Sequence 399, App
C 286	7.8	41.1	19	9	US-11-102-097-1099	Sequence 1099, App	C 359	7.6	40.0	19	9	US-11-102-097-966	Sequence 966, App
C 287	7.8	41.1	19	9	US-11-102-097-1100	Sequence 1100, App	C 360	7.6	40.0	19	9	US-11-102-097-1402	Sequence 1402, App
C 288	7.8	41.1	19	9	US-11-102-097-1101	Sequence 1101, App	C 361	7.6	40.0	19	9	US-11-102-097-2524	Sequence 2524, App
C 289	7.8	41.1	19	9	US-11-102-097-1270	Sequence 1270, App	C 362	7.6	40.0	19	9	US-11-267-769-24	Sequence 24, App1
C 290	7.8	41.1	19	9	US-11-102-097-1558	Sequence 1558, App	C 363	7.6	40.0	19	9	US-11-267-769-24	Sequence 24, App1
C 291	7.8	41.1	19	9	US-11-102-097-1559	Sequence 1559, App	C 364	7.6	40.0	19	6	US-10-511-937-857	Sequence 857, App
C 292	7.8	41.1	19	9	US-11-102-097-1560	Sequence 1560, App	C 365	7.4	38.9	19	6	US-10-511-937-1820	Sequence 1820, App
C 293	7.8	41.1	19	9	US-11-102-097-1989	Sequence 1989, App	C 366	7.4	38.9	19	6	US-10-517-441-1207	Sequence 1207, App
C 294	7.8	41.1	19	9	US-11-102-097-2079	Sequence 2079, App	C 367	7.4	38.9	19	6	US-10-517-441-1207	Sequence 1207, App
C 295	7.8	41.1	19	9	US-11-102-097-2080	Sequence 2080, App	C 368	7.4	38.9	19	6	US-10-517-441-1223	Sequence 1223, App
296	7.6	40.0	19	6	US-10-501-814-11	Sequence 11, App1	C 369	7.4	38.9	19	6	US-10-424-339-64	Sequence 64, App1
297	7.6	40.0	19	6	US-10-514-776-6	Sequence 6, App1	C 370	7.4	38.9	19	6	US-10-424-339-126	Sequence 126, App
298	7.6	40.0	19	6	US-10-514-776-203	Sequence 203, App	C 371	7.4	38.9	19	6	US-10-424-339-227	Sequence 227, App
299	7.6	40.0	19	6	US-10-515-598-11	Sequence 11, App1	C 372	7.4	38.9	19	6	US-10-424-339-289	Sequence 289, App
C 300	7.6	40.0	19	6	US-10-469-938A-68	Sequence 68, App1	C 373	7.4	38.9	19	6	US-10-424-339-404	Sequence 404, App
C 301	7.6	40.0	19	6	US-10-517-441-1513	Sequence 1513, App	C 374	7.4	38.9	19	6	US-10-424-339-509	Sequence 509, App
C 302	7.6	40.0	19	6	US-10-424-339-58	Sequence 58, App1	C 375	7.4	38.9	19	6	US-10-424-339-671	Sequence 671, App
C 303	7.6	40.0	19	6	US-10-424-339-80	Sequence 80, App1	C 376	7.4	38.9	19	6	US-10-424-339-600	Sequence 600, App
C 304	7.6	40.0	19	6	US-10-424-339-221	Sequence 221, App	C 377	7.4	38.9	19	6	US-10-424-339-679	Sequence 679, App
C 305	7.6	40.0	19	6	US-10-424-339-243	Sequence 243, App	C 378	7.4	38.9	19	6	US-10-424-339-699	Sequence 699, App
C 306	7.6	40.0	19	6	US-10-424-339-391	Sequence 391, App	C 379	7.4	38.9	19	6	US-10-424-339-723	Sequence 723, App
C 307	7.6	40.0	19	6	US-10-424-339-496	Sequence 496, App	C 380	7.4	38.9	19	6	US-10-424-339-809	Sequence 809, App
C 308	7.6	40.0	19	6	US-10-424-339-711	Sequence 711, App	C 381	7.4	38.9	19	6	US-10-424-339-820	Sequence 820, App
C 309	7.6	40.0	19	6	US-10-424-339-920	Sequence 920, App	C 382	7.4	38.9	19	6	US-10-424-339-861	Sequence 861, App
C 310	7.6	40.0	19	6	US-10-424-339-1421	Sequence 1421, App	C 383	7.4	38.9	19	6	US-10-424-339-908	Sequence 908, App
C 311	7.6	40.0	19	6	US-10-424-339-1602	Sequence 1602, App	C 384	7.4	38.9	19	6	US-10-424-339-932	Sequence 932, App
C 312	7.6	40.0	19	6	US-10-997-086-88	Sequence 88, App1	C 385	7.4	38.9	19	6	US-10-424-339-1018	Sequence 1018, App
C 313	7.6	40.0	19	6	US-10-525-726-14	Sequence 14, App1	C 386	7.4	38.9	19	6	US-10-424-339-1029	Sequence 1029, App
C 314	7.6	40.0	19	6	US-10-536-932-54	Sequence 54, App1	C 387	7.4	38.9	19	6	US-10-424-339-1070	Sequence 1070, App
C 315	7.6	40.0	19	6	US-10-525-273-29	Sequence 29, App1	C 388	7.4	38.9	19	6	US-10-424-339-1340	Sequence 1340, App

389	7.4	38.9	19	6	US-10-424-339-1521	Sequence 1521, Ap	C 462	7.4	38.9	19	9	US-11-217-936-3607	Sequence 3607, Ap
C 390	7.4	38.9	19	6	US-10-921-554-12	Sequence 12, Appl	C 463	7.4	38.9	19	9	US-11-217-936-3818	Sequence 3818, Ap
391	7.4	38.9	19	6	US-10-921-554-112	Sequence 112, Appl	C 464	7.4	38.9	19	9	US-11-217-936-3844	Sequence 3844, Ap
392	7.4	38.9	19	6	US-10-536-932-88	Sequence 88, Appl	C 465	7.4	38.9	19	9	US-11-217-936-3850	Sequence 3850, Ap
393	7.4	38.9	19	6	US-10-534-864-20	Sequence 20, Appl	C 466	7.4	38.9	19	9	US-11-217-936-3856	Sequence 3856, Ap
C 394	7.4	38.9	19	6	US-10-825-485-163	Sequence 163, Appl	C 467	7.4	38.9	19	9	US-11-217-936-3866	Sequence 3866, Ap
C 395	7.4	38.9	19	6	US-10-825-485-270	Sequence 270, App	C 468	7.4	38.9	19	9	US-11-217-936-3914	Sequence 3914, Ap
C 396	7.4	38.9	19	6	US-10-825-485-470	Sequence 470, App	C 469	7.4	38.9	19	9	US-11-217-936-3940	Sequence 3940, Ap
397	7.4	38.9	19	6	US-10-825-485-577	Sequence 577, App	C 470	7.4	38.9	19	9	US-11-217-936-3946	Sequence 3946, Ap
398	7.4	38.9	19	7	US-11-817-120-2	Sequence 2, Appl1	C 471	7.4	38.9	19	9	US-11-217-936-3952	Sequence 3952, Ap
399	7.4	38.9	19	7	US-11-813-210-31	Sequence 31, Appl1	C 472	7.4	38.9	19	9	US-11-217-936-3962	Sequence 3962, Ap
C 400	7.4	38.9	19	7	US-11-313-210-60	Sequence 60, Appl	C 473	7.4	38.9	19	9	US-11-217-936-4091	Sequence 4091, Ap
401	7.4	38.9	19	7	US-11-344-702-109	Sequence 109, Appl	C 474	7.4	38.9	19	9	US-11-217-936-4160	Sequence 4160, Ap
402	7.4	38.9	19	7	US-11-344-702-114	Sequence 114, Appl	C 475	7.4	38.9	19	9	US-11-217-936-4242	Sequence 4242, Ap
C 403	7.4	38.9	19	7	US-11-344-702-114	Sequence 114, Appl	C 476	7.4	38.9	19	9	US-11-217-936-4263	Sequence 4263, Ap
C 404	7.4	38.9	19	7	US-11-344-702-334	Sequence 334, Appl	C 477	7.4	38.9	19	9	US-11-217-936-4303	Sequence 4303, Ap
C 405	7.4	38.9	19	7	US-11-344-702-349	Sequence 349, Appl	C 478	7.4	38.9	19	9	US-11-217-936-4349	Sequence 4349, Ap
C 406	7.4	38.9	19	7	US-11-344-702-541	Sequence 541, Appl	C 479	7.4	38.9	19	9	US-11-217-936-4418	Sequence 4418, Ap
C 407	7.4	38.9	19	7	US-11-344-702-542	Sequence 542, Appl	C 480	7.4	38.9	19	9	US-11-217-936-4500	Sequence 4500, Ap
408	7.4	38.9	19	7	US-11-344-702-631	Sequence 631, Appl	C 481	7.4	38.9	19	9	US-11-217-936-4521	Sequence 4521, Ap
C 409	7.4	38.9	19	7	US-11-344-702-632	Sequence 632, Appl	C 482	7.4	38.9	19	9	US-11-217-936-4561	Sequence 4561, Ap
C 410	7.4	38.9	19	7	US-11-344-702-634	Sequence 634, Appl	C 483	7.4	38.9	19	9	US-11-182-336-54	Sequence 54, Appl
C 411	7.4	38.9	19	7	US-11-345-361-109	Sequence 109, Appl	C 484	7.4	38.9	19	9	US-11-102-097-274	Sequence 274, Appl
412	7.4	38.9	19	7	US-11-345-361-114	Sequence 114, Appl	C 485	7.4	38.9	19	9	US-11-102-097-346	Sequence 346, Appl
C 413	7.4	38.9	19	7	US-11-345-361-334	Sequence 334, Appl	C 486	7.4	38.9	19	9	US-11-102-097-347	Sequence 347, Appl
C 414	7.4	38.9	19	7	US-11-345-361-349	Sequence 349, Appl	C 487	7.4	38.9	19	9	US-11-102-097-348	Sequence 348, Appl
C 415	7.4	38.9	19	7	US-11-345-361-419	Sequence 419, Appl	C 488	7.4	38.9	19	9	US-11-102-097-375	Sequence 375, Appl
C 416	7.4	38.9	19	7	US-11-345-361-541	Sequence 541, Appl	C 489	7.4	38.9	19	9	US-11-102-097-376	Sequence 376, Appl
C 417	7.4	38.9	19	7	US-11-345-361-542	Sequence 542, Appl	C 490	7.4	38.9	19	9	US-11-102-097-377	Sequence 377, Appl
418	7.4	38.9	19	7	US-11-345-361-631	Sequence 631, Appl	C 491	7.4	38.9	19	9	US-11-102-097-378	Sequence 378, Appl
C 419	7.4	38.9	19	7	US-11-345-361-632	Sequence 632, Appl	C 492	7.4	38.9	19	9	US-11-102-097-475	Sequence 475, Appl
C 420	7.4	38.9	19	7	US-11-345-361-634	Sequence 634, Appl	C 493	7.4	38.9	19	9	US-11-102-097-476	Sequence 476, Appl
C 421	7.4	38.9	19	8	US-11-251-465-131	Sequence 131, Appl	C 494	7.4	38.9	19	9	US-11-102-097-477	Sequence 477, Appl
C 422	7.4	38.9	19	8	US-11-251-465-151	Sequence 151, Appl	C 495	7.4	38.9	19	9	US-11-102-097-478	Sequence 478, Appl
C 423	7.4	38.9	19	8	US-11-251-465-193	Sequence 193, Appl	C 496	7.4	38.9	19	9	US-11-102-097-479	Sequence 479, Appl
C 424	7.4	38.9	19	8	US-11-251-465-407	Sequence 407, Appl	C 497	7.4	38.9	19	9	US-11-102-097-560	Sequence 560, Appl
C 425	7.4	38.9	19	8	US-11-251-465-777	Sequence 777, Appl	C 498	7.4	38.9	19	9	US-11-102-097-961	Sequence 961, Appl
426	7.4	38.9	19	8	US-11-251-465-829	Sequence 829, Appl	C 499	7.4	38.9	19	9	US-11-102-097-11025	Sequence 11025, Ap
427	7.4	38.9	19	8	US-11-267-182-11	Sequence 11, Appl1	C 500	7.4	38.9	19	9	US-11-102-097-1148	Sequence 1148, Ap
428	7.4	38.9	19	8	US-11-293-507-31	Sequence 31, Appl1	C 501	7.4	38.9	19	9	US-11-102-097-1149	Sequence 1149, Ap
C 429	7.4	38.9	19	8	US-11-293-507-5406	Sequence 5406, Ap	C 502	7.4	38.9	19	9	US-11-102-097-1228	Sequence 1228, Ap
C 430	7.4	38.9	19	8	US-11-222-565-54	Sequence 5406, Ap	C 503	7.4	38.9	19	9	US-11-102-097-1234	Sequence 1234, Ap
C 431	7.4	38.9	19	9	US-11-217-936-58	Sequence 58, Appl1	C 504	7.4	38.9	19	9	US-11-102-097-1396	Sequence 1396, Ap
C 432	7.4	38.9	19	9	US-11-217-936-83	Sequence 83, Appl1	C 505	7.4	38.9	19	9	US-11-102-097-1397	Sequence 1397, Ap
433	7.4	38.9	19	9	US-11-217-936-173	Sequence 173, Appl	C 506	7.4	38.9	19	9	US-11-102-097-1473	Sequence 1473, Ap
434	7.4	38.9	19	9	US-11-217-936-178	Sequence 178, Appl	C 507	7.4	38.9	19	9	US-11-102-097-1474	Sequence 1474, Ap
C 435	7.4	38.9	19	9	US-11-217-936-395	Sequence 395, Appl	C 508	7.4	38.9	19	9	US-11-102-097-1475	Sequence 1475, Ap
436	7.4	38.9	19	9	US-11-217-936-505	Sequence 505, Appl	C 509	7.4	38.9	19	9	US-11-102-097-1476	Sequence 1476, Ap
437	7.4	38.9	19	9	US-11-217-936-684	Sequence 684, Appl	C 510	7.4	38.9	19	9	US-11-102-097-1477	Sequence 1477, Ap
C 438	7.4	38.9	19	9	US-11-217-936-761	Sequence 761, Appl	C 511	7.4	38.9	19	9	US-11-102-097-1950	Sequence 1950, Ap
C 439	7.4	38.9	19	9	US-11-217-936-792	Sequence 792, Appl	C 512	7.4	38.9	19	9	US-11-102-097-2138	Sequence 2138, Ap
440	7.4	38.9	19	9	US-11-217-936-869	Sequence 869, Appl	C 513	7.4	38.9	19	9	US-11-102-097-2139	Sequence 2139, Ap
C 441	7.4	38.9	19	9	US-11-217-936-1202	Sequence 1202, Ap	C 514	7.4	38.9	19	9	US-11-102-097-2140	Sequence 2140, Ap
442	7.4	38.9	19	9	US-11-217-936-1331	Sequence 1331, Ap	C 515	7.4	38.9	19	9	US-11-102-097-2141	Sequence 2141, Ap
C 443	7.4	38.9	19	9	US-11-217-936-1360	Sequence 1360, Ap	C 516	7.4	38.9	19	9	US-11-102-097-2712	Sequence 2712, Ap
444	7.4	38.9	19	9	US-11-217-936-1671	Sequence 1671, Ap	C 517	7.4	38.9	19	9	US-11-102-097-2840	Sequence 2840, Ap
C 445	7.4	38.9	19	9	US-11-217-936-1829	Sequence 1829, Ap	C 518	7.4	38.9	19	9	US-11-102-097-2881	Sequence 2881, Ap
446	7.4	38.9	19	9	US-11-217-936-1829	Sequence 1829, Ap	C 519	7.4	38.9	19	9	US-11-267-769-14	Sequence 14, Appl1
C 447	7.4	38.9	19	9	US-11-217-936-2151	Sequence 2151, Ap	C 520	7.4	38.9	19	9	US-11-267-807-14	Sequence 14, Appl1
C 448	7.4	38.9	19	9	US-11-217-936-2207	Sequence 2207, Ap	C 521	7.2	37.9	19	6	US-10-501-834-189	Sequence 99, Appl1
C 449	7.4	38.9	19	9	US-11-217-936-2223	Sequence 2223, Ap	C 522	7.2	37.9	19	6	US-10-501-834-182	Sequence 182, Appl
C 450	7.4	38.9	19	9	US-11-217-936-2296	Sequence 2296, Ap	C 523	7.2	37.9	19	6	US-10-511-937-2041	Sequence 2041, Ap
C 451	7.4	38.9	19	9	US-11-217-936-2446	Sequence 2446, Ap	C 524	7.2	37.9	19	6	US-10-511-937-70	Sequence 70, Appl1
452	7.4	38.9	19	9	US-11-217-936-2502	Sequence 2502, Ap	C 525	7.2	37.9	19	6	US-10-514-776-121	Sequence 121, Appl
C 453	7.4	38.9	19	9	US-11-217-936-2518	Sequence 2518, Ap	C 526	7.2	37.9	19	6	US-10-514-776-141	Sequence 141, Appl
454	7.4	38.9	19	9	US-11-217-936-2591	Sequence 2591, Ap	C 527	7.2	37.9	19	6	US-10-514-776-142	Sequence 142, Appl
C 455	7.4	38.9	19	9	US-11-217-936-2794	Sequence 2794, Ap	C 528	7.2	37.9	19	6	US-10-424-339-2117	Sequence 2117, Appl
456	7.4	38.9	19	9	US-11-217-936-3021	Sequence 3021, Ap	C 529	7.2	37.9	19	6	US-10-424-339-277	Sequence 277, Appl
C 457	7.4	38.9	19	9	US-11-217-936-3365	Sequence 3365, Ap	C 530	7.2	37.9	19	6	US-10-424-339-560	Sequence 560, Appl
C 458	7.4	38.9	19	9	US-11-217-936-3393	Sequence 3393, Ap	C 531	7.2	37.9	19	6	US-10-424-339-639	Sequence 639, Appl
C 459	7.4	38.9	19	9	US-11-217-936-3434	Sequence 3434, Ap	C 532	7.2	37.9	19	6	US-10-424-339-700	Sequence 700, Appl
C 460	7.4	38.9	19	9	US-11-217-936-3538	Sequence 3538, Ap	C 533	7.2	37.9	19	6	US-10-424-339-762	Sequence 762, Appl
461	7.4	38.9	19	9	US-11-217-936-3566	Sequence 3566, Ap	C 534	7.2	37.9	19	6	US-10-424-339-850	Sequence 850, Appl

535	7.2	37.9	19	6	US-10-424-339-909	Sequence 909, App	C 608	7.2	37.9	19	9	US-11-102-097-398	Sequence 398, App
536	7.2	37.9	19	6	US-10-424-339-971	Sequence 971, App	C 609	7.2	37.9	19	9	US-11-102-097-500	Sequence 500, App
C 537	7.2	37.9	19	6	US-10-424-339-1059	Sequence 1059, App	C 610	7.2	37.9	19	9	US-11-102-097-501	Sequence 501, App
C 538	7.2	37.9	19	6	US-10-424-339-1259	Sequence 1259, App	C 611	7.2	37.9	19	9	US-11-102-097-624	Sequence 624, App
539	7.2	37.9	19	6	US-10-424-339-1324	Sequence 1324, App	C 612	7.2	37.9	19	9	US-11-102-097-625	Sequence 625, App
540	7.2	37.9	19	6	US-10-424-339-1440	Sequence 1440, App	C 613	7.2	37.9	19	9	US-11-102-097-626	Sequence 626, App
C 541	7.2	37.9	19	6	US-10-424-339-1505	Sequence 1505, App	C 614	7.2	37.9	19	9	US-11-102-097-677	Sequence 677, App
C 542	7.2	37.9	19	6	US-10-881-580-126	Sequence 126, App	C 615	7.2	37.9	19	9	US-11-102-097-1305	Sequence 1305, App
C 543	7.2	37.9	19	6	US-10-881-580-254	Sequence 254, App	C 616	7.2	37.9	19	9	US-11-102-097-1306	Sequence 1306, App
C 544	7.2	37.9	19	6	US-10-921-554-68	Sequence 68, App	C 617	7.2	37.9	19	9	US-11-102-097-1307	Sequence 1307, App
545	7.2	37.9	19	6	US-10-921-554-69	Sequence 69, App	C 618	7.2	37.9	19	9	US-11-102-097-1308	Sequence 1308, App
546	7.2	37.9	19	6	US-10-921-554-168	Sequence 168, App	C 619	7.2	37.9	19	9	US-11-102-097-1309	Sequence 1309, App
C 547	7.2	37.9	19	6	US-10-921-554-189	Sequence 189, App	C 620	7.2	37.9	19	9	US-11-102-097-1399	Sequence 1399, App
C 548	7.2	37.9	19	6	US-10-516-314-6	Sequence 6, App	C 621	7.2	37.9	19	9	US-11-102-097-1400	Sequence 1400, App
C 549	7.2	37.9	19	6	US-10-514-558-35	Sequence 35, App	C 622	7.2	37.9	19	9	US-11-102-097-1535	Sequence 1535, App
550	7.2	37.9	19	7	US-11-299-025-124	Sequence 124, App	C 623	7.2	37.9	19	9	US-11-102-097-1536	Sequence 1536, App
C 551	7.2	37.9	19	7	US-11-344-702-356	Sequence 356, App	C 624	7.2	37.9	19	9	US-11-102-097-1657	Sequence 1657, App
C 552	7.2	37.9	19	7	US-11-344-702-418	Sequence 418, App	C 625	7.2	37.9	19	9	US-11-102-097-1658	Sequence 1658, App
C 553	7.2	37.9	19	7	US-11-344-702-433	Sequence 433, App	C 626	7.2	37.9	19	9	US-11-102-097-1666	Sequence 1666, App
C 554	7.2	37.9	19	7	US-11-344-702-547	Sequence 547, App	C 627	7.2	37.9	19	9	US-11-102-097-1667	Sequence 1667, App
C 555	7.2	37.9	19	7	US-11-345-361-356	Sequence 356, App	C 628	7.2	37.9	19	9	US-11-102-097-1688	Sequence 1688, App
C 556	7.2	37.9	19	7	US-11-345-361-418	Sequence 418, App	C 629	7.2	37.9	19	9	US-11-102-097-1689	Sequence 1689, App
C 557	7.2	37.9	19	7	US-11-345-361-433	Sequence 433, App	C 630	7.2	37.9	19	9	US-11-102-097-1745	Sequence 1745, App
C 558	7.2	37.9	19	7	US-11-345-361-547	Sequence 547, App	C 631	7.2	37.9	19	9	US-11-102-097-1746	Sequence 1746, App
559	7.2	37.9	19	8	US-11-251-465-485	Sequence 485, App	C 632	7.2	37.9	19	9	US-11-102-097-1747	Sequence 1747, App
560	7.2	37.9	19	8	US-11-251-465-487	Sequence 487, App	C 633	7.2	37.9	19	9	US-11-102-097-1748	Sequence 1748, App
561	7.2	37.9	19	8	US-11-251-465-759	Sequence 759, App	C 634	7.2	37.9	19	9	US-11-102-097-1956	Sequence 1956, App
C 562	7.2	37.9	19	8	US-11-293-697-5208	Sequence 5208, App	C 635	7.2	37.9	19	9	US-11-102-097-2051	Sequence 2051, App
C 563	7.2	37.9	19	8	US-11-321-421-278	Sequence 278, App	C 636	7.2	37.9	19	9	US-11-102-097-2052	Sequence 2052, App
564	7.2	37.9	19	8	US-11-321-991-7	Sequence 7, App	C 637	7.2	37.9	19	9	US-11-102-097-2053	Sequence 2053, App
C 565	7.2	37.9	19	9	US-11-217-936-56	Sequence 56, App	C 638	7.2	37.9	19	9	US-11-102-097-2054	Sequence 2054, App
C 566	7.2	37.9	19	9	US-11-217-936-82	Sequence 82, App	C 639	7.2	37.9	19	9	US-11-102-097-2116	Sequence 2116, App
567	7.2	37.9	19	9	US-11-217-936-171	Sequence 171, App	C 640	7.2	37.9	19	9	US-11-102-097-2463	Sequence 2463, App
568	7.2	37.9	19	9	US-11-217-936-197	Sequence 197, App	C 641	7.2	37.9	19	9	US-11-102-097-2713	Sequence 2713, App
C 569	7.2	37.9	19	9	US-11-217-936-731	Sequence 731, App	C 642	7.2	37.9	19	9	US-11-102-097-2714	Sequence 2714, App
570	7.2	37.9	19	9	US-11-217-936-839	Sequence 839, App	C 643	7.2	37.9	19	9	US-11-102-097-2882	Sequence 2882, App
C 571	7.2	37.9	19	9	US-11-217-936-1149	Sequence 1149, App	C 644	7.2	37.9	19	9	US-11-273-003-19	Sequence 19, App
C 572	7.2	37.9	19	9	US-11-217-936-1435	Sequence 1435, App	C 645	7.2	37.9	19	9	US-11-253-059-4	Sequence 4, App
573	7.2	37.9	19	9	US-11-217-936-1458	Sequence 1458, App	C 646	7.2	36.8	19	6	US-10-524-021-35	Sequence 35, App
C 574	7.2	37.9	19	9	US-11-217-936-1618	Sequence 1618, App	C 647	7.2	36.8	19	6	US-10-469-938-19	Sequence 19, App
C 575	7.2	37.9	19	9	US-11-217-936-1904	Sequence 1904, App	C 648	7.2	36.8	19	6	US-10-511-833-7	Sequence 7, App
C 576	7.2	37.9	19	9	US-11-217-936-1927	Sequence 1927, App	C 649	7.2	36.8	19	6	US-10-987-453-144	Sequence 144, App
C 577	7.2	37.9	19	9	US-11-217-936-2211	Sequence 2211, App	C 650	7.2	36.8	19	6	US-10-987-453-145	Sequence 145, App
C 578	7.2	37.9	19	9	US-11-217-936-2304	Sequence 2304, App	C 651	7.2	36.8	19	6	US-10-517-441-1224	Sequence 1224, App
C 579	7.2	37.9	19	9	US-11-217-936-2506	Sequence 2506, App	C 652	7.2	36.8	19	6	US-10-525-360-7	Sequence 7, App
C 580	7.2	37.9	19	9	US-11-217-936-4599	Sequence 2599, App	C 653	7.2	36.8	19	6	US-10-540-460-116	Sequence 116, App
C 581	7.2	37.9	19	9	US-11-217-936-4599	Sequence 2768, App	C 654	7.2	36.8	19	6	US-10-424-339-6	Sequence 6, App
582	7.2	37.9	19	9	US-11-217-936-2863	Sequence 2863, App	C 655	7.2	36.8	19	6	US-10-424-339-169	Sequence 169, App
583	7.2	37.9	19	9	US-11-217-936-2958	Sequence 2958, App	C 656	7.2	36.8	19	6	US-10-424-339-387	Sequence 387, App
584	7.2	37.9	19	9	US-11-217-936-2958	Sequence 2963, App	C 657	7.2	36.8	19	6	US-10-424-339-420	Sequence 420, App
585	7.2	37.9	19	9	US-11-217-936-2995	Sequence 2995, App	C 658	7.2	36.8	19	6	US-10-424-339-492	Sequence 492, App
C 586	7.2	37.9	19	9	US-11-217-936-3090	Sequence 3090, App	C 659	7.2	36.8	19	6	US-10-424-339-525	Sequence 525, App
C 587	7.2	37.9	19	9	US-11-217-936-3185	Sequence 3185, App	C 660	7.2	36.8	19	6	US-10-424-339-538	Sequence 538, App
C 588	7.2	37.9	19	9	US-11-217-936-3190	Sequence 3190, App	C 661	7.2	36.8	19	6	US-10-424-339-582	Sequence 582, App
589	7.2	37.9	19	9	US-11-217-936-3439	Sequence 3439, App	C 662	7.2	36.8	19	6	US-10-424-339-617	Sequence 617, App
C 590	7.2	37.9	19	9	US-11-217-936-3612	Sequence 3612, App	C 663	7.2	36.8	19	6	US-10-424-339-661	Sequence 661, App
C 591	7.2	37.9	19	9	US-11-217-936-3833	Sequence 3833, App	C 664	7.2	36.8	19	6	US-10-424-339-756	Sequence 756, App
592	7.2	37.9	19	9	US-11-217-936-3929	Sequence 3929, App	C 665	7.2	36.8	19	6	US-10-424-339-795	Sequence 795, App
593	7.2	37.9	19	9	US-11-217-936-4153	Sequence 4153, App	C 666	7.2	36.8	19	6	US-10-424-339-895	Sequence 895, App
594	7.2	37.9	19	9	US-11-217-936-4167	Sequence 4167, App	C 667	7.2	36.8	19	6	US-10-424-339-965	Sequence 965, App
C 595	7.2	37.9	19	9	US-11-217-936-4411	Sequence 4411, App	C 668	7.2	36.8	19	6	US-10-424-339-965	Sequence 965, App
C 596	7.2	37.9	19	9	US-11-217-936-4425	Sequence 4425, App	C 669	7.2	36.8	19	6	US-10-424-339-1104	Sequence 1104, App
C 597	7.2	37.9	19	9	US-11-217-936-4798	Sequence 4798, App	C 670	7.2	36.8	19	6	US-10-536-804-25	Sequence 25, App
598	7.2	37.9	19	9	US-11-217-936-4895	Sequence 4895, App	C 671	7.2	36.8	19	6	US-10-818-956-79	Sequence 79, App
C 599	7.2	37.9	19	9	US-11-374-114-3	Sequence 3, App	C 672	7.2	36.8	19	6	US-10-997-086-48	Sequence 48, App
600	7.2	37.9	19	9	US-11-008-351-63	Sequence 63, App	C 673	7.2	36.8	19	6	US-10-547-710-17	Sequence 17, App
C 601	7.2	37.9	19	9	US-11-008-351-83	Sequence 83, App	C 674	7.2	36.8	19	6	US-10-881-580-17	Sequence 17, App
C 602	7.2	37.9	19	9	US-11-267-381-34	Sequence 34, App	C 675	7.2	36.8	19	6	US-10-881-580-135	Sequence 135, App
603	7.2	37.9	19	9	US-11-301-360-127	Sequence 127, App	C 676	7.2	36.8	19	6	US-10-821-554-42	Sequence 42, App
C 604	7.2	37.9	19	9	US-11-301-360-848	Sequence 848, App	C 677	7.2	36.8	19	6	US-10-921-554-142	Sequence 142, App
C 605	7.2	37.9	19	9	US-11-102-097-381	Sequence 381, App	C 678	7.2	36.8	19	6	US-10-523-981-19	Sequence 19, App
C 606	7.2	37.9	19	9	US-11-102-097-382	Sequence 382, App	C 679	7.2	36.8	19	6	US-10-825-485-40	Sequence 40, App
C 607	7.2	37.9	19	9	US-11-102-097-397	Sequence 397, App	C 680	7.2	36.8	19	6	US-10-825-485-99	Sequence 99, App

C 681	7	36.8	19	6	US-10-825-485-105	Sequence 105, App	C 754	7	35.8	19	9	US-11-217-936-2158	Sequence 2158, Ap
C 682	7	36.8	19	6	US-10-825-485-124	Sequence 124, App	C 755	7	36.8	19	9	US-11-217-936-2246	Sequence 2246, Ap
C 683	7	36.8	19	6	US-10-825-485-207	Sequence 207, App	C 756	7	36.8	19	9	US-11-217-936-2289	Sequence 2289, Ap
C 684	7	36.8	19	6	US-10-825-485-347	Sequence 347, App	C 757	7	36.8	19	9	US-11-217-936-2329	Sequence 2329, Ap
C 685	7	36.8	19	6	US-10-825-485-406	Sequence 406, App	C 758	7	36.8	19	9	US-11-217-936-2394	Sequence 2394, Ap
C 686	7	36.8	19	6	US-10-825-485-412	Sequence 412, App	C 759	7	36.8	19	9	US-11-217-936-2453	Sequence 2453, Ap
C 687	7	36.8	19	6	US-10-825-485-511	Sequence 511, App	C 760	7	36.8	19	9	US-11-217-936-2541	Sequence 2541, Ap
C 688	7	36.8	19	6	US-10-825-485-514	Sequence 514, App	C 761	7	36.8	19	9	US-11-217-936-2584	Sequence 2584, Ap
C 689	7	36.8	19	6	US-10-542-769A-27	Sequence 27, App1	C 762	7	36.8	19	9	US-11-217-936-2624	Sequence 2624, Ap
C 690	7	36.8	19	6	US-10-542-769A-28	Sequence 28, App1	C 763	7	36.8	19	9	US-11-217-936-2791	Sequence 2791, Ap
C 691	7	36.8	19	6	US-10-479-225A-268	Sequence 268, App	C 764	7	36.8	19	9	US-11-217-936-2805	Sequence 2805, Ap
C 692	7	36.8	19	6	US-10-479-225A-271	Sequence 271, App	C 765	7	36.8	19	9	US-11-217-936-2868	Sequence 2868, Ap
C 693	7	36.8	19	7	US-11-299-025-45	Sequence 45, App1	C 766	7	36.8	19	9	US-11-217-936-3018	Sequence 3018, Ap
C 694	7	36.8	19	7	US-11-339-785-7	Sequence 7, App1.1	C 767	7	36.8	19	9	US-11-217-936-3032	Sequence 3032, Ap
C 695	7	36.8	19	7	US-11-344-702-36	Sequence 36, App1	C 768	7	36.8	19	9	US-11-217-936-3095	Sequence 3095, Ap
C 696	7	36.8	19	7	US-11-344-702-37	Sequence 37, App1	C 769	7	36.8	19	9	US-11-217-936-3162	Sequence 3162, Ap
C 697	7	36.8	19	7	US-11-344-702-53	Sequence 53, App1	C 770	7	36.8	19	9	US-11-217-936-3122	Sequence 3122, Ap
C 698	7	36.8	19	7	US-11-344-702-59	Sequence 59, App1	C 771	7	36.8	19	9	US-11-217-936-3448	Sequence 3448, Ap
C 699	7	36.8	19	7	US-11-344-702-278	Sequence 278, App	C 772	7	36.8	19	9	US-11-217-936-3465	Sequence 3465, Ap
C 700	7	36.8	19	7	US-11-344-702-420	Sequence 420, App	C 773	7	36.8	19	9	US-11-217-936-3535	Sequence 3535, Ap
C 701	7	36.8	19	7	US-11-344-702-452	Sequence 452, App	C 774	7	36.8	19	9	US-11-217-936-3585	Sequence 3585, Ap
C 702	7	36.8	19	7	US-11-344-702-669	Sequence 669, App	C 775	7	36.8	19	9	US-11-217-936-3621	Sequence 3621, Ap
C 703	7	36.8	19	7	US-11-345-361-36	Sequence 36, App1	C 776	7	36.8	19	9	US-11-217-936-3638	Sequence 3638, Ap
C 704	7	36.8	19	7	US-11-345-361-37	Sequence 37, App1	C 777	7	36.8	19	9	US-11-217-936-3693	Sequence 3693, Ap
C 705	7	36.8	19	7	US-11-345-361-53	Sequence 53, App1	C 778	7	36.8	19	9	US-11-217-936-4151	Sequence 4151, Ap
C 706	7	36.8	19	7	US-11-345-361-59	Sequence 59, App1	C 779	7	36.8	19	9	US-11-217-936-4180	Sequence 4180, Ap
C 707	7	36.8	19	7	US-11-345-361-278	Sequence 278, App	C 780	7	36.8	19	9	US-11-217-936-4191	Sequence 4191, Ap
C 708	7	36.8	19	7	US-11-345-361-420	Sequence 420, App	C 781	7	36.8	19	9	US-11-217-936-4302	Sequence 4302, Ap
C 709	7	36.8	19	7	US-11-345-361-452	Sequence 452, App	C 782	7	36.8	19	9	US-11-217-936-4325	Sequence 4325, Ap
C 710	7	36.8	19	7	US-11-345-361-669	Sequence 669, App	C 783	7	36.8	19	9	US-11-217-936-4351	Sequence 4351, Ap
C 711	7	36.8	19	8	US-11-251-610-7	Sequence 7, App1.1	C 784	7	36.8	19	9	US-11-217-936-4409	Sequence 4409, Ap
C 712	7	36.8	19	8	US-11-251-465-137	Sequence 137, App	C 785	7	36.8	19	9	US-11-217-936-4438	Sequence 4438, Ap
C 713	7	36.8	19	8	US-11-251-465-145	Sequence 145, App	C 786	7	36.8	19	9	US-11-217-936-4449	Sequence 4449, Ap
C 714	7	36.8	19	8	US-11-251-465-197	Sequence 197, App	C 787	7	36.8	19	9	US-11-217-936-4560	Sequence 4560, Ap
C 715	7	36.8	19	8	US-11-251-465-289	Sequence 289, App	C 788	7	36.8	19	9	US-11-217-936-4583	Sequence 4583, Ap
C 716	7	36.8	19	8	US-11-251-465-389	Sequence 389, App	C 789	7	36.8	19	9	US-11-294-621-104	Sequence 104, App1
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C 718	7	36.8	19	8	US-11-251-465-591	Sequence 591, App	C 791	7	36.8	19	9	US-11-301-360-848	Sequence 848, App
C 719	7	36.8	19	8	US-11-251-465-615	Sequence 615, App	C 792	7	36.8	19	9	US-11-039-632-7	Sequence 7, App1.1
C 720	7	36.8	19	8	US-11-251-465-687	Sequence 687, App	C 793	7	36.8	19	9	US-11-102-097-252	Sequence 252, App
C 721	7	36.8	19	8	US-11-251-465-713	Sequence 713, App	C 794	7	36.8	19	9	US-11-102-097-373	Sequence 373, App
C 722	7	36.8	19	8	US-11-251-465-797	Sequence 797, App	C 795	7	36.8	19	9	US-11-102-097-358	Sequence 358, App
C 723	7	36.8	19	8	US-11-251-465-853	Sequence 853, App	C 796	7	36.8	19	9	US-11-102-097-559	Sequence 559, App
C 724	7	36.8	19	8	US-11-242-139-95	Sequence 95, App1	C 797	7	36.8	19	9	US-11-102-097-560	Sequence 560, App
C 725	7	36.8	19	8	US-11-296-092-104	Sequence 104, App	C 798	7	36.8	19	9	US-11-102-097-561	Sequence 561, App
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C 727	7	36.8	19	8	US-11-219-582A-25	Sequence 25, App1	C 800	7	36.8	19	9	US-11-102-097-757	Sequence 757, App
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## ALIGNMENTS

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RESULT 1
US-10-921-554-39
; Sequence 39, Application US/10921554
; Publication No. US20060142226A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics, Inc.
; APPLICANT: Polisky, Barry
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Cholesteryl Ester Transfer
; TITLE OF INVENTION: Protein (CEPT) Gene Expression Using Short Interfering Nucleic A
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; NUMBER OF SEQ ID NOS: 326
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; TYPE: RNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target/siNA sense
US-10-921-554-39
Query Match 57.9%; Score 11; DB 6; Length 19;
Best Local Similarity 63.6%; Pred. No. 1.3e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 9 ATCTCCTTCAC 19
DB 6 AUCUCCUUCAC 16

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RESULT 2
US-10-921-554-139/C
; Sequence 139, Application US/10921554
; Publication No. US20060142226A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics, Inc.
; APPLICANT: Polisky, Barry
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Cholesteryl Ester Transfer
; TITLE OF INVENTION: Protein (CEPT) Gene Expression Using Short Interfering Nucleic Ac
; FILE REFERENCE: 04-466-A (400.206)
; CURRENT APPLICATION NUMBER: US/10/921,554
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 10/864,044
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 139
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target/siNA sense
US-10-921-554-139
Query Match 57.9%; Score 11; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 ATCTCCTTCAC 19
DB 14 ATCTCCTTCAC 4

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RESULT 3
US-11-293-697-5004
; Sequence 5004, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:

```



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; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5004
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized P
US-11-293-697-5004

Query Match          55.8%; Score 10.6; DB 8; Length 19;
Best Local Similarity 76.5%; Pred. No. 2.1e+04;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3 CACGATATCTCTTCAC 19
        |||||
Db      1 CACTGATTTCTTCAC 17

RESULT 4
US-11-217-936-416
; Sequence 416, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sitna Therapeutics, Inc.
; TITLE OF INVENTION: RNA interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 416
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-416

Query Match          52.6%; Score 10; DB 9; Length 19;
Best Local Similarity 55.6%; Pred. No. 4.6e+04;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CGCAGGTATCTCTTCA 18
        |||||
Db      2 CGCAUGUACCUCAUGCA 19

RESULT 5
US-11-217-936-526/C
; Sequence 526, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sitna Therapeutics, Inc.
; TITLE OF INVENTION: RNA interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
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; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 526
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-526

Query Match          52.6%; Score 10; DB 9; Length 19;
Best Local Similarity 72.2%; Pred. No. 4.6e+04;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CGCAGGTATCTCTTCA 18
        |||||
Db      18 CGCATGTACCTCATGCA 1

RESULT 6
US-11-217-936-1455
; Sequence 1455, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sitna Therapeutics, Inc.
; TITLE OF INVENTION: RNA interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1455
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1455

Query Match          52.6%; Score 10; DB 9; Length 19;
Best Local Similarity 50.0%; Pred. No. 4.6e+04;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      8 TATCTCCTTC 17
        :||:|
Db      8 UAUCCUCCUCC 17

RESULT 7
US-11-217-936-1924/C
; Sequence 1924, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sitna Therapeutics, Inc.
; TITLE OF INVENTION: RNA interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1924
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

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; OTHER INFORMATION: Synthetic
US-11-217-936-1924
Query Match      52.6%; Score 10; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TATCTCCTTC 17
      |||||
      12 TATCTCCTTC 3

RESULT 8
US-10-921-554-94
; Sequence 94, Application US/10921554
; Publication No. US2006014226A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics, Inc.
; APPLICANT: Polisky, Barry
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Cholesteryl Ester Transfer
; TITLE OF INVENTION: Protein (CEPT) Gene Expression Using Short Interfering Nucleic A
; TITLE OF INVENTION: (sRNA)
; FILE REFERENCE: 04-466-A (400.206)
; CURRENT FILING DATE: 2004-08-19
; PRIOR FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 10/864,044
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 94
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target/siNA sense
US-10-921-554-94

Query Match      51.6%; Score 9.8; DB 6; Length 19;
Best Local Similarity 53.8%; Pred. No. 5.9e+04;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGTATCTCCTTCA 18
      |||:|||||
      5 GGUGUCUCUCCCA 17

RESULT 9
US-10-921-554-194/c
; Sequence 194, Application US/10921554
; Publication No. US2006014226A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics, Inc.
; APPLICANT: Polisky, Barry
```

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; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Cholesteryl Ester Transfer
; TITLE OF INVENTION: Protein (CEPT) Gene Expression Using Short Interfering Nucleic Ac
; TITLE OF INVENTION: (sRNA)
; FILE REFERENCE: 04-466-A (400.206)
; CURRENT FILING DATE: 2004-08-19
; PRIOR FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 10/864,044
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 194
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target/siNA sense
US-10-921-554-194

Query Match      51.6%; Score 9.8; DB 6; Length 19;
Best Local Similarity 84.6%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGTATCTCCTTCA 18
      |||:|||||
      15 GGUGUCUCCCA 3

RESULT 10
US-11-344-702-269
; Sequence 269, Application US/11344702
; Publication No. US20060172963A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, Allan R.
; APPLICANT: Chatterton, Jon E.
; APPLICANT: Clark, Abbot P.
; TITLE OF INVENTION: RNAI-MEDIATED INHIBITION OF OCULAR HYPERTENSION TARGETS
; FILE REFERENCE: 45263-P008U01
; CURRENT FILING DATE: 2006-02-01
; PRIOR FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: US 60/648,926
; PRIOR FILING DATE: 2005-02-01
; PRIOR APPLICATION NUMBER: US 60/753,364
; PRIOR FILING DATE: 2005-12-22
; NUMBER OF SEQ ID NOS: 724
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 269
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TARGETING SEQUENCE
US-11-344-702-269
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Query Match 51.6%; Score 9.8; DB 7; Length 19;  
Best Local Similarity 84.6%; Pred. No. 5.9e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTATCTCCTTCAC 19  
|||||  
Db 5 GTATCTACTCTCAC 17

RESULT 11  
US-11-344-702-270  
; Sequence 270, Application US/11344702  
; Publication No. US20060172963A1  
; GENERAL INFORMATION:  
; APPLICANT: Shepard, Allan R.  
; APPLICANT: Chatterton, Jon E.  
; APPLICANT: Clark, Abbot F.  
; TITLE OF INVENTION: RNAI-MEDIATED INHIBITION OF OCULAR HYPERTENSION TARGETS  
; FILE REFERENCE: 45263-P008US1  
; CURRENT APPLICATION NUMBER: US/11/344,702  
; PRIOR FILING DATE: 2006-02-01  
; PRIOR APPLICATION NUMBER: US 60/648,926  
; PRIOR FILING DATE: 2005-02-01  
; PRIOR APPLICATION NUMBER: US 60/753,364  
; PRIOR FILING DATE: 2005-12-22  
; NUMBER OF SEQ ID NOS: 724  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 270  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TARGETING SEQUENCE  
US-11-344-702-270

Query Match 51.6%; Score 9.8; DB 7; Length 19;  
Best Local Similarity 84.6%; Pred. No. 5.9e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTATCTCCTTCAC 19  
|||||  
Db 4 GTATCTACTCTCAC 16

RESULT 12  
US-11-344-702-271  
; Sequence 271, Application US/11344702  
; Publication No. US20060172963A1  
; GENERAL INFORMATION:  
; APPLICANT: Shepard, Allan R.  
; APPLICANT: Chatterton, Jon E.  
; APPLICANT: Clark, Abbot F.  
; TITLE OF INVENTION: RNAI-MEDIATED INHIBITION OF OCULAR HYPERTENSION TARGETS  
; FILE REFERENCE: 45263-P008US1  
; CURRENT APPLICATION NUMBER: US/11/344,702  
; PRIOR FILING DATE: 2006-02-01  
; PRIOR APPLICATION NUMBER: US 60/648,926  
; PRIOR FILING DATE: 2005-02-01  
; PRIOR APPLICATION NUMBER: US 60/753,364  
; PRIOR FILING DATE: 2005-12-22  
; NUMBER OF SEQ ID NOS: 724  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 271  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TARGETING SEQUENCE  
US-11-344-702-271

Query Match 51.6%; Score 9.8; DB 7; Length 19;  
Best Local Similarity 84.6%; Pred. No. 5.9e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTATCTCCTTCAC 19  
|||||  
Db 3 GTATCTACTCTCAC 15

RESULT 13  
US-11-345-361-269  
; Sequence 269, Application US/11345361  
; Publication No. US20060172965A1  
; GENERAL INFORMATION:  
; APPLICANT: Shepard, Allan R.  
; APPLICANT: Chatterton, Jon E.  
; APPLICANT: Clark, Abbot F.  
; APPLICANT: Max, Martin B.  
; TITLE OF INVENTION: RNAI-MEDIATED INHIBITION OF OCULAR TARGETS  
; FILE REFERENCE: 45263-P008US2  
; CURRENT APPLICATION NUMBER: US/11/345,361  
; PRIOR FILING DATE: 2006-02-01  
; PRIOR APPLICATION NUMBER: US 60/648,926  
; PRIOR FILING DATE: 2005-02-01  
; PRIOR APPLICATION NUMBER: US 60/753,364  
; PRIOR FILING DATE: 2005-12-22  
; NUMBER OF SEQ ID NOS: 724  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 269  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TARGETING SEQUENCE  
US-11-345-361-269

Query Match 51.6%; Score 9.8; DB 7; Length 19;  
Best Local Similarity 84.6%; Pred. No. 5.9e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTATCTCCTTCAC 19  
|||||  
Db 5 GTATCTACTCTCAC 17

RESULT 14  
US-11-345-361-270  
; Sequence 270, Application US/11345361  
; Publication No. US20060172965A1  
; GENERAL INFORMATION:  
; APPLICANT: Shepard, Allan R.  
; APPLICANT: Chatterton, Jon E.  
; APPLICANT: Clark, Abbot F.  
; APPLICANT: Max, Martin B.  
; TITLE OF INVENTION: RNAI-MEDIATED INHIBITION OF OCULAR TARGETS  
; FILE REFERENCE: 45263-P008US2  
; CURRENT APPLICATION NUMBER: US/11/345,361  
; PRIOR FILING DATE: 2006-02-01  
; PRIOR APPLICATION NUMBER: US 60/648,926  
; PRIOR FILING DATE: 2005-02-01  
; PRIOR APPLICATION NUMBER: US 60/753,364  
; PRIOR FILING DATE: 2005-12-22  
; NUMBER OF SEQ ID NOS: 724  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 270  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TARGETING SEQUENCE  
US-11-345-361-270

Query Match 51.6%; Score 9.8; DB 7; Length 19;  
Best Local Similarity 84.6%; Pred. No. 5.9e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GATATCTCTTCAC 19  
| | | | |  
Db 4 GATATCTACCTCAC 16

RESULT 15  
US-11-345-361-271  
; Sequence 271, Application US/11345361  
; Publication No. US20060172965A1  
; GENERAL INFORMATION:  
; APPLICANT: Shepard, Allan R.  
; APPLICANT: Chatterton, Jon E.  
; APPLICANT: Clark, Abbot F.  
; TITLE OF INVENTION: RNAI-MEDIATED INHIBITION OF OCULAR TARGETS  
; FILE REFERENCE: 45263-P008US2  
; CURRENT APPLICATION NUMBER: US/11/345,361  
; CURRENT FILING DATE: 2006-02-01  
; PRIOR APPLICATION NUMBER: US 60/648,926  
; PRIOR FILING DATE: 2005-02-01  
; PRIOR APPLICATION NUMBER: US 60/753,364  
; PRIOR FILING DATE: 2005-12-22  
; NUMBER OF SEQ ID NOS: 724  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 271  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TARGETING SEQUENCE  
US-11-345-361-271

Query Match 51.6%; Score 9.8; DB 9; Length 19;  
Best Local Similarity 84.6%; Pred. No. 5.9e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GATATCTCTTCAC 19  
| | | | |  
Db 3 GATATCTACCTCAC 15

RESULT 16  
US-11-217-936-98/c  
; Sequence 98, Application US/11217936  
; Publication No. US20060148743A1  
; GENERAL INFORMATION:  
; APPLICANT: Jadhav, Vasant  
; APPLICANT: Carroll, Joseph  
; APPLICANT: Sirna Therapeutics, Inc.  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase  
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid  
; FILE REFERENCE: 05-727 (400/271)  
; CURRENT APPLICATION NUMBER: US/11/217,936  
; CURRENT FILING DATE: 2005-09-01  
; NUMBER OF SEQ ID NOS: 5036  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 98  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-11-217-936-98

Query Match 51.6%; Score 9.8; DB 9; Length 19;  
Best Local Similarity 84.6%; Pred. No. 5.9e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GATATCTCTTCAC 19  
| | | | |  
Db 19 GATATCTCTTCAC 7

RESULT 17  
US-11-217-936-213

; Sequence 213, Application US/11217936  
; Publication No. US20060148743A1  
; GENERAL INFORMATION:  
; APPLICANT: Jadhav, Vasant  
; APPLICANT: Carroll, Joseph  
; APPLICANT: Sirna Therapeutics, Inc.  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase  
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid  
; FILE REFERENCE: 05-727 (400/271)  
; CURRENT APPLICATION NUMBER: US/11/217,936  
; CURRENT FILING DATE: 2005-09-01  
; NUMBER OF SEQ ID NOS: 5036  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 213  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-11-217-936-213

Query Match 51.6%; Score 9.8; DB 9; Length 19;  
Best Local Similarity 53.8%; Pred. No. 5.9e+04;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 GATATCTCTTCAC 19  
| | | | |  
Db 1 GUATCCCUUCAC 13

RESULT 18  
US-11-217-936-2810/c  
; Sequence 2810, Application US/11217936  
; Publication No. US20060148743A1  
; GENERAL INFORMATION:  
; APPLICANT: Jadhav, Vasant  
; APPLICANT: Carroll, Joseph  
; APPLICANT: Sirna Therapeutics, Inc.  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase  
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid  
; FILE REFERENCE: 05-727 (400/271)  
; CURRENT APPLICATION NUMBER: US/11/217,936  
; CURRENT FILING DATE: 2005-09-01  
; NUMBER OF SEQ ID NOS: 5036  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2810  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-11-217-936-2810

Query Match 51.6%; Score 9.8; DB 9; Length 19;  
Best Local Similarity 84.6%; Pred. No. 5.9e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGTATCTCTTC 16  
| | | | |  
Db 15 ATGTAATATCTT 3

RESULT 19  
US-11-217-936-3037  
; Sequence 3037, Application US/11217936  
; Publication No. US20060148743A1  
; GENERAL INFORMATION:  
; APPLICANT: Jadhav, Vasant

```

; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAc) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3037
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-3037

Query Match      51.6%; Score 9.8; DB 9; Length 19;
Best Local Similarity 46.2%; Pred. No. 5.9e+04;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy      4 ACGGTATCTCCTT 16
Db      5 AUGGUAUACCUU 17

RESULT 20
US-10-424-339-335/c
; Sequence 335, Application US/10424339
; Publication No. US20060127891A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Belgelman, Leonid
; APPLICANT: Usman, Naeem
; APPLICANT: Haeblerli, Peter
; APPLICANT: Chowitra, Bharat
; APPLICANT: Polisky, Barry
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of MAP Kinase Gene
; TITLE OF INVENTION: Expression Or Expression Of Genes Involved In MAP Kinase Pathway
; FILE REFERENCE: 400/113 (MBHB03-388)
; CURRENT APPLICATION NUMBER: US/10/424,339
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: PCT/US 03/02510
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US 03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US 03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 1714
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 335
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense 1
```

```

US-10-424-339-335

Query Match      50.5%; Score 9.6; DB 6; Length 19;
Best Local Similarity 46.2%; Pred. No. 7.7e+04;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 ACGGTATCTCCTTAC 19
Db      19 ACGGCTGCCCTTAC 4

RESULT 21
US-10-424-339-440
; Sequence 440, Application US/10424339
; Publication No. US20060127891A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Belgelman, Leonid
; APPLICANT: Usman, Naeem
; APPLICANT: Haeblerli, Peter
; APPLICANT: Chowitra, Bharat
; APPLICANT: Polisky, Barry
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of MAP Kinase Gene
; TITLE OF INVENTION: Expression Or Expression Of Genes Involved In MAP Kinase Pathway
; FILE REFERENCE: 400/113 (MBHB03-388)
; CURRENT APPLICATION NUMBER: US/10/424,339
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: PCT/US 03/02510
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US 03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US 03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 1714
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 440
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-424-339-440

Query Match      50.5%; Score 9.6; DB 6; Length 19;
Best Local Similarity 62.5%; Pred. No. 7.7e+04;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      4 ACGGTATCTCCTTAC 19
Db      1 ACGGCTGCCCTTAC 16

RESULT 22
US-11-102-097-517/c
; Sequence 517, Application US/11102097
; Publication No. US20060160759A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Chen, et al.
; TITLE OF INVENTION: Influenza Therapeutic
; FILE REFERENCE: 0492611-0621
; CURRENT APPLICATION NUMBER: US/11/102,097
; CURRENT FILING DATE: 2005-04-08
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 517
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequences of functional target portions for RNAi to inhibit
; OTHER INFORMATION: Influenza virus.
; US-11-102-097-517

Query Match          50.5%; Score 9.6; DB 9; Length 19;
Best Local Similarity 75.0%; Pred. No. 7.7e+04;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 GCACGGTATCTCCTTC 17
Db      17 GCCCAGTACTGCTTC 2

RESULT 23
US-11-256-694-308
; Sequence 308, Application US/11256694
; Publication No. US20060088872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundberg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; PRIOR FILING DATE: 2004-04-26
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 308
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
; US-11-256-694-308

Query Match          49.5%; Score 9.4; DB 8; Length 19;
Best Local Similarity 90.9%; Pred. No. 9.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 TATCTCCTTCA 18
Db      3 TATCTACTTCA 13

RESULT 24
US-11-256-694-319
; Sequence 319, Application US/11256694
; Publication No. US20060088872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundberg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; PRIOR FILING DATE: 2004-04-26
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 319
```

```

; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
; US-11-256-694-319

Query Match          49.5%; Score 9.4; DB 8; Length 19;
Best Local Similarity 90.9%; Pred. No. 9.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 TATCTCCTTCA 18
Db      3 TATCTACTTCA 13

RESULT 25
US-11-256-694-332
; Sequence 332, Application US/11256694
; Publication No. US20060088872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundberg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; PRIOR FILING DATE: 2004-04-26
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 332
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
; US-11-256-694-332

Query Match          49.5%; Score 9.4; DB 8; Length 19;
Best Local Similarity 90.9%; Pred. No. 9.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 TATCTCCTTCA 18
Db      3 TATCTACTTCA 13

RESULT 26
US-11-256-694-333
; Sequence 333, Application US/11256694
; Publication No. US20060088872A1
; GENERAL INFORMATION:
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundberg, Joakim
; APPLICANT: Dzieglewska, Hanna
; TITLE OF INVENTION: Allele-specific Mutation Detection Assay
; FILE REFERENCE: 27.7.79627/001
; CURRENT APPLICATION NUMBER: US/11/256,694
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: PCT/GB04/001766
; PRIOR FILING DATE: 2004-04-26
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 333
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human papillomavirus
; US-11-256-694-333

Query Match          49.5%; Score 9.4; DB 8; Length 19;
Best Local Similarity 90.9%; Pred. No. 9.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 TATCTCCTTCA 18
Db      3 TATCTACTTCA 13
```

Db 3 TATCTACTTCA 13

# RESULT 27

US-11-256-694-340  
 ; Sequence 340, Application US/11256694  
 ; Publication No. US20060088872A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ahmadian, Afshin  
 ; APPLICANT: Lundeborg, Joakim  
 ; APPLICANT: Dzieglewska, Hanna  
 ; TITLE OF INVENTION: Allele-specific Mutation Detection Assay  
 ; FILE REFERENCE: 27.7.79627/001  
 ; CURRENT APPLICATION NUMBER: US/11/256,694  
 ; PRIOR FILING DATE: 2005-10-21  
 ; PRIOR APPLICATION NUMBER: PCT/GB04/001766  
 ; NUMBER OF SEQ ID NOS: 520  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 340  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: Human papillomavirus  
 US-11-256-694-340

Query Match 49.5%; Score 9.4; DB 8; Length 19;  
 Best Local Similarity 90.9%; Pred. No. 9.9e+04;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TATCTCTTCA 18  
 |||||  
 Db 3 TATCTACTTCA 13

# RESULT 28

US-11-256-694-351  
 ; Sequence 351, Application US/11256694  
 ; Publication No. US20060088872A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ahmadian, Afshin  
 ; APPLICANT: Lundeborg, Joakim  
 ; APPLICANT: Dzieglewska, Hanna  
 ; TITLE OF INVENTION: Allele-specific Mutation Detection Assay  
 ; FILE REFERENCE: 27.7.79627/001  
 ; CURRENT APPLICATION NUMBER: US/11/256,694  
 ; PRIOR FILING DATE: 2005-10-21  
 ; PRIOR APPLICATION NUMBER: PCT/GB04/001766  
 ; NUMBER OF SEQ ID NOS: 520  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 351  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: Human papillomavirus  
 US-11-256-694-351

Query Match 49.5%; Score 9.4; DB 8; Length 19;  
 Best Local Similarity 90.9%; Pred. No. 9.9e+04;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TATCTCTTCA 18  
 |||||  
 Db 3 TATCTACTTCA 13

# RESULT 29

US-11-256-694-362  
 ; Sequence 362, Application US/11256694  
 ; Publication No. US20060088872A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ahmadian, Afshin  
 ; APPLICANT: Lundeborg, Joakim  
 ; APPLICANT: Dzieglewska, Hanna

;; TITLE OF INVENTION: Allele-specific Mutation Detection Assay

;; FILE REFERENCE: 27.7.79627/001  
 ;; CURRENT APPLICATION NUMBER: US/11/256,694  
 ;; PRIOR FILING DATE: 2005-10-21  
 ;; PRIOR APPLICATION NUMBER: PCT/GB04/001766  
 ;; PRIOR FILING DATE: 2004-04-26  
 ;; NUMBER OF SEQ ID NOS: 520  
 ;; SOFTWARE: PatentIn version 3.0  
 ;; SEQ ID NO 362  
 ;; LENGTH: 19  
 ;; TYPE: DNA  
 ;; ORGANISM: Human papillomavirus  
 US-11-256-694-362

Query Match 49.5%; Score 9.4; DB 8; Length 19;  
 Best Local Similarity 90.9%; Pred. No. 9.9e+04;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TATCTCTTCA 18  
 |||||  
 Db 3 TATCTACTTCA 13

# RESULT 30

US-11-256-694-373  
 ; Sequence 373, Application US/11256694  
 ; Publication No. US20060088872A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ahmadian, Afshin  
 ; APPLICANT: Lundeborg, Joakim  
 ; APPLICANT: Dzieglewska, Hanna  
 ; TITLE OF INVENTION: Allele-specific Mutation Detection Assay  
 ; FILE REFERENCE: 27.7.79627/001  
 ; CURRENT APPLICATION NUMBER: US/11/256,694  
 ; PRIOR FILING DATE: 2005-10-21  
 ; PRIOR APPLICATION NUMBER: PCT/GB04/001766  
 ; NUMBER OF SEQ ID NOS: 520  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 373  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: Human papillomavirus  
 US-11-256-694-373

Query Match 49.5%; Score 9.4; DB 8; Length 19;  
 Best Local Similarity 90.9%; Pred. No. 9.9e+04;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TATCTCTTCA 18  
 |||||  
 Db 3 TATCTACTTCA 13

# RESULT 31

US-11-256-694-384  
 ; Sequence 384, Application US/11256694  
 ; Publication No. US20060088872A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ahmadian, Afshin  
 ; APPLICANT: Lundeborg, Joakim  
 ; APPLICANT: Dzieglewska, Hanna  
 ; TITLE OF INVENTION: Allele-specific Mutation Detection Assay  
 ; FILE REFERENCE: 27.7.79627/001  
 ; CURRENT APPLICATION NUMBER: US/11/256,694  
 ; PRIOR FILING DATE: 2005-10-21  
 ; PRIOR APPLICATION NUMBER: PCT/GB04/001766  
 ; NUMBER OF SEQ ID NOS: 520  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 384  
 ; LENGTH: 19  
 ; TYPE: DNA

ORGANISM: Human papillomavirus  
US-11-256-694-384

Query Match 49.5%; Score 9.4; DB 8; Length 19;  
Best Local Similarity 90.9%; Pred. No. 9.9e+04;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCCTTCA 18  
|||||  
Db 3 TATCTACTTCA 13

RESULT 32  
US-11-256-694-395

Sequence 395, Application US/11256694  
Publication No. US2006008872A1  
GENERAL INFORMATION:

APPLICANT: Ahmadian, Afshin  
APPLICANT: Lundberg, Joakim  
APPLICANT: Dzieglewska, Hanna  
TITLE OF INVENTION: Allele-specific Mutation Detection Assay  
FILE REFERENCE: 27.7.79627/001  
CURRENT APPLICATION NUMBER: US/11/256,694  
CURRENT FILING DATE: 2005-10-21  
PRIOR APPLICATION NUMBER: PCT/GB04/001766  
NUMBER OF SEQ ID NOS: 520  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 395  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Human papillomavirus  
US-11-256-694-395

Query Match 49.5%; Score 9.4; DB 8; Length 19;  
Best Local Similarity 90.9%; Pred. No. 9.9e+04;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCCTTCA 18  
|||||  
Db 3 TATCTACTTCA 13

RESULT 33  
US-11-256-694-406

Sequence 406, Application US/11256694  
Publication No. US2006008872A1  
GENERAL INFORMATION:  
APPLICANT: Ahmadian, Afshin  
APPLICANT: Lundberg, Joakim  
APPLICANT: Dzieglewska, Hanna  
TITLE OF INVENTION: Allele-specific Mutation Detection Assay  
FILE REFERENCE: 27.7.79627/001  
CURRENT APPLICATION NUMBER: US/11/256,694  
CURRENT FILING DATE: 2005-10-21  
PRIOR APPLICATION NUMBER: PCT/GB04/001766  
NUMBER OF SEQ ID NOS: 520  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 406  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Human papillomavirus  
US-11-256-694-406

Query Match 49.5%; Score 9.4; DB 8; Length 19;  
Best Local Similarity 90.9%; Pred. No. 9.9e+04;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCCTTCA 18  
|||||  
Db 3 TATCTACTTCA 13

RESULT 34  
US-11-217-936-727/C

Sequence 727, Application US/11217936  
Publication No. US20060148743A1  
GENERAL INFORMATION:

APPLICANT: Jachab, Vasant  
APPLICANT: Carroll, Joseph  
APPLICANT: Sirna Therapeutics, Inc.  
TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase  
TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid  
FILE REFERENCE: 05-727 (400/271)  
CURRENT APPLICATION NUMBER: US/11/217,936  
CURRENT FILING DATE: 2005-09-01  
NUMBER OF SEQ ID NOS: 5036  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 727  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-11-217-936-727

Query Match 49.5%; Score 9.4; DB 9; Length 19;  
Best Local Similarity 68.4%; Pred. No. 9.9e+04;  
Matches 13; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCCTTCAC 19  
|||||  
Db 19 CGACAGTATACACACAC 1

RESULT 35  
US-11-217-936-835

Sequence 835, Application US/11217936  
Publication No. US20060148743A1  
GENERAL INFORMATION:  
APPLICANT: Jachab, Vasant  
APPLICANT: Carroll, Joseph  
APPLICANT: Sirna Therapeutics, Inc.  
TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase  
TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid  
FILE REFERENCE: 05-727 (400/271)  
CURRENT APPLICATION NUMBER: US/11/217,936  
CURRENT FILING DATE: 2005-09-01  
NUMBER OF SEQ ID NOS: 5036  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 835  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-11-217-936-835

Query Match 49.5%; Score 9.4; DB 9; Length 19;  
Best Local Similarity 57.9%; Pred. No. 9.9e+04;  
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGCAGGTATCTCCTTCAC 19  
|||||  
Db 1 CGACAGTATACACACAC 19

RESULT 36  
US-10-825-485-284

Sequence 284, Application US/10825485  
Publication No. US20060160757A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.



```
APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Using Short Interfering Nucleic Acid (siNA)
; TITLE OF INVENTION: Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/150 (MHB04-378)
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 724
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 284
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
US-10-825-485-284

Query Match
Best Local Similarity 48.4%; Score 9.2; DB 6; Length 19;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 GGATCTCTCTTAC 19
Db 2 GGCAUCCUCCCCAC 15

RESULT 37
US-10-825-485-591/c
; Sequence 591, Application US/10825485
; Publication No. US20060160757A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hairless (HR) Gene
; TITLE OF INVENTION: Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/150 (MHB04-378)
; CURRENT APPLICATION NUMBER: US/10/825,485
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
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```
PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 724
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 591
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-825-485-591

Query Match
Best Local Similarity 48.4%; Score 9.2; DB 6; Length 19;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GGATCTCTCTTAC 19
Db 18 GGCAUCCUCCCCAC 5

RESULT 38
US-11-251-465-467/c
; Sequence 467, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-467

Query Match
Best Local Similarity 48.4%; Score 9.2; DB 8; Length 19;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGGTAATCTCTTCA 18
Db 17 CTGTGTCTGTCTCA 4

RESULT 39
US-11-217-936-1014/c
; Sequence 1014, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 05-727 (400/271)
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; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1014
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1014
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Query Match 48.4%; Score 9.2; DB 9; Length 19;
Best Local Similarity 78.6%; Pred. No. 1.3e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 14 CGCGCCGCAUCTCC 1
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## RESULT 40

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US-11-217-936-1483
; Sequence 1483, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1483
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1483
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Query Match 48.4%; Score 9.2; DB 9; Length 19;
Best Local Similarity 64.3%; Pred. No. 1.3e+05;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CGCAGCGTATCTCC 14
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DB 6 CGCGCCGCAUCTCC 19
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Search completed: August 10, 2006, 09:26:45  
Job time : 91.3333 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 08:42:03 ; Search time 1823.67 Seconds  
(without alignments)  
582.600 Million cell updates/sec

Title: US-10-636-065-29

Perfect score: 19

Sequence: 1 cgcacgctaccccttcac 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 3374

Minimum DB seq length: 19

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_est7:\*  
7: gb\_est8:\*  
8: gb\_est9:\*  
9: gb\_est10:\*  
10: gb\_est11:\*  
11: gb\_est12:\*  
12: gb\_est13:\*  
13: gb\_est14:\*  
14: gb\_est15:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 1	10.8	56.8	19	13	CL671134 PRI0163d
C 2	9.8	51.6	19	11	AZ481008 IM0302N15
C 3	8.6	45.3	19	11	AZ309116 IM0012E23
C 4	8.4	44.2	19	5	CF317235 HD--06-N1
C 5	8.2	43.2	19	5	CF929669 CF--01-R-E
C 6	8.2	43.2	19	14	AJ840508 Arabidops
C 7	8	42.1	19	5	CD532073 13104 Ara
C 8	8	42.1	19	5	CF280788 14ETL--07
C 9	8	42.1	19	5	CF299371 7LEAF--03
C 10	8	42.1	19	5	CF305417 GLEAF--01
C 11	8	42.1	19	5	CF315940 HD--05-A1
C 12	8	42.1	19	5	CF337272 JMT--07-K
C 13	8	42.1	19	11	AZ506614 IM0347A24
C 14	8	42.1	19	11	AZ995903 2M0281H19
C 15	8	42.1	19	13	CL657608 PRI012a_B
C 16	8	42.1	19	14	AJ587912 Arabidops
C 17	8	42.1	19	14	AJ600880 Arabidops
C 18	7.8	41.1	19	11	AZ308865 IM0012M14
C 19	7.8	41.1	19	11	AZ313113 IM0029N17

C 20	7.8	41.1	19	11	AZ411858	AZ411858 IM0185P01
C 21	7.8	41.1	19	11	AZ514774	AZ514774 IM0361N11
C 22	7.8	41.1	19	11	AZ585898	AZ585898 IM0391L22
C 23	7.8	41.1	19	11	AZ643528	AZ643528 IM0507H05
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C 25	7.6	40.0	19	5	CF281537	CF281537 14ETL--08
C 26	7.6	40.0	19	9	DR026632	DR026632 Osmo01180
C 27	7.6	40.0	19	11	AZ314603	AZ314603 IM0031C06
C 28	7.6	40.0	19	11	AZ505490	AZ505490 IM0346N08
C 29	7.6	40.0	19	11	AZ582154	AZ582154 IM0374C19
C 30	7.4	38.9	19	11	AZ2827164	AZ2827164 IM0103M22
C 31	7.4	38.9	19	1	A1663799	A1663799 u106a10.x
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C 34	7.4	38.9	19	11	AZ443948	AZ443948 IM0238P04
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C 36	7.4	38.9	19	11	AZ500675	AZ500675 IM0339J10
C 37	7.4	38.9	19	11	AZ834038	AZ834038 IM0116H01
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C 42	7.2	37.9	19	11	AZ341880	AZ341880 IM0074O04
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C 44	7.2	37.9	19	11	AZ612157	AZ612157 IM0438L21
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C 48	7	36.8	19	5	CF276559	CF276559 14ETL--01
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C 52	7	36.8	19	11	AZ585367	AZ585367 IM0390D06
C 53	7	36.8	19	11	AZ783569	AZ783569 IM0205O22
C 54	7	36.8	19	11	AZ799394	AZ799394 IM0056J18
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C 60	6.8	35.8	19	8	CO780487	CO780487 BL009D BO
C 61	6.8	35.8	19	8	CO781533	CO781533 BL012C HO
C 62	6.8	35.8	19	8	CM001762	CM001762 iV42B05 b
C 63	6.8	35.8	19	11	AZ372219	AZ372219 IM0124B03
C 64	6.8	35.8	19	11	AZ380009	AZ380009 IM0135L19
C 65	6.8	35.8	19	11	AZ422531	AZ422531 IM0201B16
C 66	6.8	35.8	19	11	AZ432757	AZ432757 IM0218L14
C 67	6.8	35.8	19	11	AZ440413	AZ440413 IM0231A01
C 68	6.8	35.8	19	11	AZ450047	AZ450047 IM0248A08
C 69	6.8	35.8	19	11	AZ490174	AZ490174 IM0233B05
C 70	6.8	35.8	19	11	AZ510122	AZ510122 IM0354K20
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C 72	6.8	35.8	19	11	AZ608373	AZ608373 IM0432E01
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C 76	6.8	35.8	19	11	AZ854740	AZ854740 IM0158C01
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C 84	6.6	34.7	19	3	BQ593607	BQ593607 E012766-0
C 85	6.6	34.7	19	4	CO1186	CO1186 HUMGS000788
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C 92	6.6	34.7	19	11	AZ355195	AZ355195 IM0094G22

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C 99	6.6	34.7	19 14	AJ587349	AJ587349	ArabiIdops	C 172	6	31.6	19 5	C21102	C21102
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C 108	6.4	33.7	19 3	B0594129	B0594129	E012759-0	C 181	6	31.6	19 11	AZ369420	AZ369420
C 109	6.4	33.7	19 4	C01216	C01216	HUMS000792	C 182	6	31.6	19 11	AZ394192	AZ394192
C 110	6.4	33.7	19 8	C0783138	C0783138	BL017A_G0	C 183	6	31.6	19 11	AZ403537	AZ403537
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C 113	6.4	33.7	19 9	D17097	D17097	K1ee	C 186	6	31.6	19 11	AZ446934	AZ446934
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C 116	6.4	33.7	19 11	AZ466725	AZ466725	1M0277C09	C 189	6	31.6	19 11	AZ495417	AZ495417
C 117	6.4	33.7	19 11	AZ477382	AZ477382	1M0296P16	C 190	6	31.6	19 11	AZ514408	AZ514408
C 118	6.4	33.7	19 11	AZ481877	AZ481877	1M0306B01	C 191	6	31.6	19 11	AZ589109	AZ589109
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C 120	6.4	33.7	19 11	AZ494890	AZ494890	1M0330N19	C 193	6	31.6	19 11	AZ597219	AZ597219
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C 122	6.4	33.7	19 11	AZ663240	AZ663240	1M0542H18	C 195	6	31.6	19 11	AZ646713	AZ646713
C 123	6.4	33.7	19 11	AZ771143	AZ771143	1M0573A07	C 196	6	31.6	19 11	AZ769427	AZ769427
C 124	6.4	33.7	19 11	AZ781954	AZ781954	2M0021F17	C 197	6	31.6	19 11	AZ769427	AZ769427
C 125	6.4	33.7	19 11	AZ783702	AZ783702	2M0025I08	C 198	6	31.6	19 11	AZ776860	AZ776860
C 126	6.4	33.7	19 11	AZ825698	AZ825698	2M0101O18	C 199	6	31.6	19 11	AZ779094	AZ779094
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C 130	6.2	32.6	19 3	CF1818426	CF1818426	HD--08-12	C 203	6	31.6	19 11	AZ854025	AZ854025
C 131	6.2	32.6	19 5	CO790624	CO790624	NT010A_G0	C 204	6	31.6	19 11	AZ857450	AZ857450
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C 135	6.2	32.6	19 11	AZ441505	AZ441505	1M0233M13	C 208	6	31.6	19 14	AJ587173	AJ587173
C 136	6.2	32.6	19 11	AZ489586	AZ489586	1M0322C12	C 209	6	31.6	19 14	AJ587186	AJ587186
C 137	6.2	32.6	19 11	AZ500053	AZ500053	1M0338M08	C 210	6	31.6	19 14	AJ591165	AJ591165
C 138	6.2	32.6	19 11	AZ500608	AZ500608	1M0339L05	C 211	6	31.6	19 14	ATH529932	ATH529932
C 139	6.2	32.6	19 11	AZ502110	AZ502110	1M0341C18	C 212	5.8	30.5	19 1	AA918795	AA918795
C 140	6.2	32.6	19 11	AZ510143	AZ510143	1M0354P21	C 213	5.8	30.5	19 1	A1371092	A1371092
C 141	6.2	32.6	19 11	AZ610584	AZ610584	1M0435P20	C 214	5.8	30.5	19 1	A1500684	A1500684
C 142	6.2	32.6	19 11	AZ663744	AZ663744	1M0543J01	C 215	5.8	30.5	19 1	A1664013	A1664013
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C 145	6.2	32.6	19 11	AZ805949	AZ805949	2M0067F07	C 218	5.8	30.5	19 1	AJ687665	AJ687665
C 146	6.2	32.6	19 11	AZ805949	AZ805949	2M0067F07	C 219	5.8	30.5	19 2	AJ687665	AJ687665
C 147	6.2	32.6	19 11	AZ806283	AZ806283	2M0068A16	C 220	5.8	30.5	19 3	B0599374	B0599374
C 148	6.2	32.6	19 11	AZ808212	AZ808212	2M0071D03	C 221	5.8	30.5	19 3	BO789814	BO789814
C 149	6.2	32.6	19 11	AZ815827	AZ815827	2M0084K23	C 222	5.8	30.5	19 5	CP281784	CP281784
C 150	6.2	32.6	19 11	AZ834038	AZ834038	2M0116H01	C 223	5.8	30.5	19 5	CP298134	CP298134
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C 153	6.2	32.6	19 11	AZ949895	AZ949895	2M0213N08	C 226	5.8	30.5	19 5	CP307304	CP307304
C 154	6.2	32.6	19 11	AZ956423	AZ956423	2M0222F24	C 227	5.8	30.5	19 5	CP307439	CP307439
C 155	6.2	32.6	19 13	CL678657	CL678657	PR10123C	C 228	5.8	30.5	19 8	CO777507	CO777507
C 156	6.2	32.6	19 14	AJ588791	AJ588791	ArabiIdops	C 229	5.8	30.5	19 8	CO780622	CO780622
C 157	6.2	32.6	19 14	TA11B08P	TA11B08P	ArabiIdops	C 230	5.8	30.5	19 8	CO780622	CO780622
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C 160	6	31.6	19 1	A1155325	A1155325	q88A05.r	C 233	5.8	30.5	19 11	AZ328922	AZ328922
C 161	6	31.6	19 2	AJ920596	AJ920596	AJ920596	C 234	5.8	30.5	19 11	AZ331326	AZ331326
C 162	6	31.6	19 2	BM395769	BM395769	5009-0-11	C 235	5.8	30.5	19 11	AZ345425	AZ345425
C 163	6	31.6	19 2	BM395792	BM395792	5009-0-11	C 236	5.8	30.5	19 11	AZ345449	AZ345449
C 164	6	31.6	19 2	BM396264	BM396264	5009-0-19	C 237	5.8	30.5	19 11	AZ345499	AZ345499
C 165	6	31.6	19 2	BM396331	BM396331	5009-0-2-	C 238	5.8	30.5	19 11	AZ345511	AZ345511

239	5.8	30.5	19	11	AZ345527	AZ345527	1M0080N02	C 312	5.6	29.5	19	1	AJ652627	AJ652627
240	5.8	30.5	19	11	AZ345536	AZ345536	1M0080O06	313	5.6	29.5	19	1	AJ657936	AJ657936
241	5.8	30.5	19	11	AZ345572	AZ345572	1M0080J17	314	5.6	29.5	19	1	AJ666294	AJ666294
242	5.8	30.5	19	11	AZ346709	AZ346709	1M0082M06	315	5.6	29.5	19	2	BM396413	BM396413
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244	5.8	30.5	19	11	AZ357983	AZ357983	1M0099J19	317	5.6	29.5	19	2	BM398524	BM398524
245	5.8	30.5	19	11	AZ360332	AZ360332	1M0103J04	318	5.6	29.5	19	2	BM399274	BM399274
246	5.8	30.5	19	11	AZ368655	AZ368655	1M0118P13	319	5.6	29.5	19	2	BM400783	BM400783
247	5.8	30.5	19	11	AZ368837	AZ368837	1M0119A11	320	5.6	29.5	19	2	BM401020	BM401020
248	5.8	30.5	19	11	AZ371083	AZ371083	1M0123C01	321	5.6	29.5	19	3	BM583648	BM583648
249	5.8	30.5	19	11	AZ372854	AZ372854	1M0124G22	322	5.6	29.5	19	3	BM589692	BM589692
250	5.8	30.5	19	11	AZ375581	AZ375581	1M0129E05	323	5.6	29.5	19	3	BM593604	BM593604
251	5.8	30.5	19	11	AZ386717	AZ386717	1M0145P17	324	5.6	29.5	19	4	CO25594	CO25594
252	5.8	30.5	19	11	AZ387157	AZ387157	1M0146E20	325	5.6	29.5	19	5	CF297283	CF297283
253	5.8	30.5	19	11	AZ393054	AZ393054	1M0155N21	326	5.6	29.5	19	5	CF297283	CF297283
254	5.8	30.5	19	11	AZ407748	AZ407748	1M0178C07	327	5.6	29.5	19	5	CK576562	CK576562
255	5.8	30.5	19	11	AZ410166	AZ410166	1M0182J17	328	5.6	29.5	19	7	AM248167	AM248167
256	5.8	30.5	19	11	AZ445563	AZ445563	1M0241P18	329	5.6	29.5	19	8	CO779910	CO779910
257	5.8	30.5	19	11	AZ447223	AZ447223	1M0244H13	330	5.6	29.5	19	8	CO779910	CO779910
258	5.8	30.5	19	11	AZ447247	AZ447247	1M0244G19	331	5.6	29.5	19	8	CO780487	CO780487
259	5.8	30.5	19	11	AZ452087	AZ452087	1M0251F18	332	5.6	29.5	19	8	CO781979	CO781979
260	5.8	30.5	19	11	AZ453791	AZ453791	1M0272C22	333	5.6	29.5	19	8	CO790444	CO790444
261	5.8	30.5	19	11	AZ463791	AZ463791	1M0272C22	334	5.6	29.5	19	8	CO793357	CO793357
262	5.8	30.5	19	11	AZ470220	AZ470220	1M0284M11	335	5.6	29.5	19	8	DR062800	DR062800
263	5.8	30.5	19	11	AZ480415	AZ480415	1M0301K24	336	5.6	29.5	19	9	DR103208	DR103208
264	5.8	30.5	19	11	AZ489350	AZ489350	1M0321K14	337	5.6	29.5	19	9	AZ309531	AZ309531
265	5.8	30.5	19	11	AZ510096	AZ510096	1M0354B22	338	5.6	29.5	19	11	AZ314110	AZ314110
266	5.8	30.5	19	11	AZ510106	AZ510106	1M0354E19	339	5.6	29.5	19	11	AZ316210	AZ316210
267	5.8	30.5	19	11	AZ510952	AZ510952	1M0355G15	340	5.6	29.5	19	11	AZ317020	AZ317020
268	5.8	30.5	19	11	AZ517956	AZ517956	1M0367L08	341	5.6	29.5	19	11	AZ323590	AZ323590
269	5.8	30.5	19	11	AZ579566	AZ579566	1M0367L08	342	5.6	29.5	19	11	AZ340126	AZ340126
270	5.8	30.5	19	11	AZ585820	AZ585820	1M0391I15	343	5.6	29.5	19	11	AZ346629	AZ346629
271	5.8	30.5	19	11	AZ611716	AZ611716	1M0438B15	344	5.6	29.5	19	11	AZ359598	AZ359598
272	5.8	30.5	19	11	AZ614702	AZ614702	1M0443F10	345	5.6	29.5	19	11	AZ612624	AZ612624
273	5.8	30.5	19	11	AZ626573	AZ626573	1M0466J24	346	5.6	29.5	19	11	AZ613058	AZ613058
274	5.8	30.5	19	11	AZ626779	AZ626779	1M0467A14	347	5.6	29.5	19	11	AZ637711	AZ637711
275	5.8	30.5	19	11	AZ634666	AZ634666	1M0490P03	348	5.6	29.5	19	11	AZ641145	AZ641145
276	5.8	30.5	19	11	AZ638980	AZ638980	1M0499L08	349	5.6	29.5	19	11	AZ655972	AZ655972
277	5.8	30.5	19	11	AZ647364	AZ647364	1M0513O16	350	5.6	29.5	19	11	AZ771560	AZ771560
278	5.8	30.5	19	11	AZ663184	AZ663184	1M0542L07	351	5.6	29.5	19	11	AZ782819	AZ782819
279	5.8	30.5	19	11	AZ759494	AZ759494	1M0552K06	352	5.6	29.5	19	11	AZ783477	AZ783477
280	5.8	30.5	19	11	AZ761740	AZ761740	1M0556A13	353	5.6	29.5	19	11	AZ783477	AZ783477
281	5.8	30.5	19	11	AZ769232	AZ769232	1M0569H07	354	5.6	29.5	19	11	AZ822713	AZ822713
282	5.8	30.5	19	11	AZ769437	AZ769437	1M0570A07	355	5.6	29.5	19	11	AZ826447	AZ826447
283	5.8	30.5	19	11	AZ774950	AZ774950	2M0004M16	356	5.6	29.5	19	11	AZ860660	AZ860660
284	5.8	30.5	19	11	AZ775540	AZ775540	2M0008H15	357	5.6	29.5	19	11	AZ874357	AZ874357
285	5.8	30.5	19	11	AZ784061	AZ784061	2M0026M20	358	5.6	29.5	19	11	AZ936396	AZ936396
286	5.8	30.5	19	11	AZ786336	AZ786336	2M0031H17	359	5.6	29.5	19	11	AZ974357	AZ974357
287	5.8	30.5	19	11	AZ790121	AZ790121	2M0038P21	360	5.6	29.5	19	11	AZ976225	AZ976225
288	5.8	30.5	19	11	AZ792979	AZ792979	2M0046G04	361	5.6	29.5	19	13	CU878326	CU878326
289	5.8	30.5	19	11	AZ795136	AZ795136	2M0049A16	362	5.6	29.5	19	14	AJ599527	AJ599527
290	5.8	30.5	19	11	AZ799463	AZ799463	2M0057A01	363	5.6	29.5	19	14	AA916934	AA916934
291	5.8	30.5	19	11	AZ800056	AZ800056	2M0057E20	364	5.6	29.5	19	1	AI027323	AI027323
292	5.8	30.5	19	11	AZ807034	AZ807034	2M0069B05	365	5.6	29.5	19	1	AI147066	AI147066
293	5.8	30.5	19	11	AZ820818	AZ820818	2M0093I18	366	5.6	29.5	19	1	AI183836	AI183836
294	5.8	30.5	19	11	AZ822385	AZ822385	2M0095F09	367	5.6	29.5	19	1	AI183836	AI183836
295	5.8	30.5	19	11	AZ822928	AZ822928	2M0113J08	368	5.6	29.5	19	1	AI183836	AI183836
296	5.8	30.5	19	11	AZ833844	AZ833844	2M0116O07	369	5.6	29.5	19	1	AI183836	AI183836
297	5.8	30.5	19	11	AZ842379	AZ842379	2M0140N17	370	5.6	29.5	19	1	AI695637	AI695637
298	5.8	30.5	19	11	AZ864822	AZ864822	2M0174C08	371	5.6	29.5	19	1	AI696833	AI696833
299	5.8	30.5	19	11	AZ936396	AZ936396	2M0193M02	372	5.6	29.5	19	1	AI790036	AI790036
300	5.8	30.5	19	11	AZ949954	AZ949954	2M0213J16	373	5.6	29.5	19	1	AI811474	AI811474
301	5.8	30.5	19	11	AZ951124	AZ951124	2M0215A02	374	5.6	29.5	19	1	AJ655263	AJ655263
302	5.8	30.5	19	11	AZ968667	AZ968667	2M0241A07	375	5.6	29.5	19	1	AJ746804	AJ746804
303	5.8	30.5	19	11	AZ991837	AZ991837	2M0276E17	376	5.6	29.5	19	1	AJ747293	AJ747293
304	5.8	30.5	19	14	AJ587349	AJ587349	ArabiIdops	377	5.6	29.5	19	2	BM396949	BM396949
305	5.8	30.5	19	14	AJ588602	AJ588602	ArabiIdops	378	5.6	29.5	19	2	BM399593	BM399593
306	5.8	30.5	19	14	AJ588965	AJ588965	ArabiIdops	379	5.6	29.5	19	2	BM399593	BM399593
307	5.8	30.5	19	14	AJ589265	AJ589265	ArabiIdops	380	5.6	29.5	19	2	BM396766	BM396766
308	5.8	30.5	19	14	AJ589583	AJ589583	ArabiIdops	381	5.6	29.5	19	2	BM399684	BM399684
309	5.8	30.5	19	14	AJ601030	AJ601030	ArabiIdops	382	5.6	29.5	19	3	BM582903	BM582903
310	5.8	30.5	19	14	ATH523679	AJ523679	ArabiIdops	383	5.6	29.5	19	3	BM587387	BM587387
311	5.8	30.5	19	14	ATH527400	AJ527400	ArabiIdops	384	5.6	29.5	19	4	CO1186	CO1186

C 385	5.4	28.4	19	4	COL584	C01584	HUMG000858	458	5.4	28.4	19	11	A278302	A2778302	2M0013C02
C 386	5.4	28.4	19	4	CA587820	CA587820	LBEL6D60	C 459	5.4	28.4	19	11	A2780833	A2780833	2M0018M21
C 387	5.4	28.4	19	4	CB413855	CB413855	SCAE_2576	C 460	5.4	28.4	19	11	A2783569	A2783569	2M0025O22
C 388	5.4	28.4	19	4	CB415466	CB415466	SCAE_4656	C 461	5.4	28.4	19	11	A2794440	A2794440	2M0048B15
C 389	5.4	28.4	19	5	CF294232	CF294232	30DGS--03	C 462	5.4	28.4	19	11	A2798425	A2798425	2M0055D13
C 390	5.4	28.4	19	5	CF298891	CF298891	7LEAF--02	C 463	5.4	28.4	19	11	A2803756	A2803756	2M0064M15
C 391	5.4	28.4	19	5	CF308262	CF308262	ABF--02-A	C 464	5.4	28.4	19	11	A2804026	A2804026	2M0064O07
C 392	5.4	28.4	19	5	CF311635	CF311635	ABF--06-O	C 465	5.4	28.4	19	11	A2809394	A2809394	2M0073B19
C 393	5.4	28.4	19	5	CF313581	CF313581	HD--01-MO	C 466	5.4	28.4	19	11	A2812572	A2812572	2M0079O15
C 394	5.4	28.4	19	5	CF316935	CF316935	HD--06-HO	C 467	5.4	28.4	19	11	A2822713	A2822713	2M0096M08
C 395	5.4	28.4	19	5	CF317608	CF317608	UMT--08-C	C 468	5.4	28.4	19	11	A2832901	A2832901	2M0113P12
C 396	5.4	28.4	19	5	CF542982	CF542982	S014680w-	C 469	5.4	28.4	19	11	A2833228	A2833228	2M0113U08
C 397	5.4	28.4	19	6	CNS09M6X	CF542982	Single re	C 470	5.4	28.4	19	11	A2835034	A2835034	2M0129X04
C 398	5.4	28.4	19	8	C0790624	C0790624	NT010A_G0	C 471	5.4	28.4	19	11	A2847888	A2847888	2M0148G07
C 399	5.4	28.4	19	8	C0791279	C0791279	NT012A_A0	C 472	5.4	28.4	19	11	A2854718	A2854718	2M0158N23
C 400	5.4	28.4	19	10	DV748318	DV748318	ID0AAH12C	C 473	5.4	28.4	19	11	A2855545	A2855545	2M0159P09
C 401	5.4	28.4	19	11	AZ307462	AZ307462	IM0009108	C 474	5.4	28.4	19	11	A2858446	A2858446	2M0163P08
C 402	5.4	28.4	19	11	AZ309043	AZ309043	IM0012008	C 475	5.4	28.4	19	11	A2941399	A2941399	2M0201P07
C 403	5.4	28.4	19	11	AZ309874	AZ309874	IM0017C14	C 476	5.4	28.4	19	11	A2941765	A2941765	2M0201G11
C 404	5.4	28.4	19	11	AZ314143	AZ314143	IM0030K16	C 477	5.4	28.4	19	11	A2977338	A2977338	2M0253P10
C 405	5.4	28.4	19	11	AZ328553	AZ328553	IM0052B19	C 478	5.4	28.4	19	11	A2990856	A2990856	2M0274P14
C 406	5.4	28.4	19	11	AZ330744	AZ330744	IM0056107	C 479	5.4	28.4	19	11	A2991531	A2991531	2M0275K15
C 407	5.4	28.4	19	11	AZ338061	AZ338061	IM0069B05	C 480	5.4	28.4	19	13	CL656067	CL656067	PR10125C
C 408	5.4	28.4	19	11	AZ345903	AZ345903	IM0080E23	C 481	5.4	28.4	19	13	CL657902	CL657902	PR1012B_D
C 409	5.4	28.4	19	11	AZ345954	AZ345954	IM0080C23	C 482	5.4	28.4	19	13	CL658001	CL658001	PR10130A
C 410	5.4	28.4	19	11	AZ366147	AZ366147	IM0115D20	C 483	5.4	28.4	19	13	CL668704	CL668704	PR1015Bb
C 411	5.4	28.4	19	11	AZ371078	AZ371078	IM0122A04	C 484	5.4	28.4	19	13	CL668704	CL668704	PR1015Bb
C 412	5.4	28.4	19	11	AZ392246	AZ392246	IM01524G12	C 485	5.4	28.4	19	13	CL668834	CL668834	PR1015Bd
C 413	5.4	28.4	19	11	AZ392507	AZ392507	IM0155H11	C 486	5.4	28.4	19	13	CL680274	CL680274	PR10128C
C 414	5.4	28.4	19	11	AZ393551	AZ393551	IM0156P07	C 487	5.4	28.4	19	13	CL680486	CL680486	PR10129b
C 415	5.4	28.4	19	11	AZ424552	AZ424552	IM0204L07	C 488	5.4	28.4	19	13	CL681299	CL681299	PR10130d
C 416	5.4	28.4	19	11	AZ424757	AZ424757	IM0204G02	C 489	5.4	28.4	19	13	CL693868	CL693868	PR10162d
C 417	5.4	28.4	19	11	AZ428450	AZ428450	IM0210O24	C 490	5.4	28.4	19	14	DU779955	ASXB2967	
C 418	5.4	28.4	19	11	AZ430028	AZ430028	IM0214L16	C 491	5.4	28.4	19	14	DX068083	DX068083	KB-B076L0
C 419	5.4	28.4	19	11	AZ438791	AZ438791	IM0229K01	C 492	5.4	28.4	19	14	DX069382	KB-B078G1	
C 420	5.4	28.4	19	11	AZ440106	AZ440106	IM0231G04	C 493	5.4	28.4	19	14	AJ588343	AJ588343	ArabiIdops
C 421	5.4	28.4	19	11	AZ441752	AZ441752	IM0234K06	C 494	5.4	28.4	19	14	AJ600584	AJ600584	ArabiIdops
C 422	5.4	28.4	19	11	AZ458827	AZ458827	IM0276D07	C 495	5.4	28.4	19	14	ATH525946	ATH525946	ArabiIdops
C 423	5.4	28.4	19	11	AZ478277	AZ478277	IM0298B16	C 496	5.4	28.4	19	14	ATH526841	ATH526841	ArabiIdops
C 424	5.4	28.4	19	11	AZ478277	AZ478277	IM0298B16	C 497	5.4	28.4	19	14	ATH527280	ATH527280	ArabiIdops
C 425	5.4	28.4	19	11	AZ480102	AZ480102	IM0301A20	C 498	5.4	28.4	19	14	ATH529702	ATH529702	ArabiIdops
C 426	5.4	28.4	19	11	AZ480342	AZ480342	IM0301J16	C 499	5.4	28.4	19	14	ATH529725	ATH529725	ArabiIdops
C 427	5.4	28.4	19	11	AZ485264	AZ485264	IM0312002	C 500	5.4	28.4	19	14	ATH529954	ATH529954	ArabiIdops
C 428	5.4	28.4	19	11	AZ488234	AZ488234	IM0318G24	C 501	5.4	28.4	19	14	ATH531977	ATH531977	ArabiIdops
C 429	5.4	28.4	19	11	AZ491206	AZ491206	IM0324P07	C 502	5.2	27.4	19	1	AA912825	AA912825	o143d11.s
C 430	5.4	28.4	19	11	AZ496805	AZ496805	IM0333G22	C 503	5.2	27.4	19	1	AA977115	AA977115	oq24c08.s
C 431	5.4	28.4	19	11	AZ501453	AZ501453	IM0340M13	C 504	5.2	27.4	19	1	AI017937	AI017937	cu24a06.x
C 432	5.4	28.4	19	11	AZ508288	AZ508288	IM0350A01	C 505	5.2	27.4	19	1	AI160784	AI160784	qx98g07.x
C 433	5.4	28.4	19	11	AZ508487	AZ508487	IM0350H24	C 506	5.2	27.4	19	1	AI183857	AI183857	tc73g05.x
C 434	5.4	28.4	19	11	AZ514386	AZ514386	IM0361H02	C 507	5.2	27.4	19	1	AI191818	AI191818	tn08c09.x
C 435	5.4	28.4	19	11	AZ586377	AZ586377	IM0392A15	C 508	5.2	27.4	19	1	AJ688828	AJ688828	AI688828
C 436	5.4	28.4	19	11	AZ588035	AZ588035	IM0396G17	C 509	5.2	27.4	19	1	AM075294	AM075294	AM075294
C 437	5.4	28.4	19	11	AZ596312	AZ596312	IM0409D04	C 510	5.2	27.4	19	2	BMJ96129	BMJ96129	5009-0-17
C 438	5.4	28.4	19	11	AZ600709	AZ600709	IM0418H10	C 511	5.2	27.4	19	4	BKX50886	BKX50886	BKX50886
C 439	5.4	28.4	19	11	AZ600896	AZ600896	IM0418J24	C 512	5.2	27.4	19	4	BKX554211	BKX554211	BKX554211
C 440	5.4	28.4	19	11	AZ603744	AZ603744	IM0423B15	C 513	5.2	27.4	19	4	BKX558720	BKX558720	BKX558720
C 441	5.4	28.4	19	11	AZ623310	AZ623310	IM0460G19	C 514	5.2	27.4	19	4	BKX58720	BKX58720	BKX58720
C 442	5.4	28.4	19	11	AZ651803	AZ651803	IM0532N11	C 515	5.2	27.4	19	4	BKX60068	BKX60068	BKX60068
C 443	5.4	28.4	19	11	AZ655467	AZ655467	IM0530U17	C 516	5.2	27.4	19	4	BKX60254	BKX60254	BKX60254
C 444	5.4	28.4	19	11	AZ660552	AZ660552	IM0538O08	C 517	5.2	27.4	19	4	BKX63913	BKX63913	BKX63913
C 445	5.4	28.4	19	11	AZ663032	AZ663032	IM0542M22	C 518	5.2	27.4	19	4	BKX63927	BKX63927	BKX63927
C 446	5.4	28.4	19	11	AZ663240	AZ663240	IM0542H18	C 519	5.2	27.4	19	4	BKX64633	BKX64633	BKX64633
C 447	5.4	28.4	19	11	AZ663498	AZ663498	IM0543T08	C 520	5.2	27.4	19	4	BKX67491	BKX67491	BKX67491
C 448	5.4	28.4	19	11	AZ759607	AZ759607	IM0552123	C 521	5.2	27.4	19	4	BKX68381	BKX68381	BKX68381
C 449	5.4	28.4	19	11	AZ760695	AZ760695	IM0554C07	C 522	5.2	27.4	19	4	BKX68469	BKX68469	BKX68469
C 450	5.4	28.4	19	11	AZ761834	AZ761834	IM0556E19	C 523	5.2	27.4	19	4	BKX68737	BKX68737	BKX68737
C 451	5.4	28.4	19	11	AZ768918	AZ768918	IM0569F08	C 524	5.2	27.4	19	4	C00981	C00981	C00981
C 452	5.4	28.4	19	11	AZ770542	AZ770542	IM0572K11	C 525	5.2	27.4	19	4	CA587421	CA587421	HUMG000337
C 453	5.4	28.4	19	11	AZ772336	AZ772336	IM0574K14	C 526	5.2	27.4	19	4	CA587213	CA587213	CL6L01A03
C 454	5.4	28.4	19	11	AZ772566	AZ772566	IM0583J05	C 527	5.2	27.4	19	5	CF298245	CF298245	7LEAF--01
C 455	5.4	28.4	19	11	AZ774909	AZ774909	2M0004E17	C 528	5.2	27.4	19	5	CF306225	CF306225	HDAL--03-
C 456	5.4	28.4	19	11	AZ774950	AZ774950	2M0004M16	C 529	5.2	27.4	19	5	CF312203	ABF--07-M	
C 457	5.4	28.4	19	11	AZ776733	AZ776733	2M0010E07	C 530	5.2	27.4	19	5	CF312203	ABF--07-M	

531	5.2	27.4	19	5	CF318426	CF318426 HD--08-12	C 604	5.2	27.4	19	11	A2864297	A2864297 2M0173L18
532	5.2	27.4	19	7	AM059309	AM059309 AHUTH_bas	C 605	5.2	27.4	19	11	A2868070	A2868070 2M0179I07
533	5.2	27.4	19	8	CO778963	CO778963 BL005B_B0	C 606	5.2	27.4	19	11	A2937956	A2937956 2M0196O18
534	5.2	27.4	19	8	CO779910	CO779910 BL008A_G0	C 607	5.2	27.4	19	11	A2944615	A2944615 2M0205H12
535	5.2	27.4	19	8	CO781979	CO781979 BL013D_F1	C 608	5.2	27.4	19	11	A2991573	A2991573 2M0275D23
536	5.2	27.4	19	8	CO790444	CO790444 NT009C_G1	C 609	5.2	27.4	19	13	CL873643	CL873643 abe89d05.
537	5.2	27.4	19	8	CO793357	CO793357 NT017C_D0	C 610	5.2	27.4	19	14	AJ587161	AJ587161 Arabidops
538	5.2	27.4	19	9	DN161077	DN161077 est a.Dla	C 611	5.2	27.4	19	14	AJ587166	AJ587166 Arabidops
539	5.2	27.4	19	9	DN955544	DN955544 it83Cl.g	C 612	5.2	27.4	19	14	AJ587167	AJ587167 Arabidops
540	5.2	27.4	19	9	DN985675	DN985675 MSU_2F_-2-	C 613	5.2	27.4	19	14	AJ587961	AJ587961 Arabidops
541	5.2	27.4	19	9	DR107492	DR107492 JHU140E12	C 614	5.2	27.4	19	14	AJ592461	AJ592461 Arabidops
542	5.2	27.4	19	11	AZ309914	AZ309914 IM0017P18	C 615	5.2	27.4	19	14	AJ594463	AJ594463 Arabidops
543	5.2	27.4	19	11	AZ316568	AZ316568 IM0034G14	C 616	5.2	27.4	19	14	AJ597470	AJ597470 Arabidops
544	5.2	27.4	19	11	AZ322583	AZ322583 IM0043A10	C 617	5.2	27.4	19	14	ATH525440	ATH525440 Arabidops
545	5.2	27.4	19	11	AZ324945	AZ324945 IM0047C03	C 618	5.2	27.4	19	14	ATH527642	ATH527642 Arabidops
546	5.2	27.4	19	11	AZ340577	AZ340577 IM0072H21	C 619	5.2	27.4	19	14	ATH528618	ATH528618 Arabidops
547	5.2	27.4	19	11	AZ342681	AZ342681 IM0075B23	C 620	5.2	27.4	19	14	ATH531443	ATH531443 Arabidops
548	5.2	27.4	19	11	AZ343388	AZ343388 IM0076J23	C 621	5.2	27.4	19	14	AA909236	AA909236 ox02d04.8
549	5.2	27.4	19	11	AZ345852	AZ345852 IM0080E18	C 622	5.2	27.4	19	1	AI033338	AI033338 ox02d04.8
550	5.2	27.4	19	11	AZ355195	AZ355195 IM0094G22	C 623	5.2	27.4	19	1	AI077581	AI077581 ox76a04.8
551	5.2	27.4	19	11	AZ361569	AZ361569 IM0106N21	C 624	5.2	27.4	19	1	AI187072	AI187072 qe38a01.8
552	5.2	27.4	19	11	AZ379786	AZ379786 IM0135K09	C 625	5.2	27.4	19	1	AI1524591	AI1524591 co43f09.x
553	5.2	27.4	19	11	AZ395977	AZ395977 IM0150I20	C 626	5.2	27.4	19	1	AI570374	AI570374 co78f07.x
554	5.2	27.4	19	11	AZ403969	AZ403969 IM0172B03	C 627	5.2	27.4	19	1	AI625518	AI625518 ly56d06.x
555	5.2	27.4	19	11	AZ406101	AZ406101 IM0175O11	C 628	5.2	27.4	19	1	AI648553	AI648553 t855e07.x
556	5.2	27.4	19	11	AZ427411	AZ427411 IM0209A22	C 629	5.2	27.4	19	1	AI678558	AI678558 t83h07.x
557	5.2	27.4	19	11	AZ437653	AZ437653 IM0209B14	C 630	5.2	27.4	19	1	AJ647608	AJ647608 AJ647608
558	5.2	27.4	19	11	AZ441188	AZ441188 IM0235O04	C 631	5.2	27.4	19	1	AJ650046	AJ650046 AJ650046
559	5.2	27.4	19	11	AZ457710	AZ457710 IM0261K07	C 632	5.2	27.4	19	1	AJ650046	AJ650046 AJ650046
560	5.2	27.4	19	11	AZ458883	AZ458883 IM0276D07	C 633	5.2	27.4	19	1	AJ657561	AJ657561 AJ657561
561	5.2	27.4	19	11	AZ466725	AZ466725 IM0277C09	C 634	5.2	27.4	19	1	AJ662060	AJ662060 AJ662060
562	5.2	27.4	19	11	AZ475079	AZ475079 IM0293B17	C 635	5.2	27.4	19	1	AJ666241	AJ666241 AJ666241
563	5.2	27.4	19	11	AZ480102	AZ480102 IM0301A20	C 636	5.2	27.4	19	1	AJ671616	AJ671616 AJ671616
564	5.2	27.4	19	11	AZ490111	AZ490111 IM0322H17	C 637	5.2	27.4	19	1	AJ672970	AJ672970 AJ672970
565	5.2	27.4	19	11	AZ490549	AZ490549 IM0323N03	C 638	5.2	27.4	19	1	AJ746804	AJ746804 AJ746804
566	5.2	27.4	19	11	AZ510138	AZ510138 IM0354O21	C 639	5.2	27.4	19	1	AL037236	AL037236 DXF2564L
567	5.2	27.4	19	11	AZ514467	AZ514467 IM0361B19	C 640	5.2	27.4	19	1	AM075343	AM075343 DXF2564L
568	5.2	27.4	19	11	AZ579954	AZ579954 IM0368C02	C 641	5.2	27.4	19	2	BG927923	BG927923 HNC45-1-E
569	5.2	27.4	19	11	AZ581163	AZ581163 IM0369M20	C 642	5.2	27.4	19	2	BM394350	BM394350 50072-2-3
570	5.2	27.4	19	11	AZ585898	AZ585898 IM0391L22	C 643	5.2	27.4	19	2	BM395127	BM395127 50072-2-7
571	5.2	27.4	19	11	AZ589109	AZ589109 IM0397D22	C 644	5.2	27.4	19	2	BM397569	BM397569 5009-0-34
572	5.2	27.4	19	11	AZ591963	AZ591963 IM0402P23	C 645	5.2	27.4	19	2	BM399311	BM399311 5009-0-56
573	5.2	27.4	19	11	AZ601003	AZ601003 IM0419M06	C 646	5.2	27.4	19	2	BM399863	BM399863 5009-0-62
574	5.2	27.4	19	11	AZ622447	AZ622447 IM0459I15	C 647	5.2	27.4	19	2	BM400740	BM400740 5009-0-78
575	5.2	27.4	19	11	AZ623785	AZ623785 IM0461P16	C 648	5.2	27.4	19	3	BQ789814	BQ789814 h8ge002af
576	5.2	27.4	19	11	AZ636812	AZ636812 IM0495B21	C 649	5.2	27.4	19	4	BX548528	BX548528 BX548528
577	5.2	27.4	19	11	AZ644418	AZ644418 IM0508B20	C 650	5.2	27.4	19	4	BX551805	BX551805 BX551805
578	5.2	27.4	19	11	AZ645469	AZ645469 IM0510L24	C 651	5.2	27.4	19	4	CA0646	CA0646 HUM6S000819
579	5.2	27.4	19	11	AZ645469	AZ645469 IM0510L24	C 652	5.2	27.4	19	4	CA587421	CA587421 LEB12B23
580	5.2	27.4	19	11	AZ648801	AZ648801 IM0518A10	C 653	5.2	27.4	19	4	CB412539	CB412539 SCAE_-0892
581	5.2	27.4	19	11	AZ655972	AZ655972 IM0531C16	C 654	5.2	27.4	19	4	CB412539	CB412539 SCAE_-0892
582	5.2	27.4	19	11	AZ656937	AZ656937 IM0532K13	C 655	5.2	27.4	19	4	CB413855	CB413855 SCAE_2576
583	5.2	27.4	19	11	AZ657685	AZ657685 IM0534I06	C 656	5.2	27.4	19	4	CB415466	CB415466 SCAE_4656
584	5.2	27.4	19	11	AZ659603	AZ659603 IM0537N06	C 657	5.2	27.4	19	5	CD533793	CD533793 3312J_Ara
585	5.2	27.4	19	11	AZ662546	AZ662546 IM0541P08	C 658	5.2	27.4	19	5	CF296463	CF296463 30DGS--06
586	5.2	27.4	19	11	AZ663498	AZ663498 IM0543I08	C 659	5.2	27.4	19	5	CF298887	CF298887 7LEAF--02
587	5.2	27.4	19	11	AZ665203	AZ665203 IM0546B05	C 660	5.2	27.4	19	5	CF298891	CF298891 7LEAF--02
588	5.2	27.4	19	11	AZ759898	AZ759898 IM0553A08	C 661	5.2	27.4	19	5	CF299279	CF299279 7LEAF--03
589	5.2	27.4	19	11	AZ763729	AZ763729 IM0559N16	C 662	5.2	27.4	19	5	CF303019	CF303019 ABF1--01-
590	5.2	27.4	19	11	AZ772432	AZ772432 IM0583L17	C 663	5.2	27.4	19	5	CF306449	CF306449 HDAL--03-
591	5.2	27.4	19	11	AZ775273	AZ775273 2M0007F04	C 664	5.2	27.4	19	5	CF322872	CF322872 HNN--02-E
592	5.2	27.4	19	11	AZ775865	AZ775865 2M0009P05	C 665	5.2	27.4	19	5	CF329137	CF329137 NACL--04-
593	5.2	27.4	19	11	AZ778052	AZ778052 2M0013A01	C 666	5.2	27.4	19	6	CNS08V82	CNS08V82 Single re
594	5.2	27.4	19	11	AZ782828	AZ782828 2M0024H06	C 667	5.2	27.4	19	6	CNS09MX8	CNS09MX8 Single re
595	5.2	27.4	19	11	AZ785819	AZ785819 2M0030F04	C 668	5.2	27.4	19	7	AM250665	AM250665 2822622.5
596	5.2	27.4	19	11	AZ787588	AZ787588 2M0034A07	C 669	5.2	27.4	19	8	CN498250	CN498250 F04_02622
597	5.2	27.4	19	11	AZ805995	AZ805995 2M0067P13	C 670	5.2	27.4	19	8	CN498250	CN498250 F04_02622
598	5.2	27.4	19	11	AZ812572	AZ812572 2M0079O15	C 671	5.2	27.4	19	8	COS77706	COS77706 TVEST082C
599	5.2	27.4	19	11	AZ814554	AZ814554 2M0082P13	C 672	5.2	27.4	19	8	COS78459	COS78459 TVEST093C
600	5.2	27.4	19	11	AZ818659	AZ818659 2M0088N17	C 673	5.2	27.4	19	8	CO786076	CO786076 BL285B_E0
601	5.2	27.4	19	11	AZ825396	AZ825396 2M0100N04	C 674	5.2	27.4	19	8	CO786076	CO786076 BL285B_E0
602	5.2	27.4	19	11	AZ828745	AZ828745 2M0105J19	C 675	5.2	27.4	19	8	CO786107	CO786107 BL285B_H0
603	5.2	27.4	19	11	AZ839642	AZ839642 2M0135C23	C 676	5.2	27.4	19	8	CV933279	CV933279 pWpcn_050

677	5	26.3	19	8	CX000508	CX000508	lv58b09.g	750	5	26.3	19	11	AZ808212	AZ808212	2M0071D03
678	5	26.3	19	8	CX001762	CX001762	lv42h09.b	751	5	26.3	19	11	AZ811036	AZ811036	2M0077B05
679	5	26.3	19	9	DN955504	DN955504	lt88g06.g	752	5	26.3	19	11	AZ813099	AZ813099	2M0080P09
680	5	26.3	19	9	DN955507	DN955507	lt88g10.g	753	5	26.3	19	11	AZ814554	AZ814554	2M0082P13
681	5	26.3	19	9	DR107492	DR107492	jt88g10.g	754	5	26.3	19	11	AZ818421	AZ818421	2M0082P19
682	5	26.3	19	9	DR107588	DR107588	jt88g10.g	755	5	26.3	19	11	AZ819775	AZ819775	2M0091D01
683	5	26.3	19	10	DV671474	DV671474	Col-B12 A	756	5	26.3	19	11	AZ822457	AZ822457	2M0095D16
684	5	26.3	19	11	AQ990183	AQ990183	Rfc00908	757	5	26.3	19	11	AZ826361	AZ826361	2M0102H04
685	5	26.3	19	11	AZ303949	AZ303949	IM0003M19	758	5	26.3	19	11	AZ827840	AZ827840	2M0104F01
686	5	26.3	19	11	AZ309643	AZ309643	IM0016E23	759	5	26.3	19	11	AZ829723	AZ829723	2M0107I22
687	5	26.3	19	11	AZ313113	AZ313113	IM0029N17	760	5	26.3	19	11	AZ831190	AZ831190	2M0110K18
688	5	26.3	19	11	AZ314770	AZ314770	IM0031B16	761	5	26.3	19	11	AZ834005	AZ834005	2M0116P20
689	5	26.3	19	11	AZ319924	AZ319924	IM0039C15	762	5	26.3	19	11	AZ834875	AZ834875	2M0117L13
690	5	26.3	19	11	AZ327390	AZ327390	IM0050L09	763	5	26.3	19	11	AZ835621	AZ835621	2M0129L21
691	5	26.3	19	11	AZ331082	AZ331082	IM0056C13	764	5	26.3	19	11	AZ839043	AZ839043	2M0135D04
692	5	26.3	19	11	AZ335137	AZ335137	IM0064P16	765	5	26.3	19	11	AZ842496	AZ842496	2M0141D04
693	5	26.3	19	11	AZ339847	AZ339847	IM0071C06	766	5	26.3	19	11	AZ846978	AZ846978	2M0164P24
694	5	26.3	19	11	AZ345964	AZ345964	IM0081D01	767	5	26.3	19	11	AZ848551	AZ848551	2M0174M11
695	5	26.3	19	11	AZ345964	AZ345964	IM0081D01	768	5	26.3	19	11	AZ868818	AZ868818	2M0180L11
696	5	26.3	19	11	AZ358656	AZ358656	IM0018G18	769	5	26.3	19	11	AZ871037	AZ871037	2M0183C16
697	5	26.3	19	11	AZ361569	AZ361569	IM0106N21	770	5	26.3	19	11	AZ937956	AZ937956	2M0196O18
698	5	26.3	19	11	AZ370656	AZ370656	IM0121P18	771	5	26.3	19	11	AZ954985	AZ954985	2M0220H21
699	5	26.3	19	11	AZ394490	AZ394490	IM0158D05	772	5	26.3	19	11	AZ994163	AZ994163	2M0279P05
700	5	26.3	19	11	AZ397615	AZ397615	IM0162M07	773	5	26.3	19	11	CM541244	CM541244	HPYCH41V-
701	5	26.3	19	11	AZ414372	AZ414372	IM0188G18	774	5	26.3	19	13	CM283815	CM283815	CP31h12.f
702	5	26.3	19	11	AZ422762	AZ422762	IM0201P12	775	5	26.3	19	13	CL6770097	CL6770097	PR10161a
703	5	26.3	19	11	AZ426675	AZ426675	IM0206N21	776	5	26.3	19	13	CL6771134	CL6771134	PR10163d
704	5	26.3	19	11	AZ442378	AZ442378	IM0236K18	777	5	26.3	19	13	CL671780	CL671780	PR10165C
705	5	26.3	19	11	AZ442391	AZ442391	IM0236P13	778	5	26.3	19	13	CL687732	CL687732	PR10147C
706	5	26.3	19	11	AZ445457	AZ445457	IM0241J13	779	5	26.3	19	14	AJ587169	AJ587169	Arb1d0p8
707	5	26.3	19	11	AZ447752	AZ447752	IM0244M24	780	5	26.3	19	14	AJ588791	AJ588791	Arb1d0p8
708	5	26.3	19	11	AZ465132	AZ465132	IM0274D24	781	5	26.3	19	14	AJ590235	AJ590235	Arb1d0p8
709	5	26.3	19	11	AZ477353	AZ477353	IM0296K16	782	5	26.3	19	14	AJ594370	AJ594370	Arb1d0p8
710	5	26.3	19	11	AZ477353	AZ477353	IM0296K16	783	5	26.3	19	14	AJ595406	AJ595406	Arb1d0p8
711	5	26.3	19	11	AZ478491	AZ478491	IM0298P03	784	5	26.3	19	14	AJ598857	AJ598857	Arb1d0p8
712	5	26.3	19	11	AZ480113	AZ480113	IM0301F20	785	5	26.3	19	14	ATH525591	ATH525591	Arb1d0p8
713	5	26.3	19	11	AZ480342	AZ480342	IM0301J16	786	5	26.3	19	14	ATH529281	ATH529281	Arb1d0p8
714	5	26.3	19	11	AZ480982	AZ480982	IM0302114	787	5	26.3	19	14	ATH529363	ATH529363	Arb1d0p8
715	5	26.3	19	11	AZ481449	AZ481449	IM0303N07	788	5	26.3	19	14	TA30B01Q	TA30B01Q	Arb1d0p8
716	5	26.3	19	11	AZ484303	AZ484303	IM0310K12	789	4.8	25.3	19	1	AA884867	AA884867	am21b1.s
717	5	26.3	19	11	AZ490612	AZ490612	IM0323L11	790	4.8	25.3	19	1	AA928040	AA928040	o158g09.s
718	5	26.3	19	11	AZ493714	AZ493714	IM0328T04	791	4.8	25.3	19	1	AI027323	AI027323	ow46a07.s
719	5	26.3	19	11	AZ494890	AZ494890	IM0330N19	792	4.8	25.3	19	1	AI049374	AI049374	ub33a03.x
720	5	26.3	19	11	AZ498063	AZ498063	IM0335J08	793	4.8	25.3	19	1	AI1360784	AI1360784	qx89g07.x
721	5	26.3	19	11	AZ579189	AZ579189	IM0363112	794	4.8	25.3	19	1	AI538541	AI538541	td08a11.x
722	5	26.3	19	11	AZ585367	AZ585367	IM0390D06	795	4.8	25.3	19	1	AI538541	AI538541	td08a11.x
723	5	26.3	19	11	AZ585643	AZ585643	IM0391L12	796	4.8	25.3	19	1	AI584018	AI584018	ts12e10.x
724	5	26.3	19	11	AZ586752	AZ586752	IM0392M24	797	4.8	25.3	19	1	AI804310	AI804310	tc68y08.x
725	5	26.3	19	11	AZ595885	AZ595885	IM0408L15	798	4.8	25.3	19	1	AJ647163	AJ647163	AJ647163
726	5	26.3	19	11	AZ597767	AZ597767	IM0411C22	799	4.8	25.3	19	1	AJ649246	AJ649246	AJ649246
727	5	26.3	19	11	AZ613058	AZ613058	IM0441C18	800	4.8	25.3	19	1	AJ650841	AJ650841	AJ650841
728	5	26.3	19	11	AZ621656	AZ621656	IM0455C01	801	4.8	25.3	19	1	AJ657561	AJ657561	AJ657561
729	5	26.3	19	11	AZ623493	AZ623493	IM0461M13	802	4.8	25.3	19	1	AJ657936	AJ657936	AJ657936
730	5	26.3	19	11	AZ626685	AZ626685	IM0467M01	803	4.8	25.3	19	1	AJ660078	AJ660078	AJ660078
731	5	26.3	19	11	AZ630503	AZ630503	IM0484O20	804	4.8	25.3	19	1	AJ663592	AJ663592	AJ663592
732	5	26.3	19	11	AZ639833	AZ639833	IM0501H05	805	4.8	25.3	19	1	AJ747293	AJ747293	AJ747293
733	5	26.3	19	11	AZ643124	AZ643124	IM0506P02	806	4.8	25.3	19	1	AM075423	AM075423	AM075423
734	5	26.3	19	11	AZ654214	AZ654214	IM0528H13	807	4.8	25.3	19	1	AM075491	AM075491	AM075491
735	5	26.3	19	11	AZ656517	AZ656517	IM0532P04	808	4.8	25.3	19	1	AM075504	AM075504	AM075504
736	5	26.3	19	11	AZ658282	AZ658282	IM0535C02	809	4.8	25.3	19	1	AU013837	AU013837	AU013837
737	5	26.3	19	11	AZ659191	AZ659191	IM0536J19	810	4.8	25.3	19	2	BM395626	BM395626	BM395626
738	5	26.3	19	11	AZ661787	AZ661787	IM0540I06	811	4.8	25.3	19	2	BM395679	BM395679	BM395679
739	5	26.3	19	11	AZ759944	AZ759944	IM0553O10	812	4.8	25.3	19	2	BM395733	BM395733	BM395733
740	5	26.3	19	11	AZ772136	AZ772136	IM0574K14	813	4.8	25.3	19	2	BM395769	BM395769	BM395769
741	5	26.3	19	11	AZ772446	AZ772446	IM0583O16	814	4.8	25.3	19	2	BM395792	BM395792	BM395792
742	5	26.3	19	11	AZ774477	AZ774477	2M0004A03	815	4.8	25.3	19	2	BM395830	BM395830	BM395830
743	5	26.3	19	11	AZ782743	AZ782743	2M0023D08	816	4.8	25.3	19	2	BM396147	BM396147	BM396147
744	5	26.3	19	11	AZ787654	AZ787654	2M0034B16	817	4.8	25.3	19	2	BM396288	BM396288	BM396288
745	5	26.3	19	11	AZ789771	AZ789771	2M0037D24	818	4.8	25.3	19	2	BM396403	BM396403	BM396403
746	5	26.3	19	11	AZ789827	AZ789827	2M0038C02	819	4.8	25.3	19	2	BM396507	BM396507	BM396507
747	5	26.3	19	11	AZ794653	AZ794653	2M0048G05	820	4.8	25.3	19	2	BM396664	BM396664	BM396664
748	5	26.3	19	11	AZ799057	AZ799057	2M0056B20	821	4.8	25.3	19	2	BM397535	BM397535	BM397535
749	5	26.3	19	11	AZ803930	AZ803930	2M0064N01	822	4.8	25.3	19	2	BM397535	BM397535	BM397535



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866	4.8	25.3	19	5	CF306449	CF306449 HDAL--03-	939	4.8	25.3	19	11	AZ6233110	AZ6233110 1M0460G39
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875	4.8	25.3	19	8	CN780477	CN780477 BL0109D_A0	948	4.8	25.3	19	11	AZ663184	AZ663184 1M0542L07
876	4.8	25.3	19	8	CN780622	CN780622 BL010A_F0	949	4.8	25.3	19	11	AZ665774	AZ665774 1M0543J01
877	4.8	25.3	19	8	CN783138	CN783138 BL017A_G0	950	4.8	25.3	19	11	AZ665774	AZ665774 1M0543J01
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881	4.8	25.3	19	9	D17097	D17097 D17097 K18e	954	4.8	25.3	19	11	AZ675965	AZ675965 1M0544C22
882	4.8	25.3	19	9	DN986391	DN986391 MSU 2R-2-	955	4.8	25.3	19	11	AZ6776733	AZ6776733 1M0544C22
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884	4.8	25.3	19	11	AZ308423	AZ308423 1M0011E21	957	4.8	25.3	19	11	AZ6776733	AZ6776733 1M0544C22
885	4.8	25.3	19	11	AZ309043	AZ309043 1M0012C08	958	4.8	25.3	19	11	AZ678208	AZ678208 1M0544C22
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888	4.8	25.3	19	11	AZ317339	AZ317339 1M0038G08	961	4.8	25.3	19	11	AZ6794641	AZ6794641 1M0544C22
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890	4.8	25.3	19	11	AZ329936	AZ329936 1M0054L10	963	4.8	25.3	19	11	AZ680646	AZ680646 1M0544C22
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## ALIGNMENTS

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RESULT 1
LOCUS CL671134/c 19 bp DNA linear GSS 09-JUL-2004
DEFINITION fosmid library of P. pacificus var. California Pristionchus
ACCESSION CL671134
VERSION CL671134
KEYWORDS GI:50169817
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
REFERENCE Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AUTHORS 1 (bases 1 to 19)
TITLE Neodiplogasteridae; Pristionchus.
JOURNAL ApplDB: an AcedB database for the nematode satelite organism
PUBMED 14681447
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Classes: fosmid ends.
Location/Qualifiers
1. 19
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/strain="California"
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## ORIGIN

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Query Match 56.8%; Score 10.8; DB 13; Length 19;
Best Local Similarity 85.7%; Pred. No. 8.4e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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## QY

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3 CACGGTATCTCCTT 16
19 CACGGTATCTCCTT 6

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## Db

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19 CACGGTATCTCCTT 6

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## RESULT 2

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LOCUS AZ481008 19 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0302N15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ481008
VERSION AZ481008
KEYWORDS GI:10641989
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
AUTHORS Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
TITLE Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
JOURNAL Niederhausern,A. and Wright,D., Weiss,R.
COMMENT Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0302 row: N column: 15
Seq primer: CACACGGAACACGCTATGACC
Classes: Plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[g14732114]AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and

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purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 51.6%; Score 9.8; DB 11; Length 19;  
 Best Local Similarity 84.6%; Pred. No. 2.9e+06;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 2 ACGGATTCCTT 14

Db 2 ACGGATTCCTT 14

RESULT 3 19 bp DNA linear GSS 29-SEP-2000  
 AZ309116  
 LOCUS 1M0012E23R Mouse 10kb plasmid UGCGIM library Mus musculus genomic

DEFINITION clone UGCGIM0012E23 R, genomic survey sequence.  
 AZ309116  
 ACCESSION AZ309116.1 GI:10349784

VERSION GSS.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)

JOURNAL COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center

Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0012 row: B column: 23

Seg primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

## SOURCE

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 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"  
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 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCGIM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated

Query Match 45.3%; Score 8.6; DB 11; Length 19;  
 Best Local Similarity 73.3%; Pred. No. 1.3e+07;  
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 CACGATTCCTTC 17  
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 4 CACCAATCTACTTC 18

Db 4 CACCAATCTACTTC 18

RESULT 4 19 bp mRNA linear EST 15-AUG-2003  
 CF317235  
 LOCUS HP-06-N19.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
 HP-06-N19, mRNA sequence.  
 CF317235  
 ACCESSION CF317235.1 GI:33688996

VERSION EST.  
 KEYWORDS Oryza sativa (japonica cultivar-group)  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
 clade; Eriarthroideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

JOURNAL COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 location/Qualifiers

## FEATURES

## SOURCE

1..19  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="HD-06-N19"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="OSHDA1-overexpressing transgenic rice plasmid  
 cDNA library (HD)"  
 /note="Vector: PCR4-TOP0; Site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice Histone Deacetylase overexpression  
 line."

## ORIGIN

Query Match 44.2%; Score 8.4; DB 5; Length 19;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+07;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 8 TATCTCCTTC 17  
 |||||  
 10 TATCTCCTAC 19

Db 10 TATCTCCTAC 19

RESULT 5 19 bp mRNA linear EST 12-NOV-2003  
 CF929669  
 LOCUS CP929669

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DEFINITION      CF-01-R-E08 Bos taurus CF-24-HW cDNA library Bos taurus cDNA clone
ACCESSION       CF-01-R-E08 (5'), mRNA sequence.
VERSION         CF929669
KEYWORDS        EST
SOURCE          Bos taurus (cattle)
ORGANISM        Bos taurus
                Bos taurus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                Pecora; Bovidae; Bovinae; Bos.
REFERENCE       1 (bases 1 to 19)
AUTHORS         Yoon,D.H., Lee,S.H., Lee,J.H., Sang,B.C. and Oh,S.U.
TITLE           Gene Expression Profiling of the Bovine adipose tissues
JOURNAL         Unpublished (2003)
COMMENT         Contact: Dr. Du-Hak Yoon
                National Livestock Research Institute, RDA
                564 Omoekchun-dong, Suwon, 441-350, Korea
                Tel: 82 31 290 1593
                Fax: 82 31 290 1792
                Email: dhyoon@rda.go.kr
                Insert Length: 19 Std Error: 0.00
                Seq primer: ATTAACCTCCTCAAG
                POLYA=No.

FEATURES
  source
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      /organism="Bos taurus"
      /mol_type="mRNA"
      /db_xref="taxon:9913"
      /clone="CF-01-R-E08(5')"
      /sex="Four males mixed"
      /tissue_type="adipose tissue"
      /cell_type="adipocyte"
      /dev_stage="24 months old"
      /lab_host="XLI-BlueMRF'strain"
      /clone_1lb="Bos taurus CF-24-HW cDNA library"
      /note="Vector: Uni-ZAPXR; Site_1: EcoRI; Site_2: Xho I"

ORIGIN
Query Match      43.2%; Score 8.2; DB 5; Length 19;
Best Local Similarity 76.9%; Pred. No. 2.1e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY               7 GATCTCCTTCAC 19
                  |||||
                  7 GGATCGCATCAC 19

Db
7 GATCTCCTTCAC 19

RESULT 6
A0840508
LOCUS       A0840508                19 bp      DNA      linear      GSS 08-FEB-2006
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
594F08      genomic survey sequence.
ACCESSION   A0840508
VERSION     A0840508.1 GI:52544714
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
AUTHORS     Brnaut,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepoint,L., Caboche,M. and Lecharny,A.
TITLE       T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL     EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED     12446565
REFERENCE   2 (bases 1 to 19)
AUTHORS     Balzerque,S.
TITLE       Direct Submision
            Submitted (21-SEP-2004) Balzerque S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremlieux, 91057 Evry cedex, FRANCE

```

```

COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'genoplante' (http://www.genoplante.com and
http://genoplante-info.intobio.gen.fr).

FEATURES
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      /organism="Arabidopsis thaliana"
      /mol_type="genomic DNA"
      /cultivar="Wassiliewskija"
      /db_xref="taxon:3702"
      /clone="594F08"
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      /ecotype="Wassiliewskija"
      /note="T-DNA flanking sequence
      left border"

ORIGIN
Query Match      43.2%; Score 8.2; DB 14; Length 19;
Best Local Similarity 76.9%; Pred. No. 2.1e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY               7 GATCTCCTTCAC 19
                  |||||
                  4 GAATCTCCTGAAC 16

Db
4 GAATCTCCTGAAC 16

RESULT 7
CD532073
LOCUS       CD532073                19 bp      mRNA      linear      EST 31-DEC-2003
DEFINITION  13104 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA
3', mRNA sequence.
ACCESSION   CD532073
VERSION     CD532073.1 GI:40452085
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana
            Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Guo,Y., Cai,Z. and Gan,S.
TITLE       Transcriptome of Arabidopsis leaf senescence
            Plant Cell Environ. 27 (5), 521-549 (2004)
JOURNAL     Contact: Susheng Gan
            Department of Horticulture
            Cornell University
            119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
            Tel: 607 254 5418
            Fax: 607 255 0599
            Email: sg288@cornell.edu
            Insert Length: 19 Std Error: 0.00
            Seq primer: 77
            POLYA=No.

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      /mol_type="mRNA"
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      /tissue_type="leaf"
      /dev_stage="Yellow Leaf With Greenish Base Area"
      /lab_host="E. coli"
      /clone_1lb="Arabidopsis leaf Senescence Library"
      /note="Organ: Rosette leaf; Vector: pBluescript SKII+;
            Site_1: EcoRI; Site_2: EcoRI; Senescent rosette leaves #5

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and #6 (counted from the bottom) were harvested and immediately frozen in liquid N<sub>2</sub>. The leaves were visibly yellow excepted for the leaf base areas that were still greenish."

## ORIGIN

Query Match 42.1%; Score 8; DB 5; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CTCCTTCA 19  
Db 11 CTCCTTCA 18

## RESULT 8

CF280788/c 19 bp mRNA linear EST 14-AUG-2003  
LOCUS 14ETL--07-J13.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-J13,  
mRNA sequence.  
CF280788  
ACCESSION CF280788.1 GI:33658174  
VERSION EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
KEYWORDS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
clade; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 321 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

REFERENCE 1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 321 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

source 1. .19  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="14ETL--07-J13"  
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/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_id="Rice etiolated leaf plasmid cDNA library  
(14ETL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

## ORIGIN

Query Match 42.1%; Score 8; DB 5; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CTCCTTCA 18  
Db 8 CTCCTTCA 1

## RESULT 9

CF299371 19 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--03-F22.g1 Rice leaf plasmid cDNA library II (7LEAF)  
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-F22, mRNA  
sequence.  
CF299371

ACCESSION CF299371  
VERSION CF299371.1 GI:33671132  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
clade; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 321 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

REFERENCE 1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 321 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

REFERENCE 1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 321 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

source 1. .19  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
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/lab\_host="E.coli DH10B"  
/clone\_id="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

## ORIGIN

Query Match 42.1%; Score 8; DB 5; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CTCCTTCA 18  
Db 18 CTCCTTCA 11

RESULT 10  
CF305417/c 19 bp mRNA linear EST 15-AUG-2003  
LOCUS CUD1--01-K13.b1 Rice cold treated leaf plasmid cDNA library (CUD1)  
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone CUD1--01-K13,  
mRNA sequence.  
CF305417  
ACCESSION CF305417.1 GI:33677178  
VERSION EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
clade; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 321 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

source 1. .19  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_id="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

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/organism="Oryza sativa (japonica cultivar-group)"
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/clone_lib="rice cold treated leaf plasmid cDNA library (C1D1)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

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## ORIGIN

```

Query Match      42.1%; Score 8; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+07;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      11 CTCCTTCA 18
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        12 CTCCTTCA 5

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RESULT 11
CF315940/c      19 bp      mRNA      linear      EST 15-AUG-2003
LOCUS
DEFINITION
HD--05-K18.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-K18, mRNA sequence.
CF315940
CF315940.1 GI:33687701
EST.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

```

```

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BAP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 19)

```

```

REFERENCE
AUTHORS

```

```

TITLE
JOURNAL
COMMENT

```

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

```

```

FEATURES
source
Location/Qualifiers
1..19

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

## ORIGIN

```

Query Match      42.1%; Score 8; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+07;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      11 CTCCTTCA 18
        |||||
        18 CTCCTTCA 11

```

```

RESULT 12
CF337272/c      19 bp      mRNA      linear      EST 18-AUG-2003
LOCUS
DEFINITION
JMT--07-K10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--07-K10, mRNA sequence.
CF337272
CF337272.1 GI:33822933
EST.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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```

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BAP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 19)

```

```

REFERENCE
AUTHORS

```

```

TITLE
JOURNAL
COMMENT

```

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

```

```

FEATURES
source
Location/Qualifiers
1..19

```

```

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-K10"
/tissue_type="leaf"
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/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
derived from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

```

## ORIGIN

```

Query Match      42.1%; Score 8; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+07;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      11 CTCCTTCA 18
        |||||
        11 CTCCTTCA 4

```

```

RESULT 13
AZ506614/c      19 bp      DNA      linear      GSS 05-OCT-2000
LOCUS
DEFINITION
IM0347A24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0347A24 R, genomic survey sequence.
AZ506614
AZ506614.1 GI:10687930
GSS.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

```

```

Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,

```

TITLE  
JOURNAL  
COMMENT

Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,  
Rally, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Nederhausen, A. and Wright, D., Weiser, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiser  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0347 row: A column: 24  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

SOURCE

Location/Qualifiers

1. 19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
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/clone="UGC1M0347A24"  
/sex="Male"  
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/clone\_lib="Mouse 10kb plasmid UGCM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 42.1%; Score 8; DB 11; Length 19;  
Best Local Similarity 68.8%; Pred. No. 2.7e+07;  
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CACGATATCTCTTCA 18  
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Db 18 CACTGTCTCCATTTA 3

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LOCUS  
DEFINITION 2M0281H19 Mouse 10kb plasmid UGCM2M library mus musculus genomic  
clone UGCM2M0281H19 R, genomic survey sequence.  
ACCESSION A2995903  
VERSION A2995903.1 GI:13867130  
KEYWORDS GSS.  
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ORGANISM Mus musculus  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 19)

AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,  
Rally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Nederhausen, A. and Wright, D., Weiser, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiser  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0281 row: H column: 19  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

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Location/Qualifiers

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/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
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electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
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adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ATCTCCTT 16  
|||||  
Db 5 ATCTCCTT 12

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DEFINITION PRI012a.B12 - PRI012a.B21 (19) Note: Recurring String Mixed stage  
fosmid library of P. pacificus var. California Pristionchus  
pacificus genomic, genomic survey sequence.  
ACCESSION CL657608  
VERSION CL657608.1 GI:50139393  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.

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REFERENCE 1 (bases 1 to 19)
AUTHORS Srinivasan,J., Otto,G.W., Kahlw,U., Geisler,R. and Sommer,R.J.
TITLE AppABD: an AceDB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends
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Db 7 TCTCCTTC 14
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AJ587912
ACCESSION AJ587912.1 GI:37937536
VERSION GSS; left border; T-DNA flanking sequence.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Brnaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelletier,G.,
Lepointec,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
12446565
2 (bases 1 to 19)
Balzerque,S.
Direct Submision
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and

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http://genoplante-info.infobiogen.fr.
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Best Local Similarity 100.0%; Pred. No. 2.7e+07;
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515R04, genomic survey sequence.
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ACCESSION AJ600880.1 GI:37950508
VERSION GSS; right border; T-DNA flanking sequence.
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SOURCE Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
COMMENT 1
Brnaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelletier,G.,
Lepointec,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
12446565
2 (bases 1 to 19)
Balzerque,S.
Direct Submision
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
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/clone="515R04"
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right border"
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Query Match 42.1%; Score 8; DB 14; Length 19;  
 Best Local Similarity 68.8%; Pred. No. 2.7e+07;  
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 Oy 3 CACGGTATCTCTCA 18  
 |||||  
 3 CACGGTATCTCTCA 18

RESULT 18  
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 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 41.1%; Score 7.8; DB 11; Length 19;  
 Best Local Similarity 81.8%; Pred. No. 3.5e+07;  
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 4 ACGGTATCTCC 14  
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 16 AAGTACTCC 6

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 LOCUS 1M0029N17F Mouse 10kb plasmid UGCM library Mus musculus genomic  
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 SOURCE Mus musculus (house mouse)  
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
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 (http://www.jax.org/resources/documents/dnares/). The DNA  
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 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
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 and selected for ampicillin resistance."

TITLE  
 JOURNAL  
 COMMENT

TITLE  
 JOURNAL  
 COMMENT

#### FEATURES

#### FEATURES

ORIGIN

ORIGIN

Query Match 41.1%; Score 7.8; DB 11; Length 19;  
 Best Local Similarity 81.8%; Pred. No. 3.5e+07;  
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 ACGGATCTCC 14  
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 19 ACAGATCTCC 9

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 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
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 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells

ORIGIN

Query Match 41.1%; Score 7.8; DB 11; Length 19;  
 Best Local Similarity 81.8%; Pred. No. 3.5e+07;  
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 GGTATCTCCTT 16  
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 16 GGTTCCTCATT 6

RESULT 21  
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 DEFINITION clone UGCGIM0361N11 R, genomic survey sequence.  
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 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
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 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 musculus C57BL/6J (male) was obtained from the Jackson  
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 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
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 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into

and selected for ampicillin resistance."

ORIGIN

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 41.1%; Score 7.8; DB 11; Length 19;  
 Best Local Similarity 81.8%; Pred. No. 3.5e+07;  
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 7 GATATCTCTTC 17  
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 3 GTTCTACTTC 13

RESULT 22  
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 DEFINITION IM0391L22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0391L22 F, genomic survey sequence.  
 AZ585898  
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 KEYWORDS  
 SOURCE GSS.  
 ORGANISM  
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 Mus musculus  
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 COMMENT Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0391 row: 1. column: 22  
 Seq primer: CGTTGTAAACGACGCCACT  
 Class: Plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

FEATURES  
 source  
 1. 19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0391L22"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (g14732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to

ORIGIN

adaptor mouse DNA, and transformed into  
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 41.1%; Score 7.8; DB 11; Length 19;  
 Best Local Similarity 81.8%; Pred. No. 3.5e+07;  
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 7 GATATCTCTTC 17  
 |||||  
 3 GCATCTACTTC 13

RESULT 23  
 AZ643528 19 bp DNA linear GSS 14-DEC-2000  
 LOCUS  
 DEFINITION IM0507H05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0507H05 F, genomic survey sequence.  
 AZ643528  
 VERSION  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 COMMENT Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0507 row: H column: 05  
 Seq primer: CGTTGTAAACGACGCCACT  
 Class: Plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

FEATURES  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0507H05"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (g14732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 41.1%; Score 7.8; DB 11; Length 19;  
Best Local Similarity 63.2%; Pred. No. 3.5e+07;  
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CGACGCTATCTCTTCAC 19  
Db 19 CCACGATCTCTTCTC 1

RESULT 24  
AJ587549 19 bp DNA linear GSS 15-JAN-2004  
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
DEFINITION 292A05, genomic survey sequence.

ACCESSION AJ587549  
VERSION AJ587549.1 GI:37937173  
KEYWORDS GSS: left border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE 1  
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M., and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)

REFERENCE 2 (bases 1 to 19)

AJ587549

REFERENCE Balzerque, S.

AUTHORS Direct Submmission

COMMENT Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.inbio.gen.fr>).

FEATURES Location/Qualifiers

1..19  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="292A05"  
/clone\_1lb="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Massiliensis"  
1..19  
/note="T-DNA flanking sequence left border"

## ORIGIN

Query Match 41.1%; Score 7.8; DB 14; Length 19;  
Best Local Similarity 81.8%; Pred. No. 3.5e+07;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 ATCTCTTCTC 19  
Db 4 ATCTCTTCTC 14

RESULT 25  
CF281537/c 19 bp mRNA linear EST 14-AUG-2003  
LOCUS Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--08-K01,  
DEFINITION mRNA sequence.

ACCESSION CF281537  
VERSION CF281537  
KEYWORDS EST

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BGP clade; Euphorbiaceae; Oryzae; Oryza.

1 (bases 1 to 19)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.T., Kim, U.K., Kim, Y.-K., and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

1..19  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="14ETL--08-K01"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1lb="Rice etiolated leaf plasmid cDNA library (14ETL)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

## ORIGIN

Query Match 40.0%; Score 7.6; DB 5; Length 19;  
Best Local Similarity 71.4%; Pred. No. 4.5e+07;  
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACGCTATCTTC 14  
Db 14 CGCTCGCTTCTGC 1

RESULT 26

DR026632/c 19 bp mRNA linear EST 26-MAY-2005

LOCUS Osmo01180 F. cylindrus osmotic stress library Fragilariopsis

DEFINITION cylindrus cDNA clone Fcyl180T42b03.61, mRNA sequence.

ACCESSION DR026632

VERSION DR026632.1 GI:66748995

KEYWORDS EST

SOURCE Fragilariopsis cylindrus

ORGANISM Fragilariopsis cylindrus

Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae; Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsis.

1 (bases 1 to 19)

Krell, A. and Gloeckner, G.

Analysis of an osmotic stress induced cDNA library of the psychrophilic diatom Fragilariopsis cylindrus

Unpublished (2004)

CONTACT: Krell, Andreas; Gloeckner, Gernot

Biological Oceanography, Sea Ice Research; Genome Analysis

Alfred-Wegener-Institute for Polar and Marine Research, Institute

for Molecular Biotechnology  
Am Handelshafen 12, D-27570 Bremerhaven, Germany; Beutenbergstr.  
11, D-07745 Jena, Germany  
Tel: +49 471 48311812; +49 3641 656440  
Fax: +49 471 48311425; +49 3641 656255  
Email: akrell@awi-bremerhaven.de; gernot@imb-jena.de  
PCR primers  
FORWARD: 5'M13  
BACKWARD: 3'M13  
Seq primer: 5'GTAAACGACGCCAG 3'

FEATURES  
source

Location/Qualifiers  
1. .19  
/organism="Fragilariopsis cylindrus"  
/mol\_type="rRNA"  
/db\_xref="taxon:186039"  
/clone="FCylBESTa42b03.81"  
/clone\_lib="F. cylindrus osmotic stress library"  
/note="Samples for total RNA isolation were taken  
continuous for 5 days after a salt shock treatment  
increasing salinity from 34 to 60 PSU. Total RNA  
extraction was performed with RNeasy (Ambion) and mRNA  
purification with polyA Purist (Ambion). Further steps  
were carried out as described in the Cloneminer Kit. CDNA  
size fractionation was carried out with CHROMA Spin-400  
columns and additionally on a gel."

## ORIGIN

Query Match 40.0%; Score 7.6; DB 9; Length 19;  
Best Local Similarity 71.4%; Pred. No. 4.5e+07;  
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ACAGTATCTCTTC 17  
| | | | | | | | | |  
Db 15 AGGTTCTTTTC 2

RESULT 27  
AZ314603 19 bp DNA linear GSS 29-SEP-2000  
LOCUS  
DEFINITION IM0031C06R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0031C06 R, genomic survey sequence.  
ACCESSION AZ314603  
VERSION AZ314603.1 GI:1036057  
KEYWORDS  
SOURCE GSS.  
ORGANISM Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0031 row: C column: 06  
Seq primer: CACGACGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
source

1. .19  
/organism="Mus musculus"

## ORIGIN

Query Match 40.0%; Score 7.6; DB 11; Length 19;  
Best Local Similarity 71.4%; Pred. No. 4.5e+07;  
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CACGATCTCTT 16  
| | | | | | | | | |  
Db 6 CAATGATCCCTT 19

RESULT 28  
AZ505490 19 bp DNA linear GSS 05-OCT-2000  
LOCUS  
DEFINITION IM0346N08F Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0346N08 F, genomic survey sequence.  
ACCESSION AZ505490  
VERSION AZ505490.1 GI:10686806  
KEYWORDS  
SOURCE GSS.  
ORGANISM Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0346 row: N column: 08  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
source

1. .19  
/organism="Mus musculus"

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0374C19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

## ORIGIN

```

Query Match      40.0%; Score 7.6; DB 11; Length 19;
Best Local Similarity 71.4%; Pred. No. 4.5e+07;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      3 CACGGTATCTCCTT 16
        ||| ||| ||| |||
Db      6 GACTCTCCCTCCTT 19

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## RESULT 29

AZS82154

LOCUS

1M0374C19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION

clone UUGC1M0374C19 F, genomic survey sequence.

ACCESSION

AZS82154

AZS82154.1 GI:11700755

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

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COMMENT

## source

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1.19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0374C19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

## ORIGIN

```

Query Match      40.0%; Score 7.6; DB 11; Length 19;
Best Local Similarity 71.4%; Pred. No. 4.5e+07;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      3 CACGGTATCTCCTT 16
        ||| ||| ||| |||
Db      5 CCGCTACTCTCGTT 18

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## RESULT 30

AZ827164

LOCUS

2M0103M22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION

clone UUGC2M0103M22 F, genomic survey sequence.

ACCESSION

AZ827164

AZ827164.1 GI:12997072

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

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COMMENT



Library: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: NYBG accession number #436/84"

## ORIGIN

Query Match 38.9%; Score 7.4; DB 9; Length 19;  
Best Local Similarity 88.9%; Pred. No. 5.7e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

9 ATCTCCTC 17  
|||||  
6 ATCTCTTC 14

## Db

RESULT 33  
AZ329293  
LOCUS 19 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0053A03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0053A03 R, genomic survey sequence.

ACCESSION AZ329293  
VERSION AZ329293.1 GI:10389864  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0053 row: A column: 03  
Seq primer: CACACGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

## source

1. 19  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0053A03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_11b="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and

## ORIGIN

Query Match 38.9%; Score 7.4; DB 11; Length 19;  
Best Local Similarity 88.9%; Pred. No. 5.7e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

10 TCTCCTTA 18  
|||||  
7 TCTCCATCA 15

## Db

RESULT 34  
AZ443948  
LOCUS 19 bp DNA linear GSS 04-OCT-2000  
DEFINITION 1M0238P04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0238P04 F, genomic survey sequence.

ACCESSION AZ443948  
VERSION AZ443948.1 GI:10592384  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0238 row: P column: 04  
Seq primer: CGTGTAAACGACGCCACGT  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

## source

1. 19  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0238P04"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_11b="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated



with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 38.9%; Score 7.4; DB 11; Length 19;  
Best Local Similarity 64.7%; Pred. No. 5.7e+07;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 CACGGTATCTCTTCAC 19  
1 CCCCTGTCTCTCTC 17

Db

## RESULT 35

AZ484016 19 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0339J10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0339J10 F, genomic survey sequence.

ACCESSION AZ484016  
VERSION AZ484016.1 GI:10648549

KEYWORDS

SOURCE

ORGANISM

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0310 row: J column: 10  
Seq primer: CGTTGTAACGACGCCACT  
Class: plasmid ends  
High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1. 19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0310J10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 38.9%; Score 7.4; DB 11; Length 19;  
Best Local Similarity 88.9%; Pred. No. 5.7e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TCTCCTCA 18  
10 TTCTCTCA 18

Db

## RESULT 36

AZ500675 19 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0339J10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0339J10 F, genomic survey sequence.

ACCESSION AZ500675  
VERSION AZ500675.1 GI:10680728

KEYWORDS

SOURCE

ORGANISM

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0339 row: J column: 10  
Seq primer: CGTTGTAACGACGCCACT  
Class: plasmid ends  
High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1. 19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0339J10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 38.9%; Score 7.4; DB 11; Length 19;  
Best Local Similarity 88.9%; Pred. No. 5.7e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 CTCCTTCAC 19  
16 CTCCTACAC 8

RESULT 37 19 bp DNA linear GSS 20-FEB-2001  
AZ834038 2M0116H01R Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
LOCUS clone UUGCIM0116H01 R, genomic survey sequence.  
DEFINITION  
ACCESSION AZ834038  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
GSS.  
Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D. Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

JOURNAL COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center

84112, USA  
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunne@genome.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Place: 0116 row: H column: 01

Seq primer: CACACAGGAACAGCTATGACC  
Class: Plasmid class  
High quality sequence stop: 19.

FEATURES  
Location/Qualifiers

1..19

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"

/db\_xref="taxon:10090"  
/clone="UUGCIM0116H01"

/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"

/note="Vector: pMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 38.9%; Score 7.4; DB 11; Length 19;  
Best Local Similarity 88.9%; Pred. No. 5.7e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 ATCTCTTC 17  
13 ATCTCTGC 5

RESULT 38 19 bp DNA linear GSS 15-JAN-2004  
AJ597721/c  
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
DEFINITION  
ACCESSION AJ597721  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AJ597721.1 GI:37947349  
GSS; left border; T-DNA flanking sequence.  
Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1  
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechold, N., Cruaud, C., Dekose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

2 (bases 1 to 19)  
Balzerque, S.

Direct Submission  
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from

the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at

http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'genoplante' (http://www.genoplante.com and

http://genoplante-info.infobiogen.fr).

## FEATURES

Location/Qualifiers

1..19

/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"

/clone="455F11"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Wassilewskij"

misc\_feature  
1..19 "T-DNA flanking sequence  
left border"

ORIGIN

Query Match 38.9%; Score 7.4; DB 14; Length 19;  
Best Local Similarity 88.9%; Pred. No. 5.7e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TATCTCCTT 16  
 |||||  
 Db 19 TAGCTCCTT 11

RESULT 39  
 LOCUS AM075504/c  
 DEFINITION AM075504 Chicken immune 5 - CSEQRBN30 Gallus gallus CDNA clone

AM075504 19 bp mRNA linear EST 14-SEP-2005  
 C0000798016\_T7, mRNA sequence.

AM075504  
 AM075504  
 AM075504.1 GI:75476089  
 EST.  
 Gallus gallus (chicken)  
 Gallus gallus  
 Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 19)  
 Smith, J., Speed, D., Hocking, P., Talbot, R.T., Degen, W., Schijne, V.,  
 Glass, B.J. and Burt, D.  
 Development of a chicken 5k array  
 Unpublished (2005)  
 Contact: Smith J  
 Genetics and Genomics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
 Vector pBluescript II KS(+) R. Site1: EcoRI R. Site2: NotI 5' Seq  
 Primer 17 Strain Lohman Brown layer/Rose 308 broiler cross This  
 normalized library was constructed from 1 million independent  
 clones. cDNA synthesis was initiated using an oligo(dT) primer,  
 using methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA was  
 blunt-ended, ligated to NotI adapters, digested with EcoRI,  
 size-selected, and cloned into the NotI and EcoRI compatible sites  
 of a custom modified MCS of the pBluescript (KS+) vector. The  
 library was normalized in 2 rounds using conditions adapted from  
 Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome  
 Research 6 (1996): 791, except that a significantly longer  
 reannealing hybridization was used. Clones available from the  
 ARK-Genomics Centre for Functional Genomics in Farm Animals, Roslin  
 Institute, Midlothian, EH25 9PS, UK see [www.ark-genomics.org](http://www.ark-genomics.org).

FEATURES  
 SOURCE  
 1..19  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /clone="C0000798016\_T7"  
 /issue\_type="thymus"  
 /clone\_lib="Chicken immune 5 - CSEQRBN30"

ORIGIN  
 Query Match 37.9%; Score 7.2; DB 1; Length 19;  
 Best Local Similarity 75.0%; Pred. No. 7.3e+07;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CACGCTATCTCC 14  
 |||||  
 Db 12 CGCGGAGACTCC 1

RESULT 40  
 LOCUS BX560116/c  
 DEFINITION BX560116 Glossina morsitans morsitans adult infected gut Glossina  
 morsitans morsitans cDNA clone Tse48a12\_glc, mRNA sequence.

AM075504  
 AM075504  
 AM075504.1 GI:33368195  
 EST.  
 Glossina morsitans morsitans  
 Glossina morsitans morsitans  
 Eukaryota; Metazoa; Archipoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 PUBMED  
 COMMENT

Hypoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 19)  
 Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 Adult midgut expressed sequence tags from the tsetse fly *Glossina*  
*morsitans morsitans* and expression analysis of putative immune  
 response genes  
 Genome Biol. 4 (10), R63 (2003)  
 14519198  
 Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix glc are reverse primer reads starting at 5'  
 end of the cDNA all pic reads are from  
 the 3' end.

FEATURES  
 SOURCE  
 1..19  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse48a12\_glc"  
 /issue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected  
 gut"  
 /note="country: Zimbabwe; EST from adult gut infected with  
 T. brucei"

ORIGIN  
 Query Match 37.9%; Score 7.2; DB 4; Length 19;  
 Best Local Similarity 75.0%; Pred. No. 7.3e+07;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCAAGTATCTC 13  
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 Db 17 GCAAGTATCTC 6

Search completed: August 10, 2006, 11:03:01  
 Job time : 1861.67 secs

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